

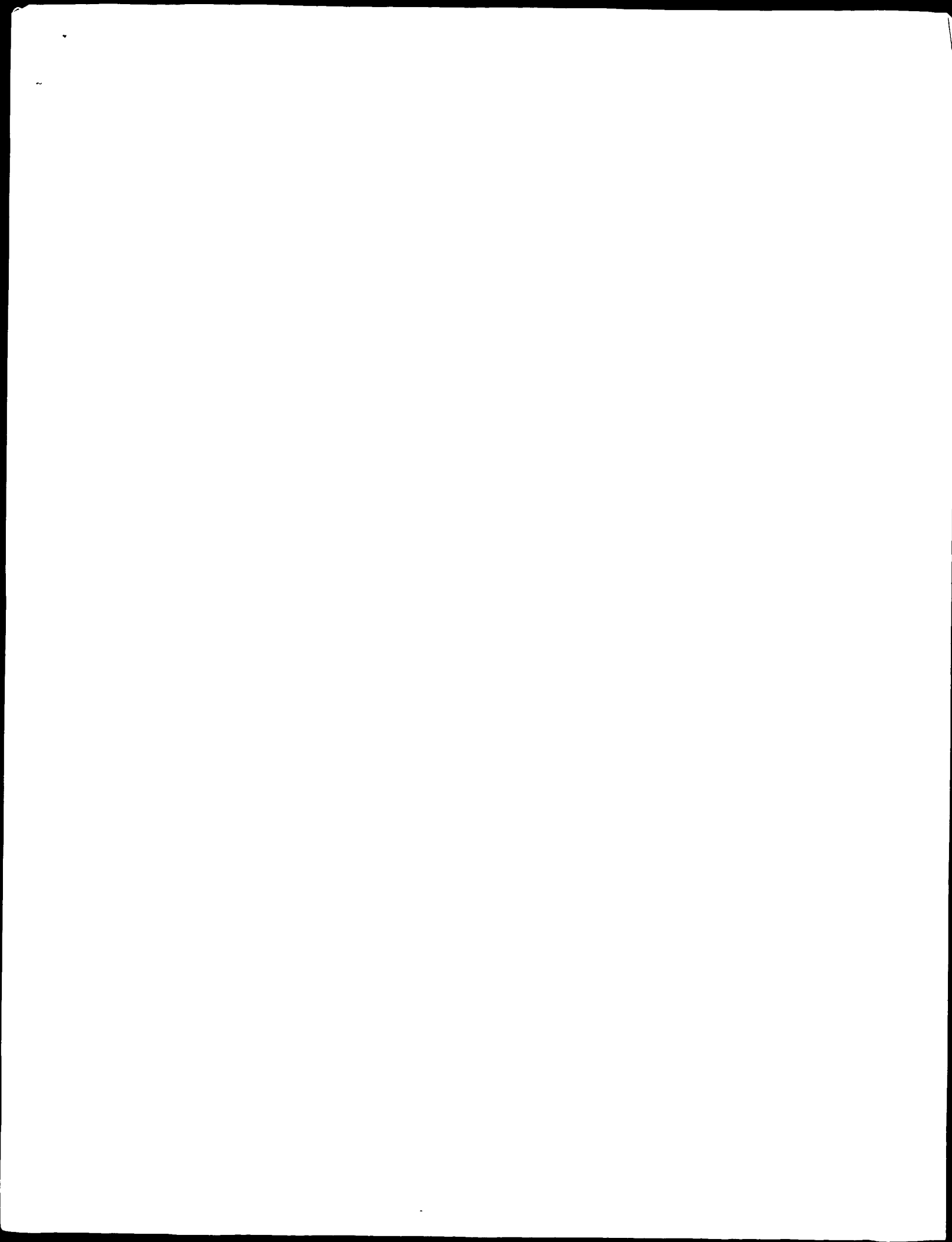
QY 9411 cctcttgaagctagaacaactatagttatcatcttcaatcttactgtgtacctt 9470
 Db 9060 cttcttgaagctagaacaactatagttatcatcttcaatcttactgtgtacctt 9119
 QY 9471 taaatagaatcttttactatcttctgttaacctaattgtgtagaatcttttaca 9530
 Db 9120 taaatagaatcttttactatcttctgttaacctaattgtgtagaatcttttaca 9179
 QY 9531 actctatactcaatcaagaacaaatctgtatatacttccctgtggaatgtactatgtagt 9590
 Db 9180 actctatactcaatcaagaacaaatctgtatatacttccctgtggaatgtactatgtagt 9239
 QY 9591 ttcagaatctcaaatcaagaacaaatctgtatatacttccctgtggaatgtactatgtagt 9650
 Db 9240 ttcagaatctcaaatcaagaacaaatctgtatatacttccctgtggaatgtactatgtagt 9299
 QY 9651 agaaactatacaactgtgaatatagaagaatacaagaagaataataaagccctctat 9710
 Db 9300 agaaactatacaactgtgaatatagaagaatacaagaagaataataaagccctctat 9359
 QY 9711 acataatgcccagcaactatcaatgtttaaatacaacaaactcaactctatcttatt 9770
 Db 9360 acataatgcccagcaactatcaatgtttaaatacaacaaactcaactctatcttatt 9419
 QY 9771 cttatctctgaagaagaactgtgtgtgtactatgaatgtgtgacatctatca 9830
 Db 9420 cttatctctgaagaagaactgtgtgtgtactatgaatgtgtgacatctatca 9479

LOCUS AF165281 9497 bp mRNA linear PRI-17-ADG-1999
 DEFINITION Homo sapiens ATP cassette binding transporter 1 (ABCI) mRNA,
 complete cds.
 ACCESSION AF165281
 VERSION AF165281.1 GI:5734100
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 9497)
 AUTHORS Rust,S., Rosier,M., Funke,H., Real,J., Amoura,Z., Piette,J.C.,
 Delauze,J.F., Brewer,H.B., Duvergier,N., Denelle,P. and Assmann,G.
 TITLES Tangier disease is caused by mutations in the gene encoding
 ATP-binding cassette transporter 1
 Nat. Genet. 22 (4), 352-355 (1999)
 JOURNAL MEDLINE 99364413
 PUBMED 10431238
 TITLE Direct Submission
 JOURNAL Submitted (01-JUL-1999) Genomics, Rhone-Poulenc Rorer, 2 rue Gaston
 Crémieux, Evry 91006, France
 FEATURES
 source
 1. 9497
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="9"
 /map="9q31"
 1. 9497
 /gene="ABCI"
 121.. 6726
 /gene="ABCI"
 /note="ABC transporter; ABC1 protein"
 /product="ATP cassette binding transporter 1"
 /protein_id="AAD49849.1"
 /db_xref="GI:5734101"
 /translation="MPSAGTLPMVGGITICANNPCRPYPPGAPGVGNFKSIVAR
 LFSDRRLILYSQKDIYSKMDKRYLRLTLOIKSSSNLKLQDLVYNETSGELYNTL

SLPKSTVDMKLRADVILRKVFLQGYOLHLTSLCNGSKSEEMIQLODQVSELCIPRE
 KLAARVLRSMNDILKPLTILNTSTSPSSKELEAKRTLLSLGTLAOLSEFNSRW
 SMROEVLFTVNNSSSSSTQYQAVSRVIRGPGGGGLKILSMYEDNNKALFSG
 NGEDEAEFVFNSTTPYCNQNDLKLKLESSPLRIIMKALKPLLYKTLITPTDPTAQ
 VNAEVAKTFOELAVPHLDGSMMEELSPKLTWPMKMSOEMDILVRLMDSDRDHPEEO
 LDLDLTADIVAFLEKHEDEVOSSNGSYTRREAPENNOAIRISRMPCVNIKTL
 EPLATEVWLINKSMELDLERKFWAGIVFGITGSELPHKVIIRMDIDVENTK
 IKDVPDGPBAPDEPMRIVWVGFAVLQDVEOAILRVLTGTERKGTVMQMPYPC
 YDDIDFLWMSRMLPMTLNIYSAVALIKIIVEKEKLEKEMIRIDGILNLSIMFS
 WFSILIFLWASGLIVLILKGLNLIPYSDPSVEFELSVFVAVTILLOCLSTLSFR
 ANLAACGCIITTYTLIPYLCAVMDPLPFLVYMWYIEANFPQGYPRWY
 GICVQNDNLFESEVEDENLITVSMMLPDLFLVYMWYIEANFPQGYPRWY
 PCRSYVMESEDESKHPSNOKRISLCEMEEPHLKLGVSIDNVYIRQKAVAV
 DGLALFVEGQILTFELHNGAGTMTSLITGLFPTSGTAYILKDLIRSEMTIRON
 LGVPOHNVFDMLTVEEHWFAFKLGSEKVKEMALMDVGLPSKLSKTSQ
 LSGCMKRLSVLALFVGGSKVYLIDPTGVDPSRGIWELLKLRQGRITLSTHH
 MDADVLGRILALISNGKLCQVSSILFALNOLGTGYLLVYKMDVSSLSGNSST
 VSTLKEDVSQSSDQSGDSHESPTLITDSALSNLIRKHSARIVYEDGHILTY
 VLPYEAKBEAFVLEHEIDRLSDIGISSYGLSETTLEIFLKAESGVDAETSDG
 TLPARNRRAFGDKQCLRPETDDADAPNDSDIDESSETDLSGMDKSYOVKGW
 KLHQOQFVALMKRLILARRSRKGFPAQIYLPVAFVICALVPSLIVPPKQPSLEQ
 PMVNEQTFVNDAPEDTGTLELNALEFDPGFRCEMGNIPDPPOQAGEEWT
 APYPTIMDLFQNGNMTMOPSPACQSSDKIKKMLPQCPGAGLPPROKONTADI
 LQDTGNISDITVKTYYQIILAKSLNKTIVNEFRYGGISYGNTOALPQOEVDA
 TKMKRHLKLKDSADRFINSJGRFTMTGLDITNNKVPFNNKGRHAISFLVATNNA
 ILRANLQKGNPSHYGTAFNHPILNFKOOLSSVAMPTSSVDLVISIVAFASVPA
 SFVFLIOEKNSAKHLOFISGVKPIVYILSNFVMDNCNVVATVLIIFLFOOKS
 VYSTENPVALALLLLYXGSIPLMTPASVFKIPSTAYVYLSVLMFLGINSVATF
 VLEFPMNKNLINDILKSVLEIPHEKCRGLIDVKNQAMDALEREENFVPL
 SMDLVGRNLFMAVEGVYFPLITVLIQYRFTIRPPVYNNKSLPINDENDEVERORI
 LDGGQNDLIEIKELITYRRKRPAWDRICVGIIPROECGLIGVAGKSSFFKMLT
 GDTVTTRGDAFLNNNSILSNIEHVHOMAGVPOFODATELTLREHVEFPALGVPE
 KEVQKVENALIRKILGKYEKTAGNNGGNKSLSTAMALIGPPVFLIDEPTGMD
 PKARFELMNAISVYKGRSVLTSHEMSECEKALCTSMALMVGREFCLASVOHLNR
 PGSGTIVIRIADGNSVPLKVPDFFGLAFPGSVKREHRLMLOYOLPSSLSLARIS
 ILSSKRLHIEDYVSQTLIDQYFVAFADQDDHDLKLSLHKQTYVDVAVLTSF
 LQDKVESTV"

BASE COUNT 2600 a 2115 c 2217 g 2364 t 1 others
 ORIGIN

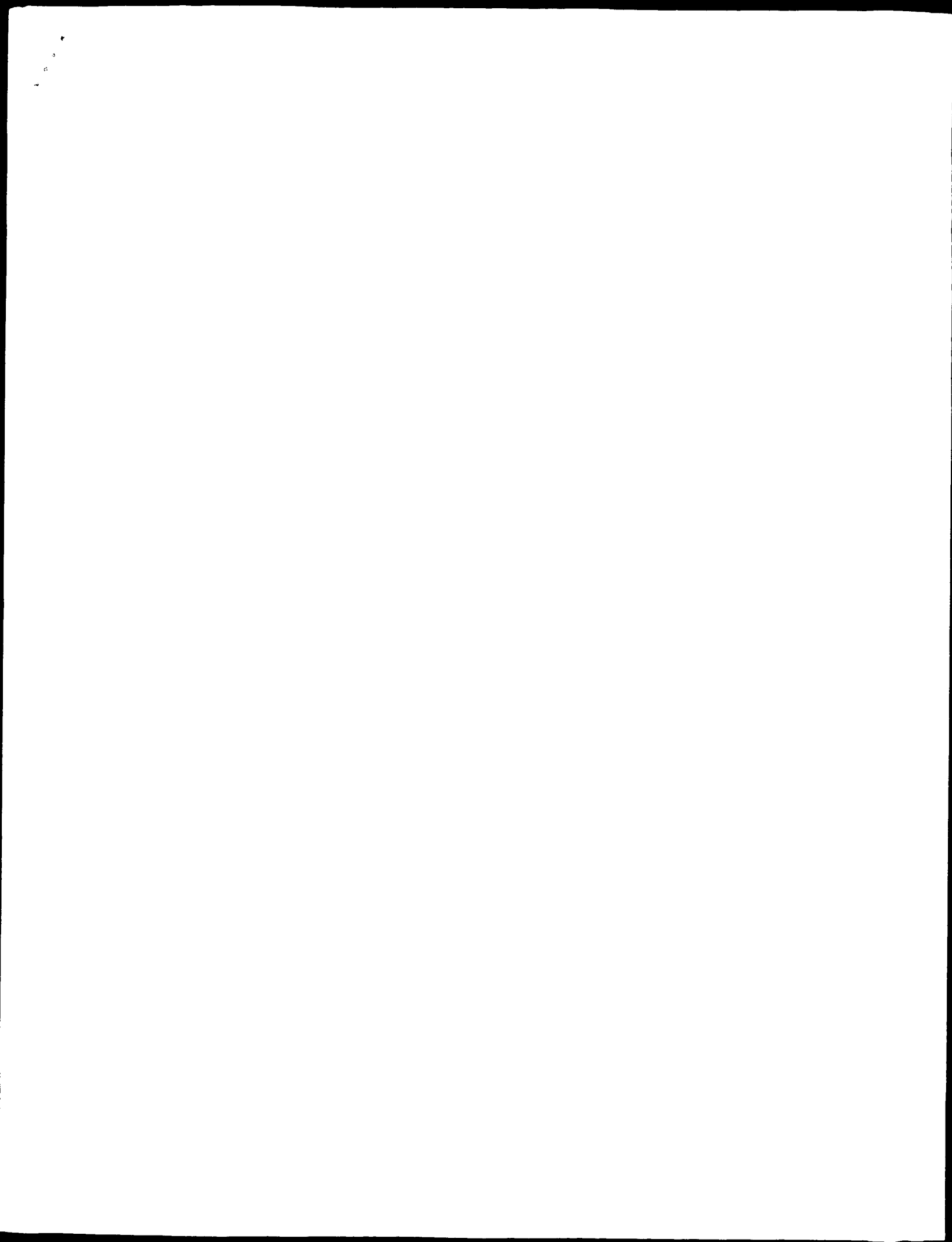
Query Match 90.4%; Score 9444.6; DB 9; Length 9497;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 9464; Conservative 0; Mismatches 15; Indels 1; Gaps 1;
 QY 351 caaatgtcagctgtactgaagtggcctctatattcttctgacatc 410
 Db 1 CAAACATGTCACCTGTACTGGAATGGCCTGCTATATTATCTGATCCTGATC 60
 QY 411 tctgttcgctgagctaccaccctatgaacaatgaatgcattccaaataaagc 470
 Db 61 TCTGTTCCGCTGAGCTACCCACCTATGAAACATGATGCATTTCCAAATAAACCC 120
 QY 471 atgcctctgcaggaacacttcttgcgttcaggggattatctgaatgcacaaccc 530
 Db 121 ATGCCCCCTGCGAGAACCTTCTTGCGGTTCAGGGGATTATCTGAAATCCCAACCC 180
 QY 531 tgttcgcttaccgactctctgaggagctcccgagatgttgtgaacttaacaatcc 590
 Db 181 TGTTCGCTTACCCGACCTCCTGCGGAGGCTCCCGAGTGTGAAACTTAAACAAATCC 240
 QY 591 attgtgctcgctgttctcaaatgtcggaggtcttttataagcagaagaagacac 650
 Db 241 ATTGTGCTCGCTGCTTTCACATGCTCGAGGCTCTTTTAAACGACGAAGAACACC 300
 QY 651 agcatgaaggaatgcgaagatctcgaagacattacacagacatcaagaatccagctca 710
 Db 301 AGCATGAAGGACATGCGCAAAAGTCTGAGACATTAACGACATCAAGAAATCCAGCTCA 360
 QY 711 aacttgaagcttaagattctctgtgtgaacaatgaaccttctgtgttctatatac 770
 Db 361 AACTTGAAGCTTCAAGATTCTCGGTGAGCAATGAACCTTCTCGGTTCTCTGATACAC 420



QY 771 aacctctctcccaagctactgtgacaaagatgctgagggctgatactctccac 830
Db 421 AACCTGCTCTCCCAAGAGTCTACTGTGACAAAGATGCTAGGGCTGATTCATCTCCAC 480
QY 831 aaggtatttttgaagagctaccaggttaactttgacaagctgctgcaatgataaata 890
Db 481 AAGGTATTTTGAAGAGCTACAGTTACATTTTACAAAGTCTGTCATAATGATCAATAA 540
QY 891 gaagagatgataactgtgtgacaaagattcttgagctttgtgcttaccaaagag 950
Db 541 GAAGAGATGATTAAGTGTGACAAAGATTCTGAGCTTGTGGCTTACCAAGAGG 600
QY 951 aaactgtctcagaagagagagtaactctgttccaacatgacactcgaagcaatccg 1010
Db 601 AAAGTGTCTCAGAGAGGAGGAGTCTGTTCCAACTGAGCAATCTGAGGCCAATCCTG 660
QY 1011 agaacataactatacatctccctcccgagcaagagagctgagctgagccacaanaa 1070
Db 661 AGAACATAAATCTACTATCTCTCTCCGAGCAAGAGAGCTGGCCGAGCAACAAAACA 720
QY 1071 ttgctgatagtcttggagacttggccagagagctgttcagcatgagaagctgagtgac 1130
Db 721 TTGCTGATAGTCTTGGAGACTGTGCCAGAGAGCTGTTCAAGCATGAGAAGCTGAGT 780
QY 1131 atgcaagagagagtgatgttcttgcacaaatgtgaacagctccagctctccacccaatc 1190
Db 781 ATGCGACAGAGAGGTGATGTTCTGACCAATGTGAACAGCTCCATCCATCCCAATC 840
QY 1191 taacagagtgctgtctgctgattgtctgcgagcatcccgagagagaggggctgaaatca 1250
Db 841 TACCAAGGTGTGTCTGATGTTCTGACCAATGTGAACAGCTCCATCCATCCCAATC 900
QY 1251 tctctcaactgtagtaggaacaaactaagaagccctcttggagagcaatgagcaatgag 1310
Db 901 TCTCTCAACTGGTATGAGAGACAACTACAAAGCCCTTGTGGAGGCAATGGCACTGAG 960
QY 1311 gaagatgtgaaactcttaagaaactctcaactctctactcaatgatttgaag 1370
Db 961 GAGATGTCTGAACCTCTTATGACAACTCTTACACTCTCTTACGAAATGATTGATGAAG 1020
QY 1371 aattggagctagctctctctcccgcaatctatctgaaagctctgaaagcgtctgct 1430
Db 1021 AATTGGAGTCTAGTCTCTTCCGCAATATCTGAAAGCTCTGAAAGCCGCTGCTGCT 1080
QY 1431 gggagaatccgtatatacactgacactccagccacaagagcagtgatgctgagtgaa 1490
Db 1081 GGGAAATCTCTGTATACACTGTGACCAAGGCAAGGAGGCTGAGTGAAGTGAAG 1140
QY 1491 aagaacttccagaaatgctgtgtctcaatctgaaagcagtgaggagaaactcagc 1550
Db 1141 AAGACTCTCCAGAACTGCTGTGTCTGATGATCTGAAAGGCTGTGGAGAGCACTCAGC 1200
QY 1551 cccaagatctgagactctcatgagaaacagccaaagaaatggaactgtccgagatgctgtg 1610
Db 1201 CCCAAGATCTGAGACTCTCATGAGAAAGCAAGAAATGAGACTGTCCGGATGCTGTG 1260
QY 1611 gacagcagggacaatgacaactcttgggaacagcagtgatgagcttgaatggaagcc 1670
Db 1261 GACAGCAGGGACAATGACACTTTTGGGAACAGCAGTGTGATGCTTGAATGGAAGCC 1320
QY 1671 caagacatgctgctgttttggccaaagcaccagagagatctccagctcaatlaatgttct 1730
Db 1321 CAAGACATCTGGGCTTGTGGCCAAACCCAGAGAGATCTCCAGTCCATTAATGCTTC 1380
QY 1731 gctgacacccggagagagagcttccaagagactaaccaggaatccggaccataatctgc 1790
Db 1381 GCTGACACCTGGAGAGAGAGCTTCAACGAGACTTAACAGGCAATCCCGACCATATCTCC 1440
QY 1791 ttcatgagagtgatcaactcgaacagactgaacccaatgaagaagaagctgagctatc 1850
Db 1441 TTCAATGAGAGTGTCAACCTGGAACAGCTTAAGCAACCATAGCAAGAGAGTGTGCTATC 1500
QY 1910 aacaagctcatgagagctgctgagtgagagagagcttctgagctgtatgttactgaga 1910

Db 1501 AACAGTCCATGAGAGCTGCTGATGAGAGAAATTCGGGCTGTGTTGTTCACTGGA 1560
QY 1911 attactcagcagcatttggagctgtcccatcatgataagaatccgaatgacatt 1970
Db 1561 ATTACTCAGCAGCAGATGAGCTCCCATCATCTCATAGTCAAGTCAAGTCAAGTCAAGT 1620
QY 1971 gacaatgtgagagagacaataaataaagatgagtgactggaacccgtgctgagct 2030
Db 1621 GACATGTGAGAGAGACAAATAAATCAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1680
QY 2031 gaeccttggagaaatgagtgatgctgagggagagcttgcacactggaagatgagtg 2090
Db 1681 GACCCCTTGAAGAGATCGGTGAGCTGTGGGGGCTTCCGCTTCTGAGAGATGTG 1740
QY 2091 gaggcagcaatcatcaaggtgtctgacggcaccgagaaagaaatggtgtctatagcaa 2150
Db 1741 GAGCAGGCAATCATAGAGTGTGAGGAGCAGGAGAAAGAAATGAGTGTATATGCA 1800
QY 2151 cagatgacctatccctgttaagttagatgacatcttctgaggggtgagtgagcgttcaatg 2210
Db 1801 CAGATCCCTATCCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
QY 2211 ccccttcatgagcgtgtgctgagttatcagtgagctgagatcatcaagagcagtg 2270
Db 1861 CCCCTTATGAGAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1920
QY 2271 tatgagaagagagcagagctgaaagacatgagcatatgagcctgagcaacagcata 2330
Db 1921 TATGAGAGAGAGCAGAGCTGAAAGAGACCATGCGATATGAGGCTGAGCAACAGCATC 1980
QY 2331 ctctgtttagctgtgtatcatgagctcatctctctctgtgagagctgagctgagta 2390
Db 1981 CTCGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
QY 2391 gctgcatcttgaagtttagaagaaactgagcctcctacagatgacccagctgtgtgtgc 2450
Db 2041 GTGCTCATCTGAGAGTGAAGAACTGCTGCTTACAGTATCCAGCGGAGTGTGTC 2100
QY 2451 ttctgtcgt 2510
Db 2101 TTCTGTGCGGTTGT 2160
QY 2511 tccagagcacaactgtgacagcagcctgtgagggagataatcaactcaagctgagcc 2570
Db 2161 TCCAGAGCACAACCTGAGAGAGAGCTGTGGGGGCTGATCTTCACTTCACTGCTGCTG 2220
QY 2571 taagtctgt 2630
Db 2221 TACGTCTGT 2280
QY 2631 ctgctgtctcgt 2690
Db 2281 CTGCTGTCTCTGT 2340
QY 2691 ggcattgagtgagtgaggaacactgtgtgagagctgtgagagagagagagagagag 2750
Db 2341 GGCATTGAGTGAGTGTGAGCAAACTGTGTGAGATCTGTGTGAGAGAGAGAGAGAGT 2400
QY 2751 cccacacttgatctcatatgagtggtgtgacactccctcctatgaggtgtgtgtgtgt 2810
Db 2401 CTCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
QY 2811 tacattgagctgtcttccagagccagtaagaaatcccaagccctgtgtatcttctgtc 2870
Db 2461 TACATTGAGAGCTGTCTTCCAGGAGGAGTACGGAATTCAGAGCCCTGTATTTCTTGC 2520
QY 2871 accaagctcatgagtggt 2930
Db 2521 ACCAAGTCTTACTGT 2580
QY 2931 aagagaatgagaaatctgcatgagagagagagagagagagagagagagagagagagag 2990

02
03
04
05
06
07
08
09
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

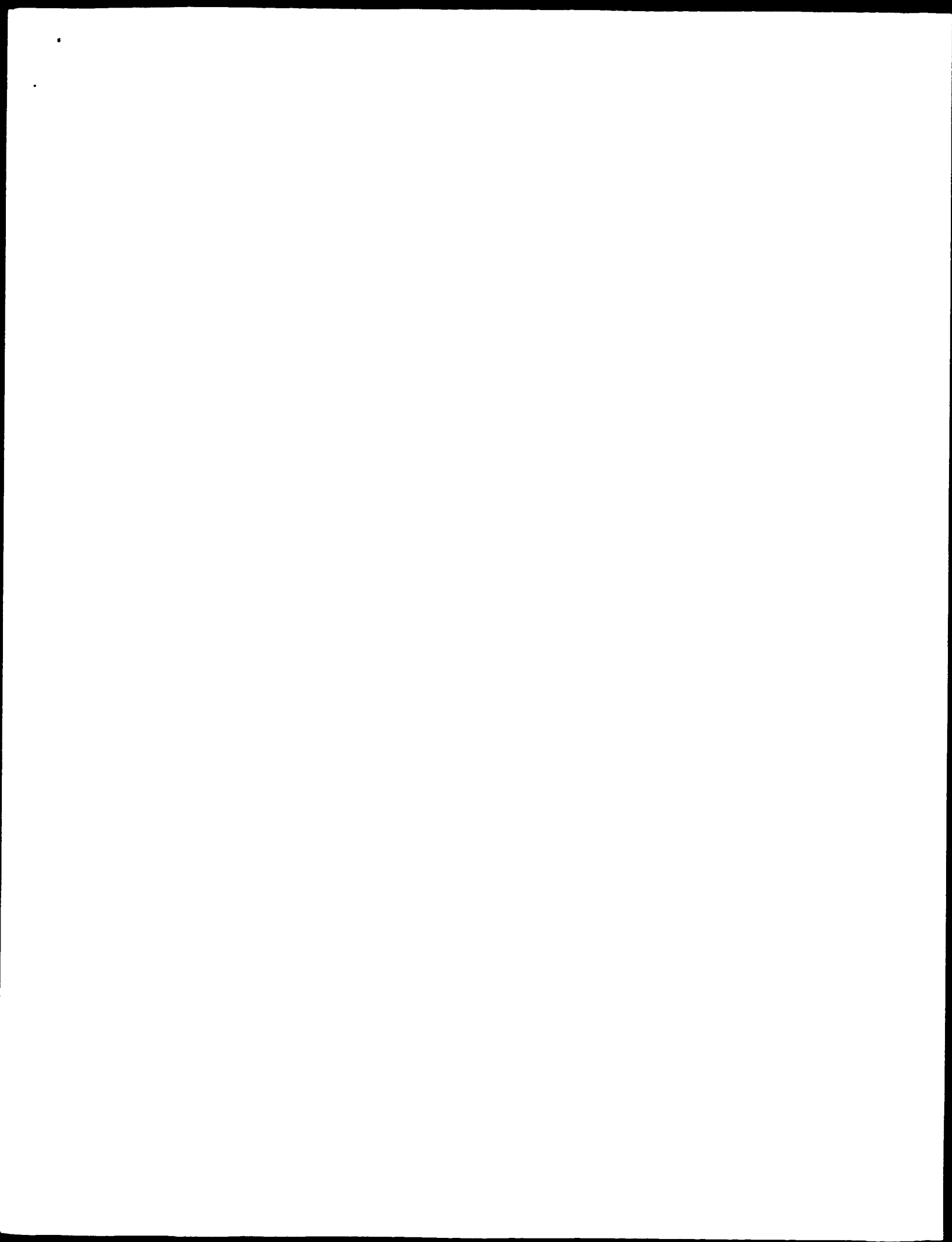


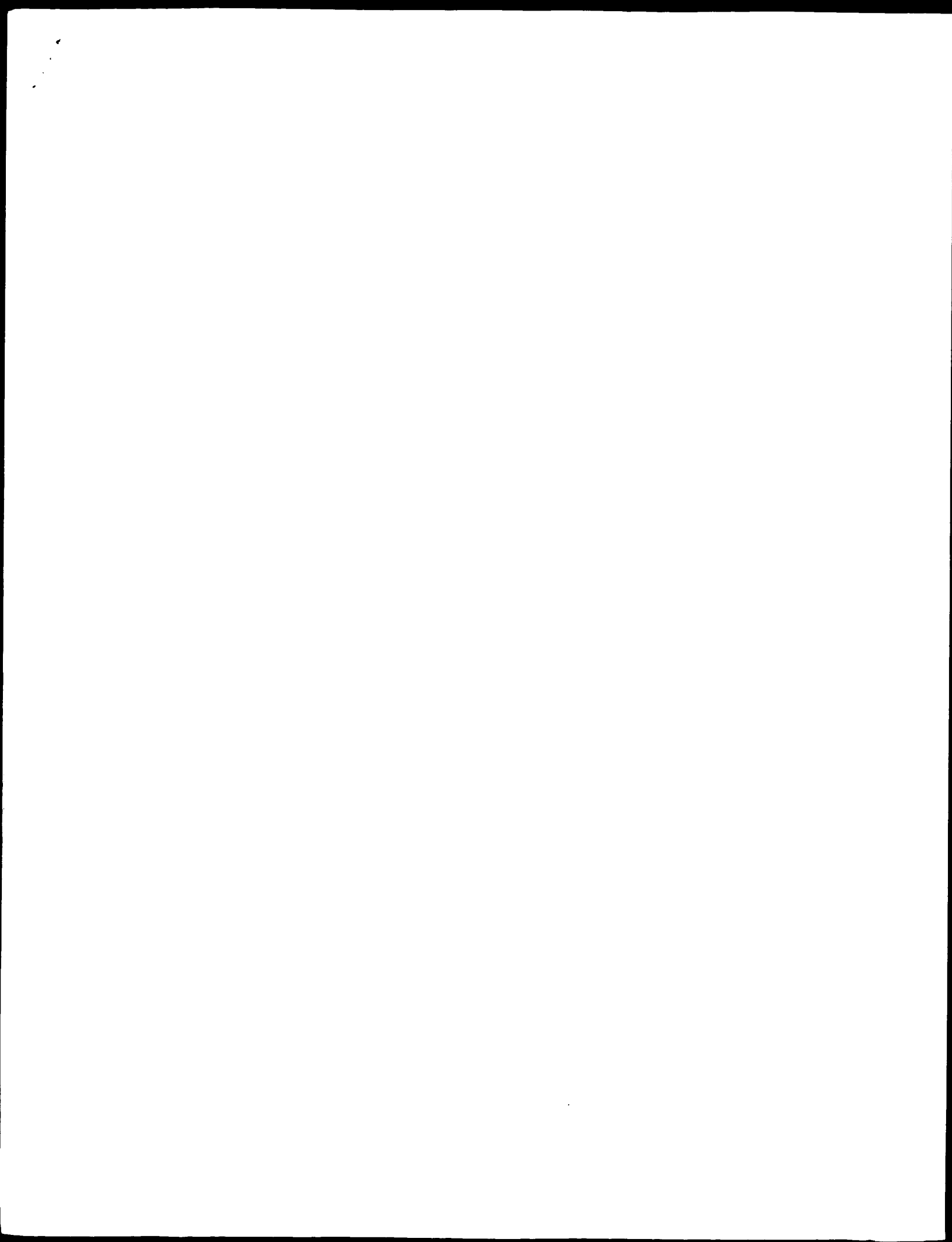
Db 2581 AAGGAATATCAGAAATCTGATGAGAGAGAACCCACCTTTGAAGCTGGGCTGTCC 2640
 QY 2591 altcagaacctgtaaaagtctacagagatggaatggaagtggtcgtcgaatggaacctgga 3050
 Db 2641 ATTGAGAACCTGTAAGAAAGTCTACCGAGATGGAGTGAAGGTGGCTGTGATGGCTGGCA 2700
 QY 3051 ctgaattttatgagggcagataactctctctctggtgccaataatggaaggggaagag 3110
 Db 2701 CTGAATTTTATGAGGGCCCAATCACCCTCTCTGGGCCCAATGAGGGGGAAGAGC 2760
 QY 3111 acccaatgtcaactctgagacgggtgtgtcccccgaacctgggacacgcctaatctctg 3170
 Db 2761 ACCACATGTCATCTGACCGGGTGTGTCCCGACCTGGGACCGCTTATATCTTG 2820
 QY 3171 ggaagaacatctgctctgagatgagacacatccgagaaacctgggggtctgtcccg 3230
 Db 2821 GGAAGAGCATTTGCTGTGATGAGCACCATCCGGCAGAACTGGGGGTGTGTCCCGAG 2880
 QY 3231 cataagctgctgttgaatgagctgctgagagaaacacatctgttctgtgtcccgcttg 3290
 Db 2881 CATTAACGTGCTGTGATGAGCTGTGATGAGAACACATCTGTGTATGCTGTGTG 2940
 QY 3291 aaagagctctctgagaaacagctgaaagcgagagatgagagatgagacatgagctgtg 3350
 Db 2941 AAAGGCTCTGTGAGAAAGCTGAGAGCGAGAGATGAGAGATGAGCTGTGTGTGTGT 3000
 QY 3351 ttgcatcaagcaagctgtaaaagcaaaacaaagcagctgtcaagtgagatgagagaaag 3410
 Db 3001 TTGGCATCAGAGCAAGCTGTAAGAAAGCAAGCCAGCTGTGAGGAGATGAGCAAGAAAG 3060
 QY 3411 ctatctgtgacctgtgacctgtgtcgtggaatctaaagtgtgcatcttctgagaaacca 3470
 Db 3061 CTATCTGTGGCTGT 3120
 QY 3471 gctgtgtgagacaccttaccgaggggaatatgagagctgtcgtcgtcgtcgtcgtcgt 3530
 Db 3121 GCTGT 3180
 QY 3531 ggcgcacacatctctctctctacacacacacacacacacacacacacacacacacacac 3590
 Db 3181 GGCACACACATCT 3240
 QY 3591 attgcacatctctccatgagagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3650
 Db 3241 ATTGCATCT 3300
 QY 3651 cagctgtgagacagctactactgacctgtgtcaagaagaatgtgaaatctctccctcagt 3710
 Db 3301 CAGCTGT 3360
 QY 3711 tccctgagaaacagtagtagcaactgtgtcaatacctgaaagaagagacagtggttctcag 3770
 Db 3361 TCCCTGAGAAACAGTAGTAGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3420
 QY 3771 agcagctgtgagctgtgacctgtgtgagacacacacacacacacacacacacacacac 3830
 Db 3421 AGCAGTTCTGT 3480
 QY 3831 tctgcatactcacaactcactcaagaagcactgtgtcgaagcccgctgtgtggaagacata 3890
 Db 3481 TCTGCTATCTCCAACTCCTCAAGAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3540
 QY 3891 gggcagtagagctgacctatgtgtcgtcatatgaagctgtcgaagagagagacgttctgtg 3950
 Db 3541 GGGCATAGCTGACCTATGT 3600
 QY 3951 ctcttcaatagatgagctgacctgtgtgagacacacacacacacacacacacacacacac 4010
 Db 3601 CTCTTATAGATGATGT 3660
 QY 4011 gaaagacacctgtgagaaatattctcgaagtggtgagagagagagagagagagagagagag 4070
 Db 3661 GAGAGACACCTGTGAGAAATATTCTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3720

QY 4071 acctgaatgtgacctgtgtccagcaagacgaacacagcggtgtgtgtgtgtgtgtgtgtgtgt 4130
 Db 3721 ACCCTGATGT 3780
 QY 4131 tgtcttcgacctgtcaactgaatgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4190
 Db 3781 TGTCTTGT 3840
 QY 4191 gaaatcagaagacagactgtgtcagtgagatgagatgagatgagatgagatgagatgagat 4250
 Db 3841 GAATCCAGAGACAGACACTGT 3900
 QY 4251 ggtgtgaaatcagaagacagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4310
 Db 3901 GGTGTGAAATCTTACAGACAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3960
 QY 4311 agacagagctcgaagagatgt 4370
 Db 3961 AGACGAGATGGAAGAGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4020
 QY 4371 ggcctgt 4430
 Db 4021 GCCCTGT 4080
 QY 4431 cctgtgagatgagacagacagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4490
 Db 4081 CCTGT 4140
 QY 4491 acctgtgaactcttaaacgacctcacaagaacctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4550
 Db 4141 ACCCTGGAATCTTAAAGCGCTTACCAAAAGACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 4200
 QY 4551 ggaacccaatccccagacagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4610
 Db 4201 GGAACCAATCCACAGACAGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4260
 QY 4611 gtcccgagacacatcagatgt 4670
 Db 4261 GTTCTCCAGACATCATGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4320
 QY 4671 cctgt 4730
 Db 4321 CCTGT 4380
 QY 4731 gcaagggggt 4790
 Db 4381 GCAGGGGGGT 4440
 QY 4791 acaggaagaacatcttgatgt 4850
 Db 4441 ACAGGAAGAAATTTGT 4500
 QY 4851 ttaagaagaacagatctgt 4910
 Db 4501 TTAAGAAGCAAGATGT 4560
 QY 4911 aatactcaagacttctcagagcaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4970
 Db 4561 AATATCTCAAGCACTTGT 4620
 QY 4971 caactaagctgt 5030
 Db 4621 CACTTAAGAGCTGT 4680
 QY 5031 atgacagagctgt 5090
 Db 4681 ATGACAGAGCTGT 4740
 QY 5091 gaaatcagcttctcagagcaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5150
 Db 4741 GCAATCACTCTTGT 4800

OY 5131 ggaaggaacccatagcaatggaattactgcttcaatcaatcccccgaatcccaag 5210
 DB 4801 GGAGGAACCTTAGCCATTATGGAATTAAGCTTTCAATCATCCCTGGAATCCACGA 4880
 OY 5211 cagagccctcaagagtgagctctatgacacacatagtgatgctctgtgccaatgt 5270
 DB 4861 CAGCAGCTCTCAGAGTGGCTCCCATGACACATCAATGATGATGCTGTCATCATCTGT 4920
 OY 5271 gtacatcttgcaatgctcctgctccagcaagcttgcctatcccgatccagagcg 5330
 DB 4921 GTCACTTTGCAATGTCCTGTCACCAAGCTTTGTGCTATTCCTGATCCAGAGCGG 4980
 OY 5331 gtccagcaagcaaaacacccctgcaatgcaatgagtgagagccctgcatcagctc 5390
 DB 4981 GTACACCAAGCAAAACACCTGCAATGCAATGAGTGAGAGCTGTATCTAGCTGCTC 5040
 OY 5391 tctaatctgtctgagataatgcaatgcaatgctgctccctgcaacatgctgcaatc 5450
 DB 5041 TCTAATTTTGTGGGATATGTCATTAATGCTGTCCTGCGACACTGTCATCATCATC 5100
 OY 5451 ttcacatgctccagcaagaatgctatgctcccaacacatgctgctgctagcctt 5510
 DB 5101 TTCATCTGCTTCCAGAGAACTGCTATGCTCCTCACCAATCTGCTGTGCTACCTCT 5160
 OY 5511 ctactctgctgataagtgatgcaatgcaatgctgctgctgctgctgctgctgct 5570
 DB 5161 CTACTTTTCTGTATGAGGATGTCATCAACCTCTCATATACCACTCTTTGTGCTTC 5220
 OY 5571 aagatcccaagcaagcctatgctgctgctgctgctgctgctgctgctgctgctgct 5630
 DB 5221 AGATCCCAAGCAACCCATGATGCTGCTCACAGCTGCAACCTCTTCAATGGCATTAAT 5280
 OY 5631 ggaagcgtggaacacccctgctgctgctgctgctgctgctgctgctgctgctgct 5690
 DB 5281 GCGAGGCTGCGCCACTTTGTGCTGAGCTGTCACCGAATGATGATATATATCAAT 5340
 OY 5691 gatactcgaatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 5750
 DB 5341 GATATCTGAGTCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5400
 OY 5751 gacatgctgcaaaacacagcaatgctgctgctgctgctgctgctgctgctgctgct 5810
 DB 5401 GACATGCTGAAAAACCAAGCAATGCTGATGCTGCAAGCTTGGGAGGATTCCTTT 5460
 OY 5811 gtgctacacatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 5870
 DB 5461 GTGTCACCATTAATCTTGGGACTTGGTGGGAGAACTTTCGCAATGGCGGAGGAGG 5520
 OY 5871 gtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 5930
 DB 5521 GTGGTGTCTTCTCTATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5580
 OY 5931 gtaaatgcaaaac 5990
 DB 5581 GTAATGCAAAAGCTATCT 5640
 OY 5991 agaattctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6050
 DB 5641 AGAATCTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5700
 OY 6051 tataagaagaagcgaagcctgctgctgctgctgctgctgctgctgctgctgctgctgct 6110
 DB 5701 TATAGAAAGAGAGCGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5760
 OY 6111 tgccttgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6170
 DB 5761 TGCCTTGGCT 5820
 OY 6171 ggaagatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6230
 DB 5821 GAGATACCACTGCTTACCAAGAGATGCTTCTTAAAGAAATAGATATCTTAAAC 5880
 OY 6231 atccatgaagatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6290

DB 5881 ATCCATGAAGTACATGACATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5940
 OY 6291 ttgacggagagaacacagtgagctgctgctgctgctgctgctgctgctgctgctgctgct 6350
 DB 5941 TTACTGGAGAGACACCTGAGTCTTGTGCTTTTGAAGAGGATCCAGAGAAAGAA 6000
 OY 6351 gtccgaaggttggtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 6410
 DB 6001 GTTGGCAAGTGTGATGAGTGAGGCGATTCGAAACTGCGCTGCTGTAAGATGGAAGAAAA 6060
 OY 6411 tatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6470
 DB 6061 TATGCTGCTGTAATGATGAGGAGCAACCAAGCTCTTCAACGCTTGGCTTTGATC 6120
 OY 6471 ggcgggctcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6530
 DB 6121 GCGCGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6180
 OY 6531 cgtctctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6590
 DB 6181 CGGTTCTTGGGAATGTCCTTAAGTGTGTCAGAGAGGAGATCAATGATGCTTAA 6240
 OY 6591 tctcaatgataagaagaatgagctcctgctgctgctgctgctgctgctgctgctgctgct 6650
 DB 6241 TCTCATGATGAGAAATGATGAGGCTTGTGCACTGATGCTGATGCTGATGCTGATGCT 6300
 OY 6651 aggtcaggtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6710
 DB 6301 AGGTTACAGTCTCTTGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6360
 OY 6711 atagtgtgcaatgcaaggtgctgctgctgctgctgctgctgctgctgctgctgctgct 6770
 DB 6361 ATAGTGTGCAATAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6420
 OY 6771 ctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6830
 DB 6421 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6480
 OY 6831 ccatctcatatctctctgctgctgctgctgctgctgctgctgctgctgctgctgct 6890
 DB 6481 CCATTTCTATTAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6540
 OY 6891 ctccacatagaagactgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6950
 DB 6541 CTCCACATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6600
 OY 6951 gccaaggaacaaatgataatgacacacacacacacacacacacacacacacacacacac 7010
 DB 6601 GCCAAGGACCAAGATGATATACCACTTAAGAACCTCTATTAACAAAAACCAAGCA 6660
 OY 7011 gtagtgagctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 7070
 DB 6661 GTATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6720
 OY 7071 gtaagaagaatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 7130
 DB 6721 GTATGAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6780
 OY 7131 gcaacatgtaagctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 7190
 DB 6781 GCACATGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6840
 OY 7191 gatactgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 7250
 DB 6841 GATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6900
 OY 7251 taagaaggaagctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 7310
 DB 6901 TACAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6960
 OY 7311 ttagtttttactataactatgtaactctatctatgtaacccaatgtaactatgaggt 7370





GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2002, 12:54:11 ; Search time 55.68 Seconds
(without alignments)
4510.378 Million cell updates/sec

Title: US-09-595-526B-2

Perfect score: 11797
Sequence: 1 MACWPQLRLIMKMLTRRRR.....VDVAVLTSFLDEKVESYV 2261

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_032802.*
1: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1982.DAT.*
4: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1983.DAT.*
5: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1984.DAT.*
6: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1985.DAT.*
7: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1986.DAT.*
8: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1987.DAT.*
9: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1988.DAT.*
10: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1989.DAT.*
11: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1990.DAT.*
12: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1991.DAT.*
13: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1992.DAT.*
14: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1993.DAT.*
15: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1994.DAT.*
16: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1995.DAT.*
17: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1996.DAT.*
18: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1997.DAT.*
19: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneeq/geneeqp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11797	100.0	2261	22	AA1981361 Amino acid sequenc
2	11797	100.0	2261	22	AA1981365 Amino acid sequenc
3	11793	100.0	2261	21	AA1981117 Human ABC1 cholest
4	11793	100.0	2261	22	AA1981362 Amino acid sequenc
5	11793	100.0	2261	22	AA1981366 Amino acid sequenc
6	11792	100.0	2261	21	AA1981109 Human ABC1 cholest
7	11789	99.9	2261	21	AA1980802 Human ABC1 cholest
8	11789	99.9	2261	22	AA1981749 Human ABC1 protein
9	11789	99.9	2261	22	AA1981363 Amino acid sequenc
10	11789	99.9	2261	22	AA1981367 Amino acid sequenc
11	11786	99.9	2261	21	AA1981111 Human ABC1 cholest

12	11786	99.9	2261	21	AA1981114 Human ABC1 cholest
13	11786	99.9	2261	21	AA1981115 Human ABC1 cholest
14	11785	99.9	2261	21	AA1981105 Human ABC1 cholest
15	11785	99.9	2261	21	AA1981110 Human ABC1 cholest
16	11784	99.9	2261	21	AA1981113 Human ABC1 cholest
17	11784	99.9	2261	21	AA1981116 Human ABC1 cholest
18	11783	99.9	2261	21	AA1981112 Human ABC1 cholest
19	11777	99.8	2261	21	AA1981104 Human ABC1 cholest
20	11774.5	99.8	2260	21	AA1981106 Human ABC1 cholest
21	11771	99.8	2261	22	AA1981183 Human ABC1 mutant
22	11767	99.7	2259	21	AA1981107 Human ABC1 FHA-3 m
23	11767	99.7	2261	22	AA19813022 Human ATP binding
24	11767	99.7	2261	22	AA19810228 Human ATP binding
25	11767	99.7	2261	22	AA19812176 Human ABC1. Homo
26	11767	99.7	2261	22	AA19812177 Human ABC1 mutant
27	11764	99.7	2261	22	AA19812188 Human ABC1 mutant
28	11763	99.7	2261	22	AA19812189 Human ABC1 mutant
29	11761	99.7	2261	22	AA19812181 Human ABC1 mutant
30	11760	99.7	2261	22	AA19818550 Human ABC1 homolo
31	11760	99.7	2263	22	AA19811956 Human ABC1 homolo
32	11760	99.7	2263	22	AA19819534 Human ABC1 mutant
33	11759	99.7	2261	22	AA19812182 Human ABC1 mutant
34	11759	99.7	2261	22	AA19812186 Human ABC1 mutant
35	11433	96.9	2201	21	AA19819380 Human ATP binding
36	11433	96.9	2201	21	AA19819380 Human ATP binding
37	11433	96.9	2201	21	AA19819380 Human ATP binding
38	11398	94.9	2143	21	AA198108108 Human ABC1 cholest
39	11015	93.4	2130	22	AA198102190 Human ABC1 mutant
40	7988	67.7	1525	19	AA198102187 Human ABC1 mutant
41	5858.5	49.7	2273	19	AA19810398 Human ABC1 mutant
42	5849	49.6	1144	22	AA198102184 Human ABC1 mutant
43	5849	49.6	1144	22	AA198102185 Human ABC1 mutant
44	5755.5	48.8	2146	22	AA198104483 Human PD-ATP-bind
45	5715	48.4	1089	22	AA198162691 Human ABC1 protein

ALIGNMENTS

RESULT 1	AA1981361	standard. Protein; 2261 AA.
XX	AA1981361	
AC	AA1981361	
XX	20-APR-2001	(first entry)
DT		
XX		
XX		Amino acid sequence of a human ABC1 polypeptide.
DE		
XX		
KW		Human: adenosine triphosphate binding cassette protein 1; ABC1;
KW		apolipoprotein-mediated mobilization; cholesterol; Tangier disease;
KW		chromosome 9q22-q31; heart disease; hypercholesterolemia;
KW		atherosclerosis; cholesterol transport.
XX		
OS		Homo sapiens.
XX		
PN		WO200078972-A2.
XX		
PD		28-DEC-2000.
XX		
PE		16-JUN-2000; 2000WO-US16765.
XX		
PR		18-JUN-1999; 9905-0140264.
PR		14-SEP-1999; 9905-0153872.
PR		19-NOV-1999; 9905-016573.
XX		
PA		(CVTH-) CV THERAPEUTICS INC.
XX		
PI		Lawn RM, Wade D, Garvin M;
XX		
DR		WPI; 2001-137812/14.
XX		
PT		Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide;

PT useful for the development of agents for the treatment of heart disease
 CC and other disorders associated with hypercholesterolemia and
 PT atherosclerosis

PS Disclosure: Page 128-143; 215pp; English.

CC The present sequence represents a human adenosine triphosphate (ATP)
 CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
 CC membranes and utilizes ATP hydrolysis to transport a wide variety of
 CC substrates across the plasma membrane. ABC1 is a pivotal protein in
 CC the apolipoprotein-mediated mobilization of intracellular cholesterol
 CC stores. ABC1 is defective in Tangier disease, a genetic disorder
 CC characterized by abnormal HDL-cholesterol metabolism. The ABC1 gene is
 CC localized to chromosome 9q22-9q31. The ABC1 genes and proteins are
 CC useful for developing pharmaceutical agents for the treatment of heart
 CC disease and other disorders associated with hypercholesterolemia and
 CC atherosclerosis. The genes are useful for developing screening assays to
 CC screen for compounds that regulate the expression of genes associated
 CC with cholesterol transport. The genes and proteins are also useful for
 CC are also useful as diagnostic indicators of cardiovascular disease and
 CC other disorders associated with hypercholesterolemia.

XX Sequence 2261 AA:

Query Match 100.0%; Score 11797; DB 22; Length 2261;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2261; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 MACHPQLRLMKMLTTRRRQTCOLLVAMPFLFLLISVRUSYPRYQHECHPNKA 60
 DB 1 macpqlrlrlmkmlttrrrtcqlllevawpflflllsvrlysypryqhechfnka 60
 QY 61 MPASGTLPMWOGITCNANNPFCRYPTRPEAGVGVGNFNKSVARLESDARLLLSKOT 120
 DB 61 mpsagtlpmwogitcnannpfcryptrpeagvgyvgnfnksvarlisdarlllyskdt 120
 QY 121 SMKMRVLTLOQIKKSSNMLKLODFLVNETSGFLYNLSLPKSTVDMKLRADILH 180
 DB 121 smkmrvltrlqgikksnmlkldflvnetsgflynlslpkstvdmkmradihlh 180
 QY 181 KVFLOGVOLHLSLSCNSKSEEMOLQDOVSELCGPKRKLAAEVLRSNMIDILKPL 240
 DB 181 kvflqgvohlslscnksseemqlgdqvselcglpkklaaevlrsnmidlkp1l 240
 QY 241 RLINSTSPFSKELAEATKTLHSLGLTLAGOELFSMKSWMROBVMFLTVNSSSSTOI 300
 DB 241 rlinstspfskelaetktlhlslgltagelismrswsmdrmqvmfltnvsssstql 300
 QY 301 YQAVSRIVCGHPBGGLKIKSLMWYEDNNYKALFGNGTEDEAEETPDNSTPYCNDLAK 360
 DB 301 yqavsrivcghpbgglikikslmwedydnnykalfgngteedaetfydstprcndlkm 360
 QY 361 NLSSPSRLIIMKALKPLVGLITVYDPDPATQVMAEVNKKTOELAVHDLFGMEELIS 420
 DB 361 nlespsrlilimkalkpllyvgkillydppdpatrqvmaevnkktoelavhdlgmeewels 420
 QY 421 PKIWTMENSOEMDLVRLMLDSRDNDHFWEQQLDGLDWTAAQIVATLAKHPEDVSSNGS 480
 DB 421 pkiwtmensoemdlvrmldsrndhfwegqldgladqivaltlakhpdevgsngs 480
 QY 481 VYTWRAFNNTNQAIRTISFMECVNLKLEPATEVWLINNSMELIDBRKFWAGIVPTG 540
 DB 481 vytwrafnntnqairtisfmevcvnlklepatevwlinsmelidbrkfwagivftg 540
 QY 541 ITPGSIELPHHVYKIRMDIDNVEPTNKTKDGYWDGPGRADPEEMRRYVWGFAVLQDVY 600
 DB 541 itpgsielephhvkykirmdidnvertnkikdgywdpgpradpedmrryvwgfa1yldv 600
 QY 601 EDAIIVLTGTEKTKGVYQOMPYPYVDIEFLRVMSRSMPLFMTLAWIYSAVAIIGKIV 660
 DB 601 eqaiivltgtekkgvymqmpypcyvddiflrvmsrsmplfmltlawiyysaavilkiv 660

QY 661 YEKEARLKEWTRIMGDNGSLNFWISLISLPLVSAGLLVYLKGNLLPVSDSVFV 720
 DB 661 yekearlkewtrimgdngslnfwisllslpllvsaagllvylkgnllpvsdsvfv 720
 QY 721 FLVFAVATLQCFLLSTLSTFRANLAAAGGIIYFTLYPYVLCVWMOYGGTTLKIFMS 780
 DB 721 flvfvatllqcfllstlstranlaaaggiiyftlypyvlycvawgdyvflkifms 780
 QY 781 LLSPVAFEGCEYFALFEEOGIGVQMDNLFESPDEEDGPNLTSSMLJDTFLYGVMT 840
 DB 781 llspvafegceyfalfeeogigvqmdnlfspdeedgpnltssmljdtflgyvmt 840
 QY 841 YIAVAPGQGIIPRPYFCTKSYWNGEESDEKSHGSKQKMSLCEMEEPHKLKGS 900
 DB 841 yiaavpgqgiiprpyfctksywngesdeshgskqkmslcmeeephklkgs 900
 QY 901 IQMLVYVYRDKMKVAADGALNLFEGQIRSFIGNHAGKTTMTSLITGFPSTGAVIL 960
 DB 901 iqmlvyvyrdkmkvadgallnlfegqirsfignhagkttmtslitgfpstgavil 960
 QY 961 GKDIREMSTIRONLGVCPQHNVLEPDMLTVEEHIMFYARLKLSEKHVKAEMQALDVG 1020
 DB 961 gkdiremstironglvcpqhnlvleehimfyarlklsekhvkaemqaldvg 1020
 QY 1021 LPSSKLSKTSQSLSGCMORKSLVATLAFVCGSKVILDEPTAGVDPRYSRKGTIELLKTRQ 1080
 DB 1021 lpskslksktsqslsgcmorkslvatlafvcskvildepagvdprysrkgtiellktrq 1080
 QY 1081 GRTIILSTHMDADVLGDRIALISHGKLCYSSSLFLKNQGTGYTLTVLKQVDESLIS 1140
 DB 1081 grtilsthmdeadvlgrlailshgkccysslflknqgtgytltlvkqvdessls 1140
 QY 1141 SCRNSSSTYSLKEDSSVQSSSDAGLGSDBESDFTLTDVSAISMLIRKHVSEARLYEDI 1200
 DB 1141 scrnssstyslkedssvqsssdaglsdhesdftldvasaismlirkhvsearlyedi 1200
 QY 1201 GHELTAVLYPEAKGAFELFHEIDRSDLSISYSGSEFTLLEITLKAESGVNAE 1260
 DB 1201 ghe1tavlypeakgafelheidrdsdlsisysgseftlleitlkaesgvnae 1260
 QY 1261 TSDGTLPARNRRAFADKQOSCLRPTEDDAADPNDSDIDPSRETDLSGMDGKSYOVK 1320
 DB 1261 tsdgtlparnrrafadkqosclrpteeddaadpndsidpsredllsgmdgksyovk 1320
 QY 1321 GKKLTQOQFVALMKRLILARRSKRGFAQIYLAFAVFCIALVNSLYPPPGKPSLELO 1380
 DB 1321 gkkltrqoqfvalmkrlilarrskrgfaqiylafavfcialvnslypppgkpslelq 1380
 QY 1381 PMWNEQYTFVNSNDAPEDTGTLELNLALTKDPGFQTRCMENGP1PDPPCOAGEEMWTAP 1440
 DB 1381 pmwneqytfvnsndapedtgtlelnaltkdpgfqrtrcmengp1ppdpcogeeemwtap 1440
 QY 1441 VPQTMDLFPQNGNMTWQNPSPACQSSDKIKMLPVCPPGAGLPPQKQKNTADILQDL 1500
 DB 1441 vpgtmdlfpqngnmtwqnpspacqssdkikmlpvcppgaglpqqkqkntadilqdl 1500
 QY 1501 TGRNISDYLVTYVYQIIKSLKINKIWEFERFGPSLGSVNTQALPPSOEYVNAIKOMK 1560
 DB 1501 tgrnisdylvtyvyqiikslkinikiwefrfgpslgsvntqalppsgeyvnaikomk 1560
 QY 1561 HLKTLAKSSADRLNLSLGRFMTGDTDRNNYKVWPNNGKGMHAISSFLLVANNALIRANLQK 1620
 DB 1561 hlklakssadrlnlsgrfmgtdtrnnkvwpnngkgmhaisfllvannaliranlqk 1620
 QY 1621 GENSHSHGTAFNPNPLNLTKOQLSEVALMTTSDVLYSICVIFAMSVPAFVFLIOER 1680
 DB 1621 genshshgtafnppnplnltkoqlsevalmttsdvlysicvifamsvpafvflioer 1680
 QY 1681 VSKAKHLOEISGVKPVLYMLSNFWMDCNVVPATVITIIIFIOOKSYSSNLPVIAL 1740
 DB 1681 vskakhloeisgvkpvlymlsnfwmdcnvvpattvitiifiooksyssnlpvial 1740
 QY 1741 LLLLYGWSITPLMYPASFVERKIPSTAVVVLTSVNLFIGINGSVATFVLELFTDNKLNIN 1800


```

Db 661 yekearlkecmrimgldnstlwfswfssilprlvsagllvvllkqnllypsdpsvfv 720
QY 721 FLVSFAVWVTLQCELLSTLFSRANLAACGGIIEFTMLPYLVCAWMDYVGTLLKIPAS 780
Db 721 flsvfavvllqgfllstlfsranlaaacggilyftllyprylcawmdyvgftllkifas 780
QY 781 LLSFVAFGCGEFALFEEOGIGVOMDNI.FESPVEEDGNLTTSISMM.LFDTFLYGVWTW 840
Db 781 llsfvafgcfefalfeegigvqwdnlfeesvveedgnlttsismmlfdtfllygmw 840
QY 841 YIEAVFPGQYIPRWYFECTKSYWCESEDEKSHPGSNOKRMSEHCEEPETLKLKGS 900
Db 841 yieavfpgqy:iprwyfpectksyw:fgcesdekshpgsnokrmseelclklgvs 900
QY 901 IONLVYVRDGMKAVNDGIALNFYEGQTSPLGNHAGKTTMTSLTGLPPTSGIAYIL 960
Db 901 ionlvvyrdgmkvavdgiainfyegqitsflgnhagkttmtslltglfpptsgtayil 960
QY 961 GNDISEMSTIRQNLGVCPOHNVLFDMLTVEHIMFYARLKLSEKHVKAEMQMALDVG 1020
Db 961 gndisemstirqnlgyvcpqhnvlfamltveehlwiyarlklsekhvkaemqmaldvq 1020
QY 1021 LPSSKLKSTSO.LSGMORLISVALAEVGSKVYLDEPTAGVDPYSRRGIWEILKYRQ 1080
Db 1021 lpsklkstsqsgsmgrklisvalafvgskvyllddeptagvdpysrrgltwelllkyrq 1080
QY 1081 GRTILLSTHHMDEADYLDGRIATITSHGKLCVGSSTLKLNOGIGYVLTLYKKDVSSLS 1140
Db 1081 grtillsthhmdeadvldgriaatitshgklccvgsstllklnoqlyvltlykkdvssls 1140
QY 1141 SCRNSSTVTVLKKEDSVSSDAGLGSDESPTLTIDVSALSNI.LRKHVSARLVEDI 1200
Db 1141 scrnsstvslylkkedsvsgssdaglgsdhesdltlidvsalsnlkrhvsarlveldi 1200
QY 1201 GHELTYYVLPYEAKEGAVLEHEIDRLSDLGISSGISETTLBEETFLKVAEESGVDAE 1260
Db 1201 gheiltyvlp:yeakegavleheidrlsdlgisssgisetllbeetflkvaeesgvdae 1260
QY 1261 TSDGTLPARRRRAFGDKQSCIRPFTEDDAADPNDSIDIPESRETLGSGMGKGSYQK 1320
Db 1261 tsdgtlparrrrafgdkqscirpfteddaadpndsidipesretllsgmgkgsgyqk 1320
QY 1321 GWTLOOQFVALLMKRLILARRSKGFFAOIV.PAVFVCIATVLSLTVPPFGYPSLEQ 1380
Db 1321 gwtlloqfvallmkrlilarrskgffaov:pa:pvfcia:tvls:lvppfgyp:sl:elq 1380
QY 1381 PMWYNEQYTFVSNDAPEDTGTELELNAITKDPFGFTRCMHGPNIPPTPCQAEEEMWTAP 1440
Db 1381 pmwyneqytfvsnndapedtgtlelnaitkdpfgftrcmhgpnipptpcqaeeemwtap 1440
QY 1441 VPOTIMLFQNGWMTQNSPACQSSDKIRKMLPVCPPGAGGLPPOKRONWTADILDL 1500
Db 1441 vpotiml:fqngwmtqns:spacqssdkirkmlpvcppgagglppokronwtadil:dl 1500
QY 1501 TGRNISDYLVKTVVQI.IAKSLKNKIWNNEFRYGGFSLVGSNTQALPPSQEVNDAIKOMK 1560
Db 1501 tgrnisdylvk:tvvqi:ia:kslknkiwnnefr:yg:gs:ntqalppsqevn:daik:omk 1560
QY 1561 HULKADSSADRFLNSLGRPMFTGLDTRNNVYKWPNNKGMAHISPLANVINNALIRANLOK 1620
Db 1561 hulkadssadrfl:ns:lg:rp:mtgl:dr:nnv:ykwpnnkgmahispl:anvin:na:li:ranlo:k 1620
QY 1621 GENPSHYGITAENHPLNLT.KOOLSEVALMTSTVDVLVSTCYFANSPFASVVFLOER 1680
Db 1621 genpshygitaenhp:lnlt:ko:olsevalmtstvdvlvstcyf:an:sp:fv:fv:lo:er 1680
QY 1681 VSKAKHLQFTSGVKPVYIWL.SNFWDMCNVVPATLVIIIFCFQOKSYVSTNLPVATL 1740
Db 1681 vskakhlqftsgvkpv:yil:snfwdmcnvvp:atlv:ii:fc:fqoksyvstn:lpvat:l 1740
QY 1741 LLLLGWSTTPLMYPASFEFKIPSTAYVVLVSNI.FTIGNSVATFVLELFTDKNLNNIN 1800
Db 1741 llllgwsttplm:ypasfe:fk:ip:st:ayvvl:vsni:ft:ig:nsvatf:vl:el:ft:dk:nl:nnin 1800

```

```

Db 1741 llllygwsitp:lmypasfv:fk:ip:st:ayvvl:vsnl:fig:ngsvatfv:el:ft:dk:nl:nnin 1800
QY 1801 DILKSYFLFFPHFCGLGKILDMYKQAMADALERFGENRFPVSPSLMDL.VGRNLPMAAVEG 1860
Db 1801 dilksyflffphfc:lg:kl:ldmy:kqam:adalerfgenr:fpv:sp:sl:mdl:vgrnlpma:aveg 1860
QY 1861 VVEFLITVLIQYRFRTRPVPNAKLSPLNDEDEVRRERROKTIIDGGQNDILEKELTKI 1920
Db 1861 vveflitvli:qy:fr:tr:pv:na:kspl:nde:devrrer:ro:ktii:dg:qndi:le:ke:lt:ki 1920
QY 1921 YRRKRRPAVDRIQVGIPECEFGELGVNAGAKSSTFMALTGDTVTYTGDAFLKNKSTLSN 1980
Db 1921 yrrkrrpavdr:icv:gi:pe:ce:fg:elgv:nag:akss:tfmaltgdtvt:ytgda:flkn:ks:tl:sn 1980
QY 1981 IHEVQNNQYOCOPATITELTGREHVEFALLGVGEKEVGKVEWAIKRLGLVYGEK 2040
Db 1981 ihevqnnqyocop:atit:eltgre:hvef:allgv:ge:kevg:kve:waik:rlglv:yge:k 2040
QY 2041 YAGNYSGGNKRRLSTAMALIGGPPVFLDEPTGMDFKARRPLMNCALSVYKGRSIVLT 2100
Db 2041 yagnysggnkr:rlst:amal:ig:gp:pvfl:de:ptgm:dfkarr:plmncal:svy:kg:rsiv:lt 2100
QY 2101 SHSMECEALCTRBAIMVNGFRCLGSVOHLKRNFGDGYITIVRIAGSNPDLKPVDFFG 2160
Db 2101 shsmecealctr:ba:imvng:fr:cl:gsvo:hlk:rnfg:dyit:ivri:agsnp:dlkp:vdffg 2160
QY 2161 LAFPSVLEKEHRNMLQYOLPSSLSLARIFSTISOSKRRLHIEDYVSQOTITDOYFVNF 2220
Db 2161 lafpsvlekehrnml:qyolp:ssls:larif:stis:oskr:rlhiedy:vsqotit:do:yfvnf 2220
QY 2221 AKDQSDDDHLKDLSLHKNQTVVDYAVLTSFLQDEKVEKYV 2261
Db 2221 akdqsddh:lkdl:slhknq:tvvd:ayvlt:sl:qde:kvekyv 2261

RESULT 3
AAB38117
ID AAB38117 standard; Protein; 2261 AA.
AC AAB38117;
DT 29-JAN-2001 (first entry)
DE Human ABC1 cholesterol transporter mutant, I883M.
XX
KW Human ABC1 cholesterol transporter; chromosome 9q31;
KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KW Tangier disease; TD; familial HDL deficiency; FNA; polymorphism;
KW cardiovascular disease; coronary artery disease; coronary restenosis;
KW cerebrovascular disease; peripheral vascular disease;
KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KW prognosis; prophylaxis; drug screening; transgenic animal; mutant;
KW nuclein.
XX
OS Homo sapiens.
XX
PN WO200055318-A2.
XX
PD 21-SEP-2000.
XX
PE 15-MAR-2000; 2000WO-IB00532.
XX
PR 15-MAR-1999; 99US-0124702.
PR 08-JUN-1999; 99US-0138048.
PR 17-JUN-1999; 99US-0139600.
PR 01-SEP-1999; 99US-0151977.
XX
PA (UYBR-) UNITV BRITISH COLUMBIA.
PA (XENO-) XENON BIORESEARCH INC.
XX
PI Hayden MR, Wilson AR, Pimstone SN;
XX

```

DR WPI: 2000-587528/55.

XX New ABC1 polypeptide is useful for treating diseases associated with
 PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
 PT disease and cancer -

PS Examples: Page -: 229pp; English.

XX The invention relates to the human ABC1 cholesterol transporter protein
 CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
 CC a member of the ATP-binding cassette (ABC transporter) superfamily of
 CC proteins, and plays a crucial role in cholesterol transport, particularly
 CC intracellular cholesterol efflux from the cell. The gene encoding ABC1 is
 CC located on chromosome 9q31, and mutations in this gene are associated
 CC with two genetic HDL (high density lipoprotein) deficiency disorders,
 CC Tangier disease (TD) and familial HDL deficiency (FHD). These diseases
 CC are distinguishable in that TD is an autosomal recessive disorder, while
 CC FHD is inherited as an autosomal dominant trait. Low levels of HDL ("good
 CC cholesterol") in the blood correlate with a high risk of cardiovascular
 CC disease, particularly coronary artery disease, but also cerebrovascular
 CC disease, coronary restenosis, and peripheral vascular disease.
 CC Conversely, a high level of HDL has protective effects against
 CC cardiovascular disease. The invention provides genetic constructs and
 CC transgenic cells and non-human animals comprising human ABC1 nucleic
 CC acids, and methods of gene therapy for the treatment or prevention of
 CC cardiovascular disease comprising the administration of an expression
 CC vector encoding ABC1 or an active fragment thereof. The invention also
 CC encompasses compounds which mimic ABC1 activity, compounds which
 CC stimulate ABC1 expression and methods of screening for such compounds.
 CC It further relates to methods for determining whether a patient has an
 CC increased risk for cardiovascular disease due to polymorphisms in the
 CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
 CC or prevent cardiovascular disease, especially coronary artery disease,
 CC cerebrovascular disease, coronary restenosis or peripheral vascular
 CC disease. They may also be used in the treatment of diseases associated
 CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
 CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
 CC The invention specifically excludes proteins with the exact amino acid
 CC sequences of Genbank Accession No: CA10005.1 and X75926, and the nucleic
 CC acid with the exact sequence as Genbank Accession No: A012376.1. The
 CC present sequence represents a mutant human ABC1 cholesterol transporter
 CC associated with an altered cholesterol level and therefore an altered
 CC risk of cardiovascular disease.
 CC Note: The present sequence is not shown in the specification, but is
 CC derived from the native human ABC1 shown on pages 152-157.
 CC
 XX
 XX
 SQ Sequence 2261 AA;

Query Match 100.0%; Score 11793; DB 21; Length 2261;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2259; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACWPOLRLILKNTLERRRRCOLLLEVAWPLFFLLILISVRLSYPEQHECHFPNKA 60
 DB 1 macwpqrlililwknltfrrtqcoqllleavwplffllilivrlsypryqhechfpka 60
 QY 61 MPASAGTLPMVQGIICNANNPCFRYPTEGPAPGVGNFNKSIYARLFSDARLLLYSQKDT 120
 DB 61 mpaagtlpmvqgiicnaannpcfryptegpapgvgvgnfnksiyarlfdsarlllysqdlt 120
 QY 121 SMQDMKRVLRTOLOIKKSSSNLKIDFLVDNETFSGFLYHNLSTPKSVVDKMLRADVILH 180
 DB 121 smrdmkrvrltloiksssnlkldflvdnetfsgfllyhnlstpkstvdkmllradvllh 180
 QY 181 KVFLOGYQLHLTSLCNGSSSEEMTQLGDQVSELGCLPEKELAAERVLRSNMDILKPDIL 240
 DB 181 kvflgqyqlhltslcnsgsseemtlqldqvselcglppeklaaervlrsnmdllkpll 240
 QY 241 RTLNSTSPFSPSKLAERATKTLHLSTGLTQAEFLFSKMSNMDQVWFLTNVSSSSROI 300
 DB 241 rtlnstspfskelaatklhlstgltaqelfsmrswsdmrqewmfltnvssssscql 300

QY 301 YQAVSRIVCGHPGCGGLIKSLMWYEDNNV KALFGSGNGTEEDAETFYDNSTPYCNDLAK 360
 DB 301 yqavsrivcghpgcgglkkslmwyednnvkalfgsgngteedaetfynstpycndlmk 360
 QY 361 NLESSPLSRIIMKALPKLILVGLTPDPATROVAEYNNKTFQELAVHDEGMIBELS 420
 DB 361 nlessplsriimkalkplilvgltpdpatrovaeynnktfqlavhdegmibels 420
 QY 421 PKITFENSGEMDLVWMLDSDRDNHFWQOQDGLMDIADIVAFIAKHPEDVSSNCS 480
 DB 421 pkitfensgemdlvwmldsdrdnhfwqoqdgldmadiavafiakhpedsnscs 480
 QY 481 VYTWREAFENNOAIRTSRMECVNLNKLDEPIATEFWMLNKSMDLDRKRWAGIVFTG 540
 DB 481 vytwreafennoairtsrmevcvnlknkldepiatefwmlnksmdldrkrwagivftg 540
 QY 541 ITPGSELPHHVKYKIRMDIDNVERTNKKIKDGTWDEPRADPEEDMKRYWGGFAYIQDVV 600
 DB 541 itpgselphhvkylrmdidnvertnkkikdgtwdepradpedmkrywggfayiqdvv 600
 QY 601 EQATIRVLTGTEKKTGYVMQOMPVCYVDIPLKWSRSMPLFMTLAMIYSVAIIKGIIV 660
 DB 601 eqatirvltgtekktyvmqompcyvdipflkwsrsmplfmtlamisvaviikgiiv 660
 QY 661 YEKEARLKEFRIMGLDINSILMFSPISSLIPLVLSAGLLVILKLGMLLPSDPSVFEV 720
 DB 661 yekearlkefrimgldinsilmfspiisslplvlsagllvilklgmlpsdpsvfev 720
 QY 721 FLISPAVNTLQCGFLISFLSBRANLAAACGIIYFTLYLRYVLCVAMODVGTGTLKIFAS 780
 DB 721 flispaavntlqcgflisflsbranalaaacgiiyftlylryvlcvaodvgtgtlkifas 780
 QY 781 ILSPVAFGCEGYFALFEQOGIGVOMDLFESPEEDGFNLTSISMALDFTLGYGMTW 840
 DB 781 ilspvafgegyfalfeqogigvomdlfespeedgfnltsismaldftlgygmw 840
 QY 841 YIEAVFPQGYCIPRPWYPCPKTSYWFGESEDEKSHPSGNOKMSEGTMEEPNHLKIGVS 900
 DB 841 yieavfpqgyciprpwypcktsywfgeesekshpsngnkselmeepnhlkigvs 900
 QY 901 IONLVKYNVDGKAVAVDGLALNFYCGITSPFLGNNGAKTTNLSILGPRPTSGTAYIL 960
 DB 901 ionlvkynvdgkavavdglalnfyctspflgnngaktttnlsilgprptsgtayil 960
 QY 961 GMDISEMSTIRONLGVCFQHNVLFDMLTVEEHIMFYARLKGISEKHVKAEMQALDVG 1020
 DB 961 gmdisemstironlgvcfqnvlfdmltveehimfyarlkgisekhvkaemqaldvg 1020
 QY 1021 LPSSKILSKTSQLSGGMOKRISVALAPVGSKVYLDEPTAGVDPYSRSGIMELLKTRQ 1080
 DB 1021 lpskilsksqslsggmqrksvalapvgskvyldeptagvdpysrrgimellktrq 1080
 QY 1081 GRITILSTHMDADVLGRIKILISHGKLCVGSGLFLKNOLGUYTYTLKKRVESLS 1140
 DB 1081 gritilsthmdadvlgrililshgklcvgsllflknolguytytlkkrvessls 1140
 QY 1141 SCRNSSFTVSYLKKEDSVQSSSDAGLGSDBHESDPLTIDVSAISNLRKHVSEARLVEDI 1200
 DB 1141 scrnssftvsylkkedsvqsssdaglsdbhesdpltidvsaissnlrkhvsearlvdi 1200
 QY 1201 GHEILTVLPEYAAKESGAFVLFHEIDRLSDLGISYSGISSTLEETFLKAESSGVDAE 1260
 DB 1201 gheiltvlpveyaakesgafvlfheidrlsdlgisysgisseetleelikaessgvdae 1260
 QY 1261 TSPGTLPARNRRAPGDKOSCLRPETDDAAPNOSDIDPESERETDLGMDGSGSYQVK 1320
 DB 1261 tspgtlparnrrapgdksclrpftddaaPNOSDIDPESERETdlsgmdgsgsyqvk 1320
 QY 1321 GWKLTQDFVALLMKRLILARRSRKGFQAVLPAVFCIALVPSLIYPPGKIPSLLEQ 1380
 DB 1321 gwkltdqdfvallmkrlilarrsrkgfqaavlpaVFCIALVPSliYppgkipslleq 1380

```

QY 1381 PMYNBOYTFVSNDAPEDTGLEILNALTKDGGFGRCEMGNPDPDTCQAGEEFTTAP 1440
    |||||||
Db 1381 pmynboeytfvsnadapedgtleilnaltkdpgfgrcmegnplpdpdcqageewttap 1440
QY 1441 VPQTIMDLFQNGNMTWQNPSPACQSSDKTKKMLPVCPPGAGGLPPPKONTADIIQDL 1500
    |||||||
Db 1441 vpqtimdlfqngnwmtnpnpacqscsdskikmlpvcppgagglppprkqntad119dl 1500
QY 1501 TGNISDYLKTYVQVLIASLNKKIWNVEFRYGGFSLGCVSTQALPPSQEVNDAIKOMK 1560
    |||||||
Db 1501 tgnisdylvktyvqliaslnkklwvnefrgygfslgvstqalppsqevndaikqmkk 1560
QY 1561 HLEKADSSADREFLNSLGFMTGLDTRNNVKKWENKNGMHAISSEPLANTINALLRANLQK 1620
    |||||||
Db 1561 hlekadsadrflnslgrfmgldtrnnvkwfnkgnhaissflnlnaallranlqk 1620
QY 1621 GENPSHYGTATNHPNLNLTKQOLSEVALMTTSVDVLVSTCVIFAMSEVPASFEVLEIQR 1680
    |||||||
Db 1621 genpshtygtatnbpnlntkqglevalmttsvdvlvsicvifamsfvpasfvlqer 1680
QY 1681 VSKAKHLDFISGVKPVYIWNLFNFWDMCNVYPATVYIIFPCROKSYSSSTMLPYLAL 1740
    |||||||
Db 1681 vskakhldfisgvkpvylwnlfndmcyvypatvyliflfcqkqsyssstmlpylal 1740
QY 1741 LLLLGKSTPLPMPASVFEKIPSTAYVVLTSVNLFIGINGSVATFVLELFTDNKLNIN 1800
    |||||||
Db 1741 llllygwstplmpasvfevipstayvvltsvnlfigingsvatfvlftdnklnin 1800
QY 1801 DILKSVFLIFPHFCGLRCLIMVKNQAMADALEEFGENRPPSPLSMVLVGRNLFANAEG 1860
    |||||||
Db 1801 dilksvflifphfcglrclimvknqamadalerrgenrppslswlvgvnlfnaveg 1860
QY 1861 VVEFLITVLQYREFIRPVPNAKLSPINDEDEVRERORILDDGGGONILEIKELTKI 1920
    |||||||
Db 1861 vveflitvlyqreffirpvnaklsplndedevrercrildgggndileikeltki 1920
QY 1921 YRRKKRPVDRICGIRPGEFGILGVNAGKSSFTMLTGDPTVTRGDAFLNKNSTLSN 1980
    |||||||
Db 1921 yrrkkrpvdricvripgecfigilgvnagkssftmldgdtvtvtrgdaflnknslsn 1980
QY 1981 IHEVHONNGYCPQPDATTELTLTGREHEFPALLRGVEKFWGVGEMATIKGLVYVYGRK 2040
    |||||||
Db 1981 ihevgnmgycpqdatteltelltgrehefiallrgvpekevvgvematikglvlyvgrk 2040
QY 2041 YAGNYSNGNKKKLTAMALLGGPPVFLDEPTTGMDPKARRLMNCALSVYKGRSVLT 2100
    |||||||
Db 2041 yagnysgnkrlstamallgppvfldepttgmdpkarrlwmncalsvykegrsvlt 2100
QY 2101 SHSMECEALCTMAIWNNGRFCTLSVOHLKRRFGGYTIIVRIGSNPDLKPVQDDFG 2160
    |||||||
Db 2101 shmecealctmaiwngnrfctlsvohlkrrfggytliivrtlagnpdlkpvqddfg 2160
QY 2161 LAFPGSVLKEKHNMLQYQLPSSLSLARLFTLSQSKRRLHLEDVSQSQTLDQVFNF 2220
    |||||||
Db 2161 lafpgsvlkekhnmlyqqlpslsarlftlsqskrrlhledysvsqtlldqvfynf 2220
QY 2221 AKDOSDDHKLKLSLKHNOTVYVAVLTSFLQDEKESYV 2261
    |||||||
Db 2221 akdosddhklklslnknotvavavltslqdekvesyv 2261

```

```

KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KM atherosclerosis; cholesterol transport.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 597
FT /note= "this is changed from Glu to Arg in Tangler
PN disease"
PN W0200078972-42.
XX
XX 28-DEC-2000.
XX
XX 16-JUN-2000; 2000WO-US16765.
XX
XX 18-JUN-1999; 99US-0140264.
XX 14-SEP-1999; 99US-0153872.
XX 19-NOV-1999; 99US-0166573.
XX
XX (CVTH-) CV THERAPEUTICS INC.
XX
XX Lawn RM, Wade D, Garvin M;
XX WPI, 2001-137812/14.
XX
PI Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PI useful for the development of agents for the treatment of heart disease
PI and other disorders associated with hypercholesterolemia and
PI atherosclerosis -
PS
PS Example 5, page 154-169; 215pp; English.
CC
CC The present sequence represents a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC a Tangler disease patient. ABC1 resides in cell membranes and utilises
CC ATP hydrolysis to transport a wide variety of substrates across the
CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC Tangler disease, a genetic disorder characterised by abnormal
CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC 9q22-9q31. The ABC1 genes and proteins are useful for developing
CC pharmaceutical agents for the treatment of heart disease and other
CC disorders associated with hypercholesterolemia and atherosclerosis. The
CC genes are useful for developing screening assays to screen for compounds
CC that regulate the expression of genes associated with cholesterol
CC transport. The genes and proteins are also useful for are also useful
CC as diagnostic indicators of cardiovascular disease and other disorders
CC associated with hypercholesterolemia.
CC
SQ Sequence 2261 AA;

```

Query Match 100.0%; Score 11793; DB 22; Length 2261;
 best Local Similarity 100.0%; Pred. No. 0;
 Matches 2260; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MACPCPOLRLILMKNLFFRRORCOULLFVAMPLEFILLISVRLSPYEDGHECFPKA 60
    |||||||
Db 1 macpcqtrillmwknlffrrqcoqillvawplifillivrlslypyeqhechfpka 60
QY 61 MPSAGTLPWVOGICINANNPCFRYPPTPGAPGVGNFNKSTIVARLFSPARLLYSOKDT 120
    |||||||
Db 61 mpsagtlpwwvgicinnanpcfrypptpgapgvgnfnkstivarlfsparrllysqdct 120
QY 121 SMKDMRKVLRTIQQIKKSSSNLKLODFLVNETSGFLYHNLSPKSTVDMKLRADYILH 180
    |||||||
Db 121 smkdmrkvlrtlqqikksnlnklqdfivnetfsgflyhnlspkstvdmkmlradvylh 180
QY 181 KYFLOGYOHLSLNGSKSEEMIOLOGPVESELCGLPKKELAERYLNSNDIYKPIIL 240
    |||||||
Db 181 kvflogyohlslnsgskseemlqlgqvsevlcglpkelaerylnsndiylkpiil 240

```


QY 241 RTLNSTSPSPSKELAEATKTLHSLGTLAQELFSMSRSGDMQOEYFELTNVSSSSSTOI 300
 Db 241 rtlnstspfskselaetkltlslgtlaqelfsmrsgdmrqewfltnvsssstqi 300
 QY 301 YQASRIVCGHPRGCGKIKISLWMDNNYKALFGNGRDEDAEPFYDSTPYCNDLMLK 360
 Db 301 yqasrivcgprggiklkslwmednnykalfgngredeaeltydnstprycndlmlk 360
 QY 361 NLESSPLRIITWKLKPLVGLKILYTPDPATROVAEYNTFOELAVEHDELEGMWELS 420
 Db 361 nlessplriitwklkplvlgkillypdpatriqvaeyntfoelavehdelegmwels 420
 QY 421 PKITFENSGEMDLVMLLDSRDNDHFWEQOJDGLDWTADQVLAFLAKHPREVQSSNS 480
 Db 421 pkitfensgemdlvmlldsrdndhfweqjdgldwtadqvalaflakhpdevqssns 480
 QY 481 VYTRBEAFNEFNQARTISRPMECVNLNKLEPIATEWYMLNKSMELDEREKFMAGIVFEG 540
 Db 481 vytrbeafnefnqartisrpfmecnlnklepiatewmlnksmellderekfmagivfeg 540
 QY 541 ITPSIELPHHVKKYKIRMDIDNERTNKIKQYWDPGPRADPFEDMKRYWNGFAYLQDYY 600
 Db 541 itpsielphhvkkkirkmdidnertnkikdywdpgpradpfedmkrywngfaylrdyv 600
 QY 601 EOAIITVLTGEEKTYGYMOQMPYCYVDIPLRYMSRMPFLMTLAWISVAVIITKGIY 660
 Db 601 eoaivitltgeektgyymoompycyvdiplrmysrmpflmtlawisvaviitkgiy 660
 QY 661 YEKEARKETWRKINGLDNISILFMSFTISLPLLVASGLLVILKGNLTPYSDPSVVEY 720
 Db 661 yekearketwrkingldnislmsftisllpllvasgllvllkgnltpydspsvvef 720
 QY 721 FLVFAVNTILQCELLISTLFSRANLAAACGIIYFTLYLPVLCVANQDYGFTLKIFAS 780
 Db 721 flsvfavntilqcellistlfsranlaaacgiiyftlylpvllcvanqdygftlkifas 780
 QY 781 ILSPAFGECEYALFEEDGIGVOMNLPESPVEEDGFNLTSISMWLDTFLYGMWTM 840
 Db 781 ilspafgeceyalfeegigvqwnlpesvpeedgfnltssismwldtfllygmwtm 840
 QY 841 YLEAVFPGOYGIIPRWYPPCTKSYWFGESDEKSHPGSNOKRMSEICMEEPHTLKIGVS 900
 Db 841 yleavfpgoygiprwyppctksywfgesdekshpgsnqrmseicmeephtlkigvs 900
 QY 901 IONLVYTRDGMKAVAVDGLALNFYEGOTTSPLGHNAGKTTTMSITNGLPPTSCTAYTL 960
 Db 901 ionlvkytrdgmkvavdglalnfyegqitstplghnagakttmsitnglptpsctaytl 960
 QY 961 GKDISEKSTIRONLGYCPOHNVLFDMLTVEEHIMFYARKLGISEKHVKAEMEQMALDVG 1020
 Db 961 gkdisekstironlgycponhvlfdmltveehimfyarklgisekhvkaemeqmaldv 1020
 QY 1021 LPSRSKIKSTSQLSGGMRKLSVALAFVGSKVVILDEPTAGVDPYSRGIIWELLKTYRQ 1080
 Db 1021 lpsrskikstsqlsggmrklsvalafvgskvvildeptagvdpysrgiwellktyrq 1080
 QY 1081 GRTIISTHMHMEADVLDRIATISHGKLCVSGSLFLKNLGGYVTLTKKRVESLS 1140
 Db 1081 grtiisthmmhmedvldriatishgklcvsgslflknlggyvtlkkrvessls 1140
 QY 1141 SCRNSSSTVYLLKEDSVSSQSSDAGLSDEHSDTLTIDVSAISNLTIRKHYSEARLVEDI 1200
 Db 1141 scrnssstvylkedsvssqssdaglsdhesdtltdvasaisnltirkhysearlv 1200
 QY 1201 GHELTIVLPEYAKBGAVELFHEITDDRSLDGLISSYISSETTLEFRLTKAEESSVDAAE 1260
 Db 1201 gheiltivlpeyakbgavelfheitddrslsdglissyissettleftrlkaeesvdae 1260
 QY 1261 TSDGTLPARNRRAFGDKOSCLRPTEDDAADPNDSIDDPESRETDLSGMDGKSYGVK 1320
 Db 1261 tsdgtlparnrtrafgdkosclrpfeeddaadpndsidpsestdllsgmdgksygvk 1320
 QY 1321 GWKLTQOQFVALLMKRLLIARRSRKGFQAQIVLPAVFCIALVSLIYPPGKTIPLSLQ 1380

Db 1321 gwkltdqgfvallwklrliaarrskffagivlpavfvcialvslivppfkgypslslq 1380
 QY 1381 PMMYNEQYTFVSDNADPEDGTLELNAALTKDPEGFCIRMEGNIPIDPTQOAGEEWTAP 1440
 Db 1381 pmyneqytfvsndapedgtlelnaaltkdpgfircmegnripdptqageewt 1440
 QY 1441 VPQITMDLPONGMNTMKNPSPACOCSSDKHKMLPVCPPGAGLPPPOKONTADILDL 1500
 Db 1441 vptitmdlpgngmntmknpspacocssdklkmllpvcppgaglpppoqkntadil 1500
 QY 1501 TGRNIDSYLVKTYVOIITAKSLKNNKIMWNEFRYGFSLGVSNTOALPPSOEVDAIKOMK 1560
 Db 1501 tgrnidsvlvktyvoitakslknnkimwnefrygfslgvsnbqalppsqevdaik 1560
 QY 1561 HLKIAKSSADRFINSIGRMTGLDTRNNKVMFNNKGMHAISSFLANVINNALIRANLQK 1620
 Db 1561 hlkiakssadrflnsigrmtgltrnnkvwmfnkghaissflvnnaliranlqk 1620
 QY 1621 GENSHGITAFNHPNLTKQOOLSEVALMTTSYDVLSICVIFAMSFPVASFVFLQER 1680
 Db 1621 genshgitafnhpnltkqoolsevalmttsydvlsicvifamsfpvafvflqer 1680
 QY 1681 VSKAKHLQFISGVKPVITWLSNFWDMCNVVPATVLIIFICEQOKSYVSTNLPLVAL 1740
 Db 1681 vskakhlqfisgvkpvitwlsnfwdmcnvvpatlviificeqoksyvstnlplval 1740
 QY 1741 LLLLYGWSITPLMTPASVFRKIPSTAVVLTSVNLFGINGSVATVTELFPTNKNLNIN 1800
 Db 1741 llllygwsitplmtpasvfrkipstavvltsvnlfgingsvatvtefptnknlnin 1800
 QY 1801 DILKSVLIFPHFCIGRLIDMVKNOAMADALERFGENREVSPLSMDLVGRNLFAMAVG 1860
 Db 1801 dilksvflfphfcigrldmvrknqamadalerrfgenrvtspslwlvgrnlfama 1860
 QY 1861 VWFLLITVLIOYRFFIRPRVNAKLSPINDEDEYRREKORILDDGQNDILEIKELTKI 1920
 Db 1861 vwffllitvlloyrffirprvnaqlspindeedyrrekorilddgqndileikel 1920
 QY 1921 YRRKKRPVADRICVGIIPGECFGLGVNAGKSGTFMNLGDTVTVRGDAFLKKNSTLSN 1980
 Db 1921 yrrkkrpvadricvgiipgecfglgvnagksgtfmnlgdtvtvrgdafllkknst 1980
 QY 1981 IHEVHQNNGYCPQOPADITELLTGREHEFFALLKGVPEKEVGYEMAIRKLGLVKYGEK 2040
 Db 1981 ihvhnngycpqopaditelltgreheffallkgvpekevgyemairklglvkyg 2040
 QY 2041 YAGNTSGGNKKRLSTAMALIGPPVYFLDEPTGMDKARREFLMNCALSVYKGRSVLFT 2100
 Db 2041 yagntsggnkrlstamaligppvylfdeptgmdkarrflmncalsvykggrsvl 2100
 QY 2101 SHSMECEALCTRNAIMVNGRPRLCGSVQHLKKNFCDGYTTIVRIAGSNPDLKPYODPFG 2160
 Db 2101 shsmecealctrnaimvngprlclgsvqhlkknfcdgyttivriagsnplkpyod 2160
 QY 2161 LAFPGSVLKEKHNNLQYQOLPSSLSLARIFSILSOSKKRHLHEDIVSYQTTLDQVYVF 2220
 Db 2161 lafpgsvlkehnnlqyqolpsslslarifsilsoqkkrhlhedyvsqttldqv 2220
 QY 2221 AKDQSDHDLKDLSTLHKNOTVVDVAVLSPLODEKVKRSYV 2261
 Db 2221 akdqsddhldkdlstlhknotvvdvavlsplodekvkrsyv 2261
 RESULT 5
 AAB31366
 ID AAB31366 standard: Protein: 2261 AA.
 XX AAB31366;
 AC AAB31366;
 XX 20-APR-2001 (first entry)
 DT 20-APR-2001 (first entry)
 XX amino acid sequence of ABC1 polypeptide from Tangier disease patient.
 DE

XX	Human: adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9q22-q31; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport.
XX	Homo sapiens.
XX	Key
XX	Location/Qualifiers
XX	Misc-difference 597
XX	/note= "this is changed from Glu to Arg in Tangier disease"
XX	MO200078971-A2.
XX	28-DEC-2000.
XX	16-JUN-2000; 2000MO-US16591.
XX	18-JUN-1999; 99US-0140264.
XX	14-SEP-1999; 99US-0153872.
XX	19-NOV-1999; 99US-0166573.
XX	(CVTH-) CV THERAPEUTICS INC.
XX	(UNIV) UNIV WASHINGTON.
XX	Lawn RM, Wade D, Oram JF, Garvin M;
XX	WPI; 2001-137811/14.
XX	N-PSDB; AAF24707.
XX	Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis -
XX	Claim 25; Page 150-165; 211pp; English.
XX	The present sequence represents a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide, and is isolated from a Tangier disease patient. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.
XX	Sequence 2261 AA;
XX	Query Match 100.0%; Score 11793; DB 22; Length 2261;
XX	Best Local Similarity 100.0%; Pred. No. 0;
XX	Matches 2260; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX	1 MACWQRLRLMKNTFRRCOTCLLEAYWLFIFLIIISVRLSPYEQHECHFPNKA 60
XX	1 macwqrlrlmkntfrfrrcqtclleaywlfiflilsvrlyspyeqhechfpnka 60
XX	1 MPASATLEPMVOGIIICNANNPCFRYPTEGAPGPGVGNFKNSIYARLFSDARRLLYSQKDT 120
XX	1 mpasatlepmvogiiicnannpcfryppegapgvgnfnksiyarlfdsarrlllysqdkt 120
XX	121 SMKDKRKVLKRLQOIKKSSSNLKLODFVNDNETSGFLYHNLSLPKSTVDDKMLRADVILH 180
XX	121 smkdkrkvlrltqlqksssnlkigdfvndnetsgfilyhnlsipkstvdkmlradvllh 180

Qy	181	KELQGVOLHJLSTLCNCSKSEEMTQUCODEVSELGCPREKILAAERVLRSNMJLAPTL	240
Db	181	Kvlllqyqqlhlsicngsksseemlqdygdevselcgjplekilaaeervlrsnmjllkpll	240
Qy	241	RTLNSTPFPSEKLEAEATKTLHLSJGTTLAQEJFMSKRSNDMHOEWPLTJNVNSSSSQOI	300
Db	241	rltnstspfskelaeatktllhsjgtlaqelfsmrswsdmgewmlltnvnssstqj	300
Qy	301	YQAVSRIVCGHPGGGLKTKSLMTWEDNNYKALFSGNGTEDEDAETFDNSTTPYCNDJLMK	360
Db	301	yqavsrivcghepgggkiklslnwdednnkalfsgngteedaetfydnsttqycondlmk	360
Qy	361	NLESPSLRITMVALPRLVGLKILTPDPAPAROMAVKNTPOELAVFHLDEGMWELS	420
Db	361	nleaspsrlitwvalkprllvgklltprdpaparcymaevnktfelavfhldegmwels	420
Qy	421	PKIWTPEWNSOEMDLVRMLLSDRDNHFEQOJDLGJMTAODIYAFLAKHPEDVOSNGS	480
Db	421	pkIwtPewnsqemdlvrmllsdrdnhfeqjldglwtaqdiavafIakhpedsngs	480
Qy	481	VYTMREAFENETNOAJRTISRFECECNLMLKEPIATEWYLKMSHELLDEKRPAGIYFTG	540
Db	481	vytmreafeetngaiftlstrfimecynlmlkepiaevyllkmselldekrpagiylftg	540
Qy	541	ITPGSITELPHHVKYKIRMDIDNVERTNKIKDGYMDPGRADPEFDMRWYGCFAIYLDYV	600
Db	541	ltpgsitelphvkylrmdidvertnkikdgydpdpradpedefdmrwygcfaiylrdyv	600
Qy	601	EOALHVLNLTGTEKKTKGYVMQMPHYCYDOLFVLKRSKMLPMTLAMIYSAVVIITKGIY	660
Db	601	eqalhlvlnltgtekktgyvmqmpyacyddolfvlrsmrsmplmtlamiysavvillkgitv	660
Qy	661	YEKEARLEKTRKMGIDNSIMFSEWISSLPPLVYSGLLVILIKIGNLLPYSDPSVAVY	720
Db	661	yekearleketrimgidnsimfwisssllpplvysgllvllikignllpydspsvavt	720
Qy	721	FLTSVAVVYIIIOCFILSTLFSRANLAAACGGIYFTLYLPVLCVAMODYGFTLKIFAS	780
Db	721	fltsvavvylilicflstlfsrnlaaaaggilyftlylpvlylcvamodygftlkifas	780
Qy	781	LJSPAFGCGEYEFALFEEOGIGVOMNLFESPVEEDGFNLUTSISIMLFDPIFVGMWU	840
Db	781	ljspafgfcgeyefalfeegdygvomnlfespeedgfnlltsisimlfdclfygmwku	840
Qy	841	YIEANFPGQYGIIPRPWTFPCTKSTWCESEDESKSHPSNOKRMSLCEMEEPETHLKGS	900
Db	841	yieanfpgqygiiprpwtfpctksywfceesedekshpsnokrmslcmeeepethlkgs	900
Qy	901	IQNTLVKVRDDCMKAVNOGLANFEYEGITFSLHNGAGTTMSILTGLFPTSTAYIL	960
Db	901	iqnltkvyrddcmkavnglalnfyegitfslhmgagktlmsiltglfptstayil	960
Qy	961	GKDIRSEKSTIRONLGYCPOHNVLFDMLVYEEHIMPYARLKGISEKHVAKMEQJALDVG	1020
Db	961	gkdirsemstlrqnlgycpohnvlfdmlyeehiwfyarlkglsekhvakemeqjalvg	1020
Qy	1021	LPSSEKTSKTSQSLSGMGORLSVALAFVSGSKVILIDETPAGVDYXSRGIMWELLAKRQ	1080
Db	1021	lpssktsktsqslsgmqrlsvalafvsgskvllidpetagvdyxsrgrimwellkryq	1080
Qy	1081	GRTIILSTHMHDEADVGDJIALIISGKILCCGVSSLFLNQJGTGYTLVLVKPDVESTLS	1140
Db	1081	grtillsthhmdeadvgdjialisgkllccgvsslflnqjgtgytlvlvkpdvestls	1140
Qy	1141	SCRSSSTSVYLLKKEBVSQSSSDAGLSDHESDTLTJDVSAISMLIRKHVSEARLYEDI	1200
Db	1141	scrssstsvyllkkesvsgsssdaglsghesdcltjdvasaismlirkhvsearlyedi	1200
Qy	1201	GHELTLYVPEAKECAPFELFIEIDDRJSDJISYSGISETTLIEFTFLKAAESSGDAL	1260
Db	1201	gheltlyvpeakegafvelfheidrtisdjissysisettleeftlkaeessgdal	1260

QY 1261 TSDSTLPARRRRRAFGDKOSCLRPTEDDADPNDSIDIPESHREPTLLSGMDKGSYQVK 1320
 DB 1261 tsdgtlparrrrra fgdkgsc lrpftedda dndsid ipeshreptllsgm dkgsgsyqvk 1320
 QY 1321 GWKLTQOOFVALLMKRLILRRSRKGFPAQIVLPAVFVCIALVFSLVPEFGKPSLEIQ 1380
 DB 1321 gwkl tqoofv allmkrl ilrrsrkg fpaqiv lpa vfvci alv fslv pefgkpsleiq 1380
 QY 1361 PMWTNEQTYVSNAPEDTGTLELNLATDPDPCGRMCNGNITPOTPOAGEEWTAP 1440
 DB 1361 pmwtn eqtyv snapedt gtleln latdpdpcgrmcngn itp ot poage ewtap 1440
 QY 1441 VPOTIMDFONGNMTQNPSPACCCSDSKIKKMLPVCPPGAGLPPORRONTADILQDL 1500
 DB 1441 vpotimdf ong nmtqnp spaccs dskik kmlpvc ppgag lppor rontad ilqdl 1500
 QY 1501 TGRNIDYLVKTYVOIILAKSLKNKIWNERRYGGFSLGVSNTQALPPSOVNAIQQMK 1560
 DB 1501 tgrnid ylvk tyvo iilak slkn kiwn erry ggsf slgvs ntqal pps o vna iqqmk 1560
 QY 1561 HLKTLAKOSSADRLNSLGRFMTGLDTRNNYKVMFNKNGWHAISSEFLVNNALIRANKOK 1620
 DB 1561 hlktlak ossadrl nslgrf mtgl dtrnn ykvm fnkng wha isse flvnn alir ank ok 1620
 QY 1621 GENPSHYGITAFNHPNLNLTKOOLSEVALMTTSDVLVSLCIVIFAMSFVPASFVFLIOER 1680
 DB 1621 genpshygitaf nhpnl nltkool seval mtt s dvlv slc ivi famsfvp asfv flioer 1680
 QY 1681 VSKAKHLOFISGVKRYVYWLNSFNFWDMKNYVVPATVITITIFICQOKSYSTRTPLAL 1740
 DB 1681 vskakh lof isgvk ryv ywl nsfnfw dmkn yvvp atvit itif icqok systrt plal 1740
 QY 1741 LLLYGMSTPLMYPASVVFRIPTAYVLTVMLEFGINGSVATFVLELFTDKLNIN 1800
 DB 1741 lll ygmstplm ypasv vfr ipta yvlt vmle fgings vatf vlelft dkl nin 1800
 QY 1801 DILKSVFLIEPHFCGLGRLIDMKYKQAMADALERGENRFPSPISMDLYGNINLFAMAVEG 1860
 DB 1801 dilksv flieph fcglgr lidmk ykq amadal ergen rfp spis mdlygn inlf amaveg 1860
 QY 1861 VVEFLITVLIQYRFRIRPPVNAKLSPLNDEDEDEVRERQRILIDGGGNDILEIKELTKI 1920
 DB 1861 vveflitv liqy rfrir ppvna klspln dede dvrer qril idggg ndilei keltki 1920
 QY 1921 YRRRRKPAVDRIQVIGPECEFGLLGVNGAKSSFFKMLTGDYTYTRDADALNNKSLISN 1980
 DB 1921 yrrrrk pavidri qv igpece fgllgv ngakss ffkml tgd ytytr dadal nnksl is n 1980
 QY 1981 IHEVHONMGYCPQFOAITEFLTGREHVEFFALLRGVPEKEGKVGEMAIRKILGVKYEK 2040
 DB 1981 ihev honmg ycpqfoa ite fltgre hveff allrgv pekeg kvgem airkilgvkyek 2040
 QY 2041 YAGNSGNGNRKRLSTAMALIGSPVVEFLDEPTTGMDPKARFLMNCALSVYKEGSRVLT 2100
 DB 2041 yagngs ngnrkrl stamal igspv veflde pttgmd pkarfl mncal svykegsrvlt 2100
 QY 2101 SHMECEALCTFMAIMWGRFRICSGYOHKLNRRGDGTYTVIRAGSNPDLKPVQDEFG 2160
 DB 2101 shmece alctfma imwgr fricsg yohk lnrrgd gtytv irag snpdlkpv qde ffg 2160
 QY 2161 LAEPGSVLKEKHHNMLOYOLPSSLSLARIFFSLISQSKRLHIEDYSVSQTTLDGVFVNF 2220
 DB 2161 laepgs vlkek hhnml o yolp ss sls lariff slis qskrl hiedys vsqttldgv fvnf 2220
 QY 2221 AKDOSDDHLKJLSLHKNOTVADVAVLTSFLQDEKKESEYV 2261
 DB 2221 akd osddhlk jlsl hkn otvadv avlts flqde kkeseyv 2261

RESULT 6
 AAB38109
 ID AAB38109 standard; Protein; 2261 AA.
 XX

AC AAB38109;
 XX 29-JAN-2001 (first entry)
 DT Human ABC1 cholesterol transporter mutant, R219K.
 XX
 DE Human ABC1 cholesterol transporter mutant, R219K.
 XX
 KW Human ABC1 cholesterol transporter; chromosome 9q31;
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
 KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
 KW cardiovascular disease; coronary artery disease; coronary restenosis;
 KW cerebrovascular disease; peripheral vascular disease;
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
 KW prognosis; prophylaxis; drug screening; transgenic animal; mutant;
 KW muten.
 KW
 OS Homo sapiens.
 XX
 PN WO200055318-A2.
 XX
 PD 21-SEP-2000.
 XX
 PE 15-MAR-2000; 2000WO-1B00532.
 XX
 PR 15-MAR-1999; 99US-0124702.
 PR 08-JUN-1999; 99US-0138048.
 PR 17-JUN-1999; 99US-0139600.
 PR 01-SEP-1999; 99US-0151977.
 XX
 PA (UYBR-) UNITI BRITISH COLUMBIA.
 PA (XENO-) XENON BIORESEARCH INC.
 PI Hayden MR, Wilson AR, Plimstone SN;
 DR WPI, 2000-587528/55.
 XX
 PT New ABC1 polypeptide is useful for treating diseases associated with
 PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
 PT disease and cancer -
 XX
 PS Examples; Page --: 229pp; English.
 XX
 CC The invention relates to the human ABC1 cholesterol transporter protein
 CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
 CC a member of the ATP-binding cassette (ABC transporter) superfamily of
 CC proteins, and plays a crucial role in cholesterol transport, particularly
 CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
 CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
 CC located on chromosome 9q31, and mutations in this gene are associated
 CC with two genetic HDL (high density lipoprotein) deficiency disorders,
 CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
 CC are distinguishable in that TD is an autosomal recessive disorder, while
 CC FFA is inherited as an autosomal dominant trait. Low levels of HDL ("good
 CC cholesterol") in the blood correlate with a high risk of cardiovascular
 CC disease, particularly coronary artery disease, but also cerebrovascular
 CC disease, coronary restenosis, and peripheral vascular disease.
 CC Conversely, a high level of HDL has protective effects against
 CC cardiovascular disease. The invention provides genetic constructs and
 CC transgenic cells and non-human animals comprising human ABC1 nucleic
 CC acids, and methods of gene therapy for the treatment or prevention of
 CC cardiovascular disease comprising the administration of an expression
 CC vector encoding ABC1 or an active fragment thereof. The invention also
 CC encompasses compounds which mimic ABC1 activity, compounds which
 CC stimulate ABC1 expression and methods of screening for such compounds.
 CC It further relates to methods for determining whether a patient has an
 CC increased risk for cardiovascular disease due to polymorphisms in the
 CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
 CC or prevent cardiovascular disease, especially coronary artery disease,
 CC cerebrovascular disease, coronary restenosis or peripheral vascular
 CC disease. They may also be used in the treatment of diseases associated
 CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
 CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
 CC The invention specifically excludes proteins with the exact amino acid

CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
 CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The
 CC present sequence represents a mutant human ABC1 cholesterol transporter
 CC associated with an altered cholesterol level and therefore an altered
 CC risk of cardiovascular disease.
 CC Note: The present sequence is not shown in the specification, but is
 CC derived from the native human ABC1 shown on pages 152-157.
 XX
 SQ Sequence 2261 AA:

Query Match 100.0%; Score 11792; DB 21; Length 2261;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2259; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACMPQLRLMLKNTLERRRQTCOLLLEVAWPLFILLISVRLSTPPEQHECHPDKA 60
 Db 1 macmpqlrlmlkntlerrrqtcolleavawplfllllsvrlstpyeqhechfpnka 60
 QY 61 MRSAGTLPWVGITICANNPCFRPTPGAPGVGNFNKSIYARLFSDARRLLTSOKDT 120
 Db 61 mrsagtlpwvgiticanpccfrptpggapgvgnfnksiyarlfsdarrlltysqadt 120
 QY 121 SMKDMKRYRTLOQIKSSSNKLQDFLVNTEFSGFLYHNLSPKSTVDKMLRADVTLH 180
 Db 121 smkdmkrvrtloqiksssnklqdflvntefsgflyhnlspkstvdkmrlradvllh 180
 QY 181 KVFLOGYQLHLTSLNGSKSEEMIOLEDOEVELGCLPREKLAARLRLSMDLTKRTL 240
 Db 181 kvflogyqlhltslsgskseemioledevelgclpreklaarlrslsmdltkrtl 240
 QY 241 RLNSTSPPEPKELAEARKTLHLSTGLTAADELFSMRSDMKQOEYMLTLNVSSTSTOI 300
 Db 241 rlNSTSPPEPKelaarktlhlstgltaaDELFSmrSDmkQOEYmLTlnVSSSTSTOI 300
 QY 301 YQAVSRICGHEGSGGLTKISLWYEDNNYKALFGNGTEEDAEHYDNSTTPYCNDLMK 360
 Db 301 yqavsrivcghegggltkislwYedNNyKAlFGngTEedAEHyDNstTPYcndLMk 360
 QY 361 NLESPLSRITIKALKPLLVGKIILYPTDPATROVMAEVNKTFOELVFHDLSEMEELS 420
 Db 361 nlesplsrItIKAlKPLLVGKIILyPTDPATROVMAEVNktFOElVFHdlSEMEELS 420
 QY 421 PKITFMENSOEMDLVRMLDSDRNDHPWEOGLDGLDWTADIVAFIAKAPEDVOSSNGS 480
 Db 421 pkItfMENsgemdlVRMLdsDRNDHPWEOGLDGLDWTADIVAFIAkAPEDVOSSngs 480
 QY 481 VYTWREAPNETNOAIRTSRFMECVNLKLEPIATEVWLINKSMELDERKFNAGIYFTG 540
 Db 481 vytwreaPnetNOAIRtsRFMEcvNLKLEPIATEVWLInKSMELdeRKfNAGIyftG 540
 QY 541 ITPGSIELPHHVKKIKRMDIDNVERTKIKDGVWDEPRADPEDMKRYVWGFAVLDVV 600
 Db 541 ItpgsIElPHHVKKIKrMDIDNVERTKIKDGVWDEPRADPEdMKRYVWGfAVLDVV 600
 QY 601 EQAIRVLSTGTEKKTGYVMOOMPVCYVDDIFLRVMSRSMPLFMPTLAWISVAVITKGY 660
 Db 601 eQAIrVLstGTEKktGYVMOOMPVCYVDDIFLRvMSRSMPLFMPTLAWISvAVITkGY 660
 QY 661 YEKEARLKEKRMIMGIDNSTLMSWFTSSILPLVSAGLLVLLKLGNTLPSVSDPSVTV 720
 Db 661 yeKEARlKEKRMIMGIDNSTlMSWFTSSILPlVSAgLLVLLKLGNTLPSVSDPSvTV 720
 QY 721 FLTSVFAVVTILOGLISTLFSRANLAAAGGIYFLLYLYLVLCVAMQOXYGFTLKTFRS 780
 Db 721 fltsVFAVvtILOGLISTlFSRANLAAAGGIYfLLYLYLVlLCVAMQOXYGfTLKtFRS 780
 QY 781 LLSPVAFGCGCEYFALFEEOGIGVOMDNLFESPVEEDGNLTSTISMMFLDFELGVMTM 840
 Db 781 llsPVAFGCGCEyFAlFEEOGIgVOMDNLFESpVEEDGNLTstISMMfLDFELGVmtM 840
 QY 841 YLEAVPGCYGIRPWPYFCCTSYMGERSDEKSHPGSKQKMSLCEMEEPETHLKCVS 900
 Db 841 yLeAVPGCYgIRPWPYfCCTSYMGERSDEKshPGSKQKMSLCEMEEPETHlkCVs 900

Db 841 yLeavfpgqyGIRPWPYfPctksYwfgEesdeKshpgsnqkrIseIcmeepethlkIcYs 900
 QY 901 IONLVKYYRDGKAVVDGALNFEYEGOTTSLGHNAGAKTTMTSLTGLFPPTSGTAYIL 960
 Db 901 IOnLVKYYrDGkAVVDGAlNFEYEGOTTsLGhNAGAKTTMTsLTLGLFPPTSGtAYIl 960
 QY 961 GKDIRESEKSTIRONLGYVCPQHNVLFDMLTVEEHIMFWYARLKLSEKHYKVAEMQALDVG 1020
 Db 961 gKdIResEKstIRONlGYVcPQHnVLFdMLtVEEHImFWYARlKLSEkHYKvAEmqALdVg 1020
 QY 1021 LPSSKLKSTQSOLSGMOKRISVALAPYGSKVYILDEPPIAGVDYPRRGITWELLKYRQ 1080
 Db 1021 lPssKLkSTQSOLSGMOKRISvAlAPYGSKVYILDEpPIAGVDYPRRGITWELLkYrQ 1080
 QY 1081 GRTIILSTHMDADVLDGRIATISHKLCCVSSLELKNOLGXYLLTVKKDYESLS 1140
 Db 1081 gRTIILstHMDAdvLDGRIATIShKLCCvSSLElKNOLGXYLLtVKKDyESLS 1140
 QY 1141 SCRRSSSTVSTLKKEDSVSOSSSDAGLSDHESDTLTIDVSAISNLRKHVSEARLVEDI 1200
 Db 1141 sCRSSStVstLKKEDSVsOSSSDAGlSDHESDTLTIDvSAISnLRKhVSEARlVEdI 1200
 QY 1201 GHEFTYVLYPEAAKEGAFVELFHEIDRLSDLGISSTGSETTLEELFLKVAEESGVDAE 1260
 Db 1201 gHEfTYVLYPeAAKEGAFvELFHEIDrLSDLGISStGSETTLEElFLKvAEESGVdAE 1260
 QY 1261 TSQGTLPARRNRRAFGDKQSCLRPTEDAADPNDSIDPESREPTDLSGMDCKSGSYOK 1320
 Db 1261 tSQGTLPArRNRRAfGDKQsCLRPTEDAADPNdSIDPeSREPTDLSGMdCKSGSYOK 1320
 QY 1321 GWKLTQOQFALLMKRLRLIARRSRKGFPAQIYLPANFVCIALVSLVPPFGKYPSELDQ 1380
 Db 1321 gWkLTQOqFAlLMKRLRLIARSRKGFPAQIYLPANfVCIAlVSLVPPfGKYpSEldQ 1380
 QY 1381 PMWYNQDYTFVNSDAPEDGTLELNALFKDPGFGRCWGNPDPPTPOQAEEMETAP 1440
 Db 1381 pMWYNQDYTFvNSDAPEDGTleLNaLFKDPGFGRCWGNpDPPTPOQAEEmETAP 1440
 QY 1441 VPQTIMDLQONGWIMQNSPACQSSDKIKKMLPVCPPGAGLPPPOKKOTADILDL 1500
 Db 1441 vPQTimdlQONGwIMQNSPACQSSDKIKmLPVCPPGAGLPPPOKKOTADIlDL 1500
 QY 1501 TGRNISDYLVKTYVQIITIASLKNKILWVNEFRGFGSLGVSNNQALPQOEVDALIKOKK 1560
 Db 1501 tGRNISdyLVkTYVQIITIASlKNKILWvNEFRGFGSLGVSnnQALPQOEVDAlIKOKk 1560
 QY 1561 HLKLAQSSADRLNSLGRFMTGLDTRNNVYKWFENKGMHAISFLVYINNAILRANLQK 1620
 Db 1561 hLKLAQSSADrLNSLGRfMTGLDTRNNVYKwFENKGMHAISfLVYINnaILRANlQK 1620
 QY 1621 GENPSHYGTTAFNHNPLNLTKOQLSVALMTTSVDVLSICYIFAMSPVPASFVFLIOER 1680
 Db 1621 gENPSHYGTTAFnHNPLNLTKOQLSvAlMTTSVDVLSICYIFAMSPVPASFVfLIOER 1680
 QY 1681 VSKAHLOFISGVKPVYIWLSNFWDMCNVYVPATLVYIIFICQOQKSYSTMLPYLAL 1740
 Db 1681 vSKAHLOfISGVKpVYIwLSNfWDMCNVYVPATLVYIIFICQOQKSYSTmLPYlAl 1740
 QY 1741 LLLYGSITPLMYPASVFKIPSTAYVLTSLVLFICINGSVATFVLELFTDKLNIN 1800
 Db 1741 lLLYGSITPlMYPASvFKIPSTAYVLTslVLFICINGSvATFVLElFTDKlNIN 1800
 QY 1801 DILKSVFLIPHFCLGRLLDMVKNQAMADALEFGENRRFSPISMPLVGRNLFAMAVEG 1860
 Db 1801 dILKSVfLIPHFCLGRllDMVKNQAMADAlEFGENRRfSPISMPLVGRNLfAMAVEg 1860
 QY 1861 VVEFLITVLIORYRFFIRPRYNAKLSPLNDEDEDVRRERORILIDGGQNDILEIKELTKI 1920
 Db 1861 vVEFLITVLIORyRFFIRPRYnAKLSPlnDEDEDVRRERORIlIDGGQNDIlEIkELTKI 1920
 QY 1921 YRRRRKPAVNRICGIRPGECFGLGVNAGKSTFEMLTGDTTYRGAFLKNSILSN 1980
 Db 1921 yRRRRKPAVnRICGIRPGECfGLGVNAGKSTfEMLTGDTTYRGAfLKNSIlSN 1980

QY 1981 IHEVHONMGYCPQFIDAITELLTGREHVEFPALLRGVPEKEVGKVGEMAIRKLGIVKGEK 2040
 DB 1981 IHEVHONMGYCPQFIDAITELLTGREHVEFPALLRGVPEKEVGKVGEMAIRKLGIVKGEK 2040
 QY 2041 YAGNYSGNGNRKRLSTMTALIGGPPVFLDEPTGMDPKARFLMNCALSVYKEGSRVLT 2100
 DB 2041 YAGNYSGNGNRKRLSTMTALIGGPPVFLDEPTGMDPKARFLMNCALSVYKEGSRVLT 2100
 QY 2101 SHSMECEALCTMAIMWGRFECGVSOLKLRNREDGTTIVYRAGSNPDLKPYQDFEG 2160
 DB 2101 SHSMECEALCTMAIMWGRFECGVSOLKLRNREDGTTIVYRAGSNPDLKPYQDFEG 2160
 QY 2161 LAPPGSVLKEKHNMLQYOLPSSLSLARIFSLISQSKRLHIEDYVSQTTLDQVFNF 2220
 DB 2161 LAPPGSVLKEKHNMLQYOLPSSLSLARIFSLISQSKRLHIEDYVSQTTLDQVFNF 2220
 QY 2221 AKDQSDDDHLKDLSLKRNQTVDAVLTSLFLODEKYEKSYV 2261
 DB 2221 AKDQSDDDHLKDLSLKRNQTVDAVLTSLFLODEKYEKSYV 2261

RESULT 7
 AAB38082 standard; Protein; 2261 AA.
 AAB38082:
 29-JAN-2001 (first entry)
 Human ABC1 cholesterol transporter.

Human ABC1 cholesterol transporter; chromosome 9q31;
 ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
 Tangier disease; TD; familial HDL deficiency; FHD; polymorphism;
 cardiovascular disease; coronary artery disease; coronary restenosis;
 cerebrovascular disease; peripheral vascular disease;
 Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
 X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
 prognosis; prophylaxis; drug screening; transgenic animal.

Homo sapiens.
 WO200055318-A2.
 21-SEP-2000.
 15-MAR-2000; 2000WO-IB00532.
 15-MAR-1999; 99US-0124702.
 08-JUN-1999; 99US-0138048.
 17-JUN-1999; 99US-0139600.
 01-SEP-1999; 99US-0151977.
 (UYBR-) UNIV BRITISH COLUMBIA.
 (XENO-) XENON BIORESEARCH INC.
 Hayden MR, Wilson AR, Pimstone SN;
 MPI: 2000-587528/55.
 N-PSDB: AAC69120.
 New ABC1 polypeptide is useful for treating diseases associated with
 ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
 disease and cancer -
 Claim 5; Page 152-157; 229pp; English.

The invention relates to the human ABC1 cholesterol transporter protein
 (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
 a member of the ATP-binding cassette (ABC transporter) superfamily of
 proteins, and plays a crucial role in cholesterol transport, particularly
 intracellular cholesterol trafficking in monocytes and fibroblasts, being

involved in cholesterol efflux from the cell. The gene encoding ABC1 is
 located on chromosome 9q31, and mutations in this gene are associated
 with two genetic HDL (high density lipoprotein) deficiency disorders,
 Tangier disease (TD) and familial HDL deficiency (FHD). These diseases
 are distinguishable in that TD is an autosomal recessive disorder, while
 FHD is inherited as an autosomal dominant trait. Low levels of HDL ("good
 cholesterol") in the blood correlate with a high risk of cardiovascular
 disease, particularly coronary artery disease, and peripheral vascular
 disease, coronary restenosis, and peripheral vascular disease.
 Conversely, a high level of HDL has protective effects against
 cardiovascular disease. The invention provides genetic constructs and
 transgenic cells and non-human animals comprising human ABC1 nucleic
 acids, and methods of gene therapy for the treatment or prevention of
 cardiovascular disease comprising the administration of an expression
 vector encoding ABC1 or an active fragment thereof. The invention also
 encompasses compounds which mimic ABC1 activity, compounds which
 stimulate ABC1 expression and methods of screening for such compounds.
 It further relates to methods for determining whether a patient has an
 increased risk for cardiovascular disease due to polymorphisms in the
 ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
 or prevent cardiovascular disease, especially coronary artery disease,
 cerebrovascular disease, coronary restenosis or peripheral vascular
 disease. They may also be used in the treatment of diseases associated
 with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
 disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
 The invention specifically excludes proteins with the exact amino acid
 sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
 acid with the exact sequence as GenBank Accession No: AJ012376.1. The
 present sequence represents the human ABC1 cholesterol transporter.

Sequence 2261 AA:

Query Match 99.9%; Score 11789; DB 21; Length 2261;
 Best Local Similarity 99.98%; Pred. No. 0;
 Matches 2258; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACMPQLRLILMKNLFFRRQTCQLLEAVMPLTFILILSVRLSYPPYQHECHFPNKA 60
 DB 1 macmpqrlililwkhltffrrtqqlileavmplfifililsvrlsyppyeqhechfpnka 60
 QY 61 MPFAGTLPWVGITICMANNCFRPTPGEGAPGVGNKSTVARLPSDARILLYSQXDT 120
 DB 61 mpsagtlpwwvgiticonannpcfrrptpggeapgvgnknksivarlsdsarilllysqxdt 120
 QY 121 SMKMKRKYRLTLOQIKKSSNLKLODFVDMETPSGFLYNNLSLPKSTVDKMLRADVILH 180
 DB 121 smkkmrkylrltloqikksnslkldfivdmetsgfllynnlsipkstvdkmlradvilh 180
 QY 181 KYFLQGYQLHLTSLCNGSKSSEMIQLDQEVSELGGLPKREKLAARVYLRSMNDILKPL 240
 DB 181 kyflgylqlhltslncgskssnmikldfivdnetstgfllynnlsipkstvdkmlradvilh 180
 QY 241 RFLNSTSPSPSKELAEAKRTLLHSLGTLOAELEFMRSMQDROCPVMTLTVNSSSSSTOI 300
 DB 241 rflnstspfskelaekrtllhslgtlaeelfsmrsvdmrvgmfltvnsssstql 300
 QY 241 RLNSTSPFSKELAETKLLHSLGTLAGELFSMRVSDMRGVMFLTVNSSSTQI 360
 DB 241 rlnstspfskelaetkllhslgtlagelfsmrvsdmrvgmfltvnsssstql 360
 QY 301 YQAVSRIVCGHPGEGGLKISLWYEDNNYKALGSGNTERDAETFYDNSTTPYCDNLAK 360
 DB 301 yqavsrivcghpegglkikslwyednnykalgsgnterdaetfydnsttpycondlkm 360
 QY 361 NLESPPLSRITWKALKPLLVGKILYTPPATROYMAEVNKTPOBLAVFHDLEGMWELS 420
 DB 361 nlespplsrilwkalkpllvvgkilytpptatroymaevnktfoblavfhdlegmwels 420
 QY 421 PKIWTFMENSQEMDLVRMLDSDRNDHFWEOQLGSLDTADIDYAFIAKHPEDVQSSNGS 480
 DB 421 pkiwtfmensqemdlvrmldsdrndhfwegqlgsltdadidyafiakhpvedvqssngs 480
 QY 481 VYTWREAFNETQALITTSRFECEVNLKLEPIATEVWLINXSMELDERKFWAGIVFTG 540
 DB 481 vytwreafnetqalittsrfecvnlklepiatevwlinskmelederfkfwagivftg 540

QY 541 ITPGSIPLPHHKYKIRMDIDNVERTNKIKGQYWDGPRADPFEDMRVWGFGAYLDDV 600
 Db 541 ITPGSIPLPHHKYKIRMDIDNVERTNKIKGQYWDGPRADPFEDMRVWGFGAYLDDV 600
 QY 601 EGAIRVLTGTEKTKGVYMOQMPYPCYVDJELFRVMSMSMLPMTLMTYSAVATIKGIV 660
 Db 601 EGAIRVLTGTEKTKGVYMOQMPYPCYVDJELFRVMSMSMLPMTLMTYSAVATIKGIV 660
 QY 661 YEKERLKEHMLGJLNDJSLMFSWISLPLLVSAAGLVLLKGLNLTPSDPSVAV 720
 Db 661 YEKERLKEHMLGJLNDJSLMFSWISLPLLVSAAGLVLLKGLNLTPSDPSVAV 720
 QY 721 FLVSAVAVTIQCFILISLFSRANLAAAGGIIYFTLYLPVLCVAAQDVGFLTKIPAS 780
 Db 721 FLVSAVAVTIQCFILISLFSRANLAAAGGIIYFTLYLPVLCVAAQDVGFLTKIPAS 780
 QY 781 LLSVAEGEGCEYFALFEEDGIGVOMDNLFPESPEEDGFNLTTISIMWLEFPTLYGWTW 840
 Db 781 LLSVAEGEGCEYFALFEEDGIGVOMDNLFPESPEEDGFNLTTISIMWLEFPTLYGWTW 840
 QY 841 YIEAVFGQYGIIPRPWYPCYKSWFEESDEKSHPSNOKRMSEICMEEPHLKLGVS 900
 Db 841 YIEAVFGQYGIIPRPWYPCYKSWFEESDEKSHPSNOKRMSEICMEEPHLKLGVS 900
 QY 901 IONLVKVRDGMKVAVDGLALNFEGQITSEFLHNGAKTTMSILTLGLPPTSGRAYIL 960
 Db 901 IONLVKVRDGMKVAVDGLALNFEGQITSEFLHNGAKTTMSILTLGLPPTSGRAYIL 960
 QY 961 GKDJRSKSTIRONLGYCPOHNLFDMLTVEEHITWYARLKLSEKHVKAEMBOALDVG 1020
 Db 961 GKDJRSKSTIRONLGYCPOHNLFDMLTVEEHITWYARLKLSEKHVKAEMBOALDVG 1020
 QY 1021 LPSKSLKSTISOLSGMQRKLSVALAFVGGSKVYIIDEPAAGVDPVSRKGTWLLKLYRQ 1080
 Db 1021 LPSKSLKSTISOLSGMQRKLSVALAFVGGSKVYIIDEPAAGVDPVSRKGTWLLKLYRQ 1080
 QY 1081 GRTIILSTHMDADVLGDRIRAITSHQKLCVSSFLKNQJGTGYLLTVKKDVESSIS 1140
 Db 1081 GRTIILSTHMDADVLGDRIRAITSHQKLCVSSFLKNQJGTGYLLTVKKDVESSIS 1140
 QY 1141 SCRNSSSTVYLYKKEDSVSSSSDAGISDHSDELTIIVSAISNLIRKHVSARLVEOI 1200
 Db 1141 SCRNSSSTVYLYKKEDSVSSSSDAGISDHSDELTIIVSAISNLIRKHVSARLVEOI 1200
 QY 1201 GHELTIVLYPEAKEGAFVELFHEIDRLSDLGISSTYGISETTLEIFLKAESGVDAE 1260
 Db 1201 GHELTIVLYPEAKEGAFVELFHEIDRLSDLGISSTYGISETTLEIFLKAESGVDAE 1260
 QY 1261 TSDGTLPARNRRAFGDKOSCLRPFTEDDADPNDSIDPESRETYLLSGMDGKSYQVK 1320
 Db 1261 TSDGTLPARNRRAFGDKOSCLRPFTEDDADPNDSIDPESRETYLLSGMDGKSYQVK 1320
 QY 1321 GMLTIOQGFVALLMKRLLIARSRKGFQOIVLPAFVCIALVFSLIYVPGFKYPSLEIQ 1380
 Db 1321 GMLTIOQGFVALLMKRLLIARSRKGFQOIVLPAFVCIALVFSLIYVPGFKYPSLEIQ 1380
 QY 1381 PMWYNQYTFEVNDAPEDTGTELELINALTKDPGFGTRCMEGNPDPDTPCOAGEEBMTAP 1440
 Db 1381 PMWYNQYTFEVNDAPEDTGTELELINALTKDPGFGTRCMEGNPDPDTPCOAGEEBMTAP 1440
 QY 1441 VPQITMDLEFQNGNMTWQNPSPACOCSSDKIKKMLPVCPPGAGGLPPQKOKTADILDD 1500
 Db 1441 VPQITMDLEFQNGNMTWQNPSPACOCSSDKIKKMLPVCPPGAGGLPPQKOKTADILDD 1500
 QY 1501 TGRNSIDTLYVKTYYOIIAKSLKNKIMVNEFRYGFSLGVSNTOALPPSOEVNDATKQMK 1560
 Db 1501 TGRNSIDTLYVKTYYOIIAKSLKNKIMVNEFRYGFSLGVSNTOALPPSOEVNDATKQMK 1560
 QY 1561 HLKLAQSSADGFLNSLGFPMGLDTRNNVYKWFNNKQMHAISSFLYINNAIIRANIOK 1620
 Db 1561 HLKLAQSSADGFLNSLGFPMGLDTRNNVYKWFNNKQMHAISSFLYINNAIIRANIOK 1620
 QY 1621 GENPSHYGITAEHNPDLNLTQOOLSEVALMTTSVDVLVSCIVFAKSEVPASVAVFLIGER 1680

Db 1621 genpshygitaeahnpdlntkqolsevalmttsvdlvscivfaksevpasvavfliger 1680
 QY 1681 VSKAKHLQRTSGVKPVYIWLNSFWDMCNVYPATLVIIIFTCQOKSYVSTNLPVIAL 1740
 Db 1681 VSKAKHLQRTSGVKPVYIWLNSFWDMCNVYPATLVIIIFTCQOKSYVSTNLPVIAL 1740
 QY 1741 LLLLYGMSITPLMYPASFEKIPSTAYVYVLTSNVLEIGNSAVAFVLELFDNKLNNIN 1800
 Db 1741 LLLLYGMSITPLMYPASFEKIPSTAYVYVLTSNVLEIGNSAVAFVLELFDNKLNNIN 1800
 QY 1801 DLKSVFLIFPHECLGRLIDWKYNOAMADALEREENFVPLSDVIGRNLFFMAVEG 1860
 Db 1801 DLKSVFLIFPHECLGRLIDWKYNOAMADALEREENFVPLSDVIGRNLFFMAVEG 1860
 QY 1861 VYFELLTVLIQRFIRPRPVNAKISPLNDEBEDYRREKORILDCGGONDILEIKELTKI 1920
 Db 1861 VYFELLTVLIQRFIRPRPVNAKISPLNDEBEDYRREKORILDCGGONDILEIKELTKI 1920
 QY 1921 YRRKRPAVDRLICVGIPECEGFLGVNAGAKSTFEKMLTGDTTWRGDAPLNKSTISN 1980
 Db 1921 YRRKRPAVDRLICVGIPECEGFLGVNAGAKSTFEKMLTGDTTWRGDAPLNKSTISN 1980
 QY 1981 IHEVHONMGYCPQDAITELLTGREHVEFFALLRGVPERKGVKGEWAIRKILGVYGEK 2040
 Db 1981 IHEVHONMGYCPQDAITELLTGREHVEFFALLRGVPERKGVKGEWAIRKILGVYGEK 2040
 QY 2041 YAGNYSGGNKRKLTAMALIGSPVYFLDEPTGMDPKARFIMNICALSYKESRYLT 2100
 Db 2041 YAGNYSGGNKRKLTAMALIGSPVYFLDEPTGMDPKARFIMNICALSYKESRYLT 2100
 QY 2101 SISMECEALCTRMAIMVNGREFCLGSVOHLKNRGRDGYTIVRAGSNPLKVPDFFG 2160
 Db 2101 SISMECEALCTRMAIMVNGREFCLGSVOHLKNRGRDGYTIVRAGSNPLKVPDFFG 2160
 QY 2161 LAEPGSVLYKEKRRNLQYOLPSSLSLARIFSISQSKRRLHIEDYSQTTLDQVYNE 2220
 Db 2161 LAEPGSVLYKEKRRNLQYOLPSSLSLARIFSISQSKRRLHIEDYSQTTLDQVYNE 2220
 QY 2221 AKQSDDDHLKDLARKQYVAVVAVLNSFLQDERKVESYV 2261
 Db 2221 AKQSDDDHLKDLARKQYVAVVAVLNSFLQDERKVESYV 2261

RESULT 8
 ID AAB71749 standard; protein: 2261 AA.
 XX AAB71749;
 AC 17-MAY-2001 (first entry)
 DT
 DE Human AbCl protein.
 KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; AbCl.
 XX Homo sapiens.
 OS
 PN MO200115676-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 01-SEP-2000; 2000MO-IB01492.
 XX
 PR 01-SEP-1999; 9905-0151977.
 PR 15-MAR-2000; 200005-0526193.
 PR 23-JUN-2000; 200005-0213958.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (XENO-) XENON GENETICS INC.
 XX
 PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
 XX

XX WPI: 2001-244356/25.

PT Treating a lower than normal high density lipoprotein-cholesterol
(HDL-C) level, a higher than normal triglyceride level, or a
PT cardiovascular disease, by administering a compound that modulates LXR-
PT or RXR-mediated transcriptional activity -

XX Claim 16: Fig 2: 317pp: English.

XX The present invention relates to a method for treating a patient
CC diagnosed as having a lower than normal high density
CC lipoprotein-cholesterol (HDL-C) level, a higher than normal
CC triglyceride level, or a cardiovascular disease, involving
CC administering a compound that modulates LXR- or RXR-mediated
CC transcriptional activity or ABC1 expression or activity.
CC The LXR gene product may be used in an assay to identify
CC compounds useful for the treatment of a disease or condition selected a
CC lower than normal HDL cholesterol level, a higher than normal
CC triglyceride level, and a cardiovascular disease.

XX Sequence 2261 AA:

Query Match 99.9%: Score 11789; DB 22; Length 2261;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2258; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACPQRLRLMKNLTRRRQTCQLLEAVMPLEFLILISVRLSYPPYEQHECHFNKA 60
DB 1 macppqrlrlmknltrrrqtcqlleavmpfllilsvrlsyppyeqhechfnka 60
QY 61 MPSAGTLPMWOGIICNANPCFRYPPEAGPVGYNFNKSIYARLPFSDKRLLIXSQDT 120
DB 61 mpsagtlpmwogiiicnannpcfryppeagpyvgynfnksiyarlfpsdkrllixsqdt 120
QY 121 SMKMRKRVLTLOQIKSSNKLKLOPLVDNTEFSGFLYHNLSLPKSTYDKMLRADVILH 180
DB 121 smkmrkrrvltloqikssnklkloplvdnntefsgflyhnlslpkstdkmlradvilh 180
QY 181 KVFLOGYOLHLTSLCNGSKSEEMIQLODOFVSELGSLPEKTLAAERVLRSNMIDILKPL 240
DB 181 kvflogyolhltslcngskseemiqldofvselcslpekltlaaervlrsnmidilkpl 240
QY 241 RFLNSTSPFBSKELAEATKTLHSLGLAOLFSMSMSMSMRQEWELTNVNSSSSSTQI 300
DB 241 rflnstspfbskelaektktlhslglaoelfsmssmsmsmrqeweltnvnsssstqi 300
QY 301 YQAVSRIYCGHPGEGGLIKISLWYEDNNYKALFGGNGTEDEAEFYDNSTTPYCNLDMK 360
DB 301 yqavsriycghpegglkikslwylednnykalfgngteedaefydnsttpycndlmk 360
QY 361 NLESSPLSRIITWALKLPVGLKILYTPDPATROVAEAVNKTQEOBLAVFHDEEGMDEIS 420
DB 361 nlessplsriitwalklpvglkilytpdpatrovaeavnktqeoelavfhdeegmdeis 420
QY 421 PKIYTFMNSQBNMLVRLMLDSRDNDHFWGQULGLWMTQDIAVFLAKRPEVOSSNGS 480
DB 421 pkiytfmnsqbnmlvrlmldsrdndhfwgqulglwmtqdiaavlakrpevoSSNGS 480
QY 481 VYTMREAFENETNOAIRTISRFMECVNLKLEPIATEVWLINKSMEILLDERKFMAGIVTG 540
DB 481 vytmreafenetnoairtisrfmecvnlklepiatevwlinskmeillderkfmagivtg 540
QY 541 ITPGSIELPHVKKIRMDINVERTKIKIGYWDPRADPRADPFDMYVWGCAVYLODYV 600
DB 541 itpgsielephvkkirmdinvertkikigywdpradpradpfdmYVWGCAVYLODYV 600
QY 601 BOAIIIRVLGTGKTKGVYMOOMPYPYVDIDFLRMSKSMPLFMTLAMIISVAVIIGIV 660
DB 601 boaiiirvlgtgktkgvymoompypyvdiidflrmsksmplfMTLAMIISVAVIIGIV 660
QY 661 YEKEARLKETMRIMGLDINSILFWSFISLIPLLVSAGLLVILKGNLLPYSDPSVYV 720
DB 661 yekearlketmrimgldinsilfwsfislipllvsagllvilkgnllpySDPSVYV 720

DB 661 yekearlketmrimgldinsilfwsfislipllvsagllvilkgnllpySDPSVYV 720
QY 721 FLSVAVVTIIOCFILSTLFSRANLAAACGGIYFTLTLPVLCVANOVDVGTIKTFAS 780
DB 721 flsvavvtiioCFILSTLFSRANLAAACGGIYFTLTLPVLCVANOVDVGTIKTFAS 780
QY 781 LLSVPAFGGCVFPLAFEEGQIGVQMDNLFESPVEDCFNLTTISIMMLFETFLYGYMTW 840
DB 781 llsvpaFGGCVFPLAFEEGQIGVQMDNLFESPVEDCFNLTTISIMMLFETFLYGYMTW 840
QY 841 YIEAVPQGYGIPRPYFPCTKSYWFEESDEKSHPGSNQKRMSEICMEEPRLKLGVS 900
DB 841 yieavpQGYGIPRPYFPCTKSYWFEESDEKSHPGSNQKRMSEICMEEPRLKLGVS 900
QY 901 IONLVYVRDGMKVAVDGLALFPEGQITSEFGHGACKTTMTSLTNGLPPTSGTAVIL 960
DB 901 ionlvYVRDGMKVAVDGLALFPEGQITSEFGHGACKTTMTSLTNGLPPTSGTAVIL 960
QY 961 GKDISEMSTIRQNLGVCPOHNVLEFMDLTVBEHIFWYARLKLSEKHVKAEMEQNALDVG 1020
DB 961 gkdiseMSTIRQNLGVCPOHNVLEFMDLTVBEHIFWYARLKLSEKHVKAEMEQNALDVG 1020
QY 1021 LPSSKLKSTSQLSGQMOKRLSYALAFVCGSKVYLIDERTAGVDPRSRGIMELLIXYRQ 1080
DB 1021 lpsklkSTSQLSGQMOKRLSYALAFVCGSKVYLIDERTAGVDPRSRGIMELLIXYRQ 1080
QY 1081 GRITLSTHMDADVLGDRILATISHGKLCVGSSEFLKNQGTGYVTLVKKEDSILS 1140
DB 1081 gritlSTHMDADVLGDRILATISHGKLCVGSSEFLKNQGTGYVTLVKKEDSILS 1140
QY 1141 SCRNSSSTVSYLKKEDEVSOSSSDAGISDBHSDTLTIDVSAISNLIRKHVSEARLVEDI 1200
DB 1141 scrnssstVSYLKKEDEVSOSSSDAGISDBHSDTLTIDVSAISNLIRKHVSEARLVEDI 1200
QY 1201 GHELTLYLPLEAKKEGAFVFLFHEIDRLSDIGISSYSEITTEIEFLKVAEEGVDAE 1260
DB 1201 gheLTLYLPLEAKKEGAFVFLFHEIDRLSDIGISSYSEITTEIEFLKVAEEGVDAE 1260
QY 1261 TSQDCTLPARNRRAFGDKQCLPFTEDDADPNDDIPDESRETDLSGMDGKSYOVK 1320
DB 1261 tsqDCTLPARNRRAFGDKQCLPFTEDDADPNDDIPDESRETDLSGMDGKSYOVK 1320
QY 1321 GWKLTQOOFVALLMKRLILARRSKGFFAOIYLPAYVCIALVLSLIVPFGKYSLEIQ 1380
DB 1321 gwKLTQOOFVALLMKRLILARRSKGFFAOIYLPAYVCIALVLSLIVPFGKYSLEIQ 1380
QY 1381 PWMYNEQYTFVSNAPEDTGTLELINALTKDPGFRGCMGPNIPPTPCOAGEEWTAP 1440
DB 1381 pwmYNEQYTFVSNAPEDTGTLELINALTKDPGFRGCMGPNIPPTPCOAGEEWTAP 1440
QY 1441 VPQITMDLFONGNMTWQNPSPACQSSDKIKMLPYCPGAGGLPPQRKONTADILQDL 1500
DB 1441 vpqITMDLFONGNMTWQNPSPACQSSDKIKMLPYCPGAGGLPPQRKONTADILQDL 1500
QY 1501 TGRNISDYLVKTYVOIILAKSLKNIWYNERRYGFSLGYSVNTQALPPSQGVNDAIKOMK 1560
DB 1501 tgrNISDYLVKTYVOIILAKSLKNIWYNERRYGFSLGYSVNTQALPPSQGVNDAIKOMK 1560
QY 1561 HLXIAKQSSABRPLNSLGRFMTGLDTERNNYKVWPNKNGMAIISFLVAVINNALIRANLQK 1620
DB 1561 hlXIAKQSSABRPLNSLGRFMTGLDTERNNYKVWPNKNGMAIISFLVAVINNALIRANLQK 1620
QY 1621 GENPSHYGITAFAHNPULNLTROOLSEVALMTTSVDVILSICVIFAMSFVPSVYVLIQER 1680
DB 1621 genPSHYGITAFAHNPULNLTROOLSEVALMTTSVDVILSICVIFAMSFVPSVYVLIQER 1680
QY 1681 VSKAHNLOPISGVKRYIWNLSNFVWDMQNVYVPAFLVILIFICFOOKSYSSNLPVLAL 1740
DB 1681 vskAHNLOPISGVKRYIWNLSNFVWDMQNVYVPAFLVILIFICFOOKSYSSNLPVLAL 1740
QY 1741 LLLLVGMSITPLMYPASVFKIPSTAYVVLTSVNLFTGINGSVATVLELFTDNKLNNIN 1800
DB 1741 lllLVGMSITPLMYPASVFKIPSTAYVVLTSVNLFTGINGSVATVLELFTDNKLNNIN 1800


```

QY 1801 DILKSVFLIFPHFCIGKGLIMVKNQAMADALBERGENREVSPLSMDLIGRNIPMAVAEG 1860
DB 1801 dILKSVfLIpfhfcIgrgLIldmVknqamadalErgerfvsplswdlvgnLIamaVeG 1860
QY 1861 VWFELITVLIVGPFIRPRPNNAKLSPLNDEDEVRREROBILINGGONDLLEIKELTKI 1920
DB 1861 vWfELITvLIgyrffIRprpnakLSplndedevrrerqLIldg99qndLIelkELtkI 1920
QY 1921 YRRKRKPAVDRIQVIGIPPECFGILGVNAGKSSFTFKMLTGTDTTVTRGDAFLANKSLISN 1980
DB 1921 yrrkrkpavdrIcvgIppECFGIlgvnagKssftfKmlTgdtvttrgdaflnkslIsn 1980
QY 1981 IHEHONMGVPOPDATITELTGREHEFFALLKGVEPEKGVKGEWAIRKLGIVKGEK 2040
DB 1981 ihehnmvgvcpqdaItellTgreheffallIrgvepekvkgewaIrklgIvKgeK 2040
QY 2041 YAGNYSGGNKRKRLSTAMALIGPVPVFLDEPTTGMDPKARFLMNCALSVKKEGRSVLTF 2100
DB 2041 yaGnysggnkrkrlstamaLIgppvPvfldepttgmDpkarflmncalsvkkgErsvltf 2100
QY 2101 SHSMECEALCTRAIMVGNRFRIGISVQHLKRFNGYITTVRIAGSNPDLKPVODFGS 2160
DB 2101 shsmecealctmaImvngfrfclgsvqhlkrfngyIttvriagSnPdlkpvodfgs 2160
QY 2161 LAFPGSVLKKEKRNMLQYOLPSSLSLARIFSILOSRRRLIEDYSVSTTLDOYFVNF 2220
DB 2161 lafpgsvlKkEkRnmlqYolpsslslarIfsIlOSkrRLIEDysvsttlDOYfvnf 2220
QY 2221 AKQOSDDHLKDLISLHNQTVVDAVLTSLDDBKVKESYV 2261
DB 2221 akqosddhLkdlSLhnqtvvdavltSLldDbkVkesyV 2261

```

RESULT 9

```

AAB31363
ID AAB31363 standard; Protein; 2261 AA.
AC AAB31363;
DT 20-APR-2001 (first entry)
DE Amino acid sequence of ABC1 polypeptide from Tangier disease patient.
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 587
FT note="this is changed from Arg to Trp in Tangier disease"
PN WO200078972-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-US16765.
XX
PR 18-JUN-1999; 99US-0140264.
PR 14-SEP-1999; 99US-0153872.
PR 19-NOV-1999; 99US-016573.
XX
PA (CVTH-) CV THERAPEUTICS INC.
XX
PI Lawn RM, Wade D, Garvin M;
XX
DR WPI; 2001-137812/14.
XX
PT Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,

```

```

PT useful for the development of agents for the treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX
PS Disclosure; Page 176-191; 215pp; English.
XX
CC The present sequence represents a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC ATP hydrolysis to transport a wide variety of substrates across the
CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC Tangier disease, a genetic disorder characterised by abnormal
CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC 9q22-9q31. The ABC1 genes and proteins are useful for developing
CC pharmaceutical agents for the treatment of heart disease and other
CC disorders associated with hypercholesterolemia and atherosclerosis. The
CC genes are useful for developing screening assays to screen for compounds
CC that regulate the expression of genes associated with cholesterol
CC transport. The genes and proteins are also useful for are also useful
CC as diagnostic indicators of cardiovascular disease and other disorders
CC associated with hypercholesterolemia.
CC
XX
SQ Sequence 2261 AA;

```

```

Query Match 99.9%; Score 11789; DB 22; Length 2261;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 MACWQOLRLMLKNTLFFRRRCOLLLEVAMPFLFLLISVRLSYPRYEDGHECHFPKA 60
DB 1 macwqolrlmlkntLffrrrcollLevampflfllIsVrLsypryEdghechfpka 60
QY 61 MESAGTLFWVQGITCMANNPCFRYPPTGEGAPGVVGNFKSIVARLFSDARLLYSOKDT 120
DB 61 mpsagtlfwvgIcIcmannpcfrYpPtgeGApgvvgnfKsIvArLfSdarllYsQkdt 120
QY 121 SMKDKRKYLRRLQOIKRSSNLIKLODFLVNDETSGFLYHNLSLPKSTVDKMLRADYILH 180
DB 121 smkdkrkyLrRLqOIkrSSnLIkLOdflvNDETsgflYhnlsLPkStvdKmlradYilH 180
QY 181 KYFLQYOLHTSLCNGSKSEEMIOLODQVESEICGPKKEKLAAEVYLSNMNMLKPTL 240
DB 181 kVflgYolhtslcngskseemIOldQvseIcgpKkeKlaaEvYlSnmnmlKptl 240
QY 241 RFLNSTSPFSKELAEATKYLHSLGTLAQLFSMRSMWDMROEVMFLTVNSSSSSTQI 300
DB 241 rflnstspfskElEaTKylhslgTLaqlfsmrsmwDmroEvmflTvnsssstqI 300
QY 241 rflnstspfskElEaTKylhslgTLaqlfsmrsmwDmroEvmflTvnsssstqI 300
QY 301 YQAVSRIVCGHPEGGGGLKIKSLNMYEDNNYKALFGNGTEDEAETFYDNSTTTPYCNLAK 360
DB 301 yqavsrIvcghpegggLkIKslNmyEdnnYkAlfgngteDeaETfyDnSttTPyCnLak 360
QY 361 NLESSPLSRILWKALEKLVGKILYTPDTPATROVAEAVKTKFOELAVFDLGGMEELS 420
DB 361 nlessplsrIlwkaLEkLVgkILytpDtpatRoVAeavKtkfoELavfdLgGmeels 420
QY 421 PKITFMENSGEMDVYMLLDSRDNDHFWEQDLGDLMTKODIVAPLAKHPEDVSSNGS 480
DB 421 pkItfmenSGemdvYmLLdsrdndHFweQDLgdlMTkOdIvApLakhpEdvSSngs 480
QY 481 VYTWREAFNETNOAIRTISRPMECVNLNKLEPIATEVWLNKSMELLDKPKFAGIVFG 540
DB 481 vytwreaFnetnOairtIsrPmECvnlNkLEpIateVwlNkSmELldKpkfAGivfg 540
QY 541 ITPGSIELPHHVKKYKIRMDIDNVERTNKLKDGWDBGPADRPEDMRYWGGFAYLQDVP 600
DB 541 ItpgsIElphhvKkyKIRmdIDnvertNklKdgWdbgpADrpEdmRYwGgFaylQdvp 600
QY 601 EOALIRVLGTGEEKTGYYMQOMYPCYVDIDFLRWKSRKMPFLMTLAMYISAAVITKGIIV 660
DB 601 eOalIrVlgtGekTgYymqOMyPcyvDIIdflrWkSRkMpfLmTLamYISAAvITkGIiv 660

```



```

QY 661 YEKARLKEKTRMIRGLDINSILMESWTSLSLPLLVASAGLLVILKLGKLNLLPSDSGVVY 720
Db 661 YEKARLKEKTRMIRGLDINSILMESWTSLSLPLLVASAGLLVILKLGKLNLLPSDSGVVY 720
QY 721 FLVSFAVVTIIQCLSLISLPSRAALAAAGGIIITLYLTVYLVAVMADVGTLLKIFKS 780
Db 721 FLVSFAVVTIIQCLSLISLPSRAALAAAGGIIITLYLTVYLVAVMADVGTLLKIFKS 780
QY 781 LLSPAFGFGECEYFALFEEOGIGVOMDNLESPYEEDEGFMILTSTISAMLPDTELYGVMTW 840
Db 781 LLSPAFGFGECEYFALFEEOGIGVOMDNLESPYEEDEGFMILTSTISAMLPDTELYGVMTW 840
QY 841 YLEAVFPGQYIIPRWTFPCTKSTYFGBESDEKSHPSNOKRMEICMEEPFHLKLGVS 900
Db 841 YLEAVFPGQYIIPRWTFPCTKSTYFGBESDEKSHPSNOKRMEICMEEPFHLKLGVS 900
QY 901 IONLVKVRDGMKAVNDSALNFEYGOTTSFLGHNGAKTTMSILTLGPPPTSGTAYIL 960
Db 901 IONLVKVRDGMKAVNDSALNFEYGOTTSFLGHNGAKTTMSILTLGPPPTSGTAYIL 960
QY 961 GKDISEKSTIKONLGYCPOHNVLFDMLTVEEHIMFYARLKGLSEKHVKAEMEQMALDVG 1020
Db 961 GKDISEKSTIKONLGYCPOHNVLFDMLTVEEHIMFYARLKGLSEKHVKAEMEQMALDVG 1020
QY 1021 LPSSKLSKTSQSLSGMOKRUSVALAEVGSKVYLDEPFTAGVDPYRSGRIWELLKXKQ 1080
Db 1021 LPSSKLSKTSQSLSGMOKRUSVALAEVGSKVYLDEPFTAGVDPYRSGRIWELLKXKQ 1080
QY 1081 GRITIISTHHMEADVLDRIATISHGKLCGSSLFKNLGTGYITLVKRVESLSL 1140
Db 1081 GRITIISTHHMEADVLDRIATISHGKLCGSSLFKNLGTGYITLVKRVESLSL 1140
QY 1141 SCRNSSSTVSYLKKEEDSVSQSSSDAGLSDHESDITLIDVAISNLIRKHVSEARLVEDI 1200
Db 1141 SCRNSSSTVSYLKKEEDSVSQSSSDAGLSDHESDITLIDVAISNLIRKHVSEARLVEDI 1200
QY 1201 GHELTIVLYLEAKKEGAFVLEFHEIDRLSDLGISYCISETTLEETFLKAAESGVDAE 1260
Db 1201 GHELTIVLYLEAKKEGAFVLEFHEIDRLSDLGISYCISETTLEETFLKAAESGVDAE 1260
QY 1261 TSDGTLPARNRRAFGDKOSCLRPFTEDDAADPNDSIDDPESRETDLSGMDKGSYOVK 1320
Db 1261 TSDGTLPARNRRAFGDKOSCLRPFTEDDAADPNDSIDDPESRETDLSGMDKGSYOVK 1320
QY 1321 GWRILTQOQFVALLWKRLILARSRKGFPAQIVLPAVFCIALVESLTYPPGKYSLDQ 1380
Db 1321 GWRILTQOQFVALLWKRLILARSRKGFPAQIVLPAVFCIALVESLTYPPGKYSLDQ 1380
QY 1381 PMWYNQYFVNSDAPEDDTLELINALTKDPGFRCEGPNRPDTPCOAGEEEMTAP 1440
Db 1381 PMWYNQYFVNSDAPEDDTLELINALTKDPGFRCEGPNRPDTPCOAGEEEMTAP 1440
QY 1441 VPQITMDLFONGMWTQONSAPACQSSDKIKKMLPYCPGAGGLPPORQONTADILDL 1500
Db 1441 VPQITMDLFONGMWTQONSAPACQSSDKIKKMLPYCPGAGGLPPORQONTADILDL 1500
QY 1501 TGRNISDYLVKTYOIIAKSLKMKIYNNEFRYGGFSLGYSNQAALPQGEVNDAIKOMK 1560
Db 1501 TGRNISDYLVKTYOIIAKSLKMKIYNNEFRYGGFSLGYSNQAALPQGEVNDAIKOMK 1560
QY 1561 HLKLAQSSADRFNLNSIGRPMTGLDTRNNKYVFNKNGHAISSFLNVLNNAILRANLQK 1620
Db 1561 HLKLAQSSADRFNLNSIGRPMTGLDTRNNKYVFNKNGHAISSFLNVLNNAILRANLQK 1620
QY 1621 GENPSHYGITAHPNLPLTQOQSEVALMTTSDVILVSCIVTFAMSFVASFVFIQOR 1680
Db 1621 GENPSHYGITAHPNLPLTQOQSEVALMTTSDVILVSCIVTFAMSFVASFVFIQOR 1680
QY 1681 VSKAKHLOFTSGVPVITYWLSNFWMDCNVVPATLVIITFCFOOKSYVSSSTNLPEVL 1740
Db 1681 VSKAKHLOFTSGVPVITYWLSNFWMDCNVVPATLVIITFCFOOKSYVSSSTNLPEVL 1740

```

```

QY 1741 LLLLYGWSITPLMYPASEVEKIBSTAYVVLTSVNLFTIGINGSVATFVLELFPDKNLNTN 1800
Db 1741 LLLLYGWSITPLMYPASEVEKIBSTAYVVLTSVNLFTIGINGSVATFVLELFPDKNLNTN 1800
QY 1801 DILKSVFLIPHPFCLGKGLIDMKYKNQAMADLERFEGNRVPSLSMDIVGRNLFAAAVAG 1860
Db 1801 DILKSVFLIPHPFCLGKGLIDMKYKNQAMADLERFEGNRVPSLSMDIVGRNLFAAAVAG 1860
QY 1861 VVFELITVLIOYRPFIRPRPVNAKLSPLNDEDEVDREQRRIIDGGGOMDILEIKELTKI 1920
Db 1861 VVFELITVLIOYRPFIRPRPVNAKLSPLNDEDEVDREQRRIIDGGGOMDILEIKELTKI 1920
QY 1921 YRRKRKPAVDRIICVGIIPGECFGLLVNGAGKSTFEMLTGDTTVTRGDAFLKNKILSN 1980
Db 1921 YRRKRKPAVDRIICVGIIPGECFGLLVNGAGKSTFEMLTGDTTVTRGDAFLKNKILSN 1980
QY 1981 IHEVHQNMGYCPQDPAITELLTGREHVEFPALLRGVEKEVGKGEWAIRKLGIVYGEK 2040
Db 1981 IHEVHQNMGYCPQDPAITELLTGREHVEFPALLRGVEKEVGKGEWAIRKLGIVYGEK 2040
QY 2041 YAGNYSGGKRRKLSFAMALIGCPVYFLDEPPTGMDPKARFLMNCALSVYKGRSVLT 2100
Db 2041 YAGNYSGGKRRKLSFAMALIGCPVYFLDEPPTGMDPKARFLMNCALSVYKGRSVLT 2100
QY 2101 SHSMECEALCTPMAIMVNGREFCLGSVOHLKNRFGDGYTVIRIAGSNPDLPYQDFG 2160
Db 2101 SHSMECEALCTPMAIMVNGREFCLGSVOHLKNRFGDGYTVIRIAGSNPDLPYQDFG 2160
QY 2161 LAFPGSVLKEKRKNMLQYOLPSSLSLARIFSTISQSKRLHIEDYSVSTOTLDQVVF 2220
Db 2161 LAFPGSVLKEKRKNMLQYOLPSSLSLARIFSTISQSKRLHIEDYSVSTOTLDQVVF 2220
QY 2221 AKDQSDDDLKDLSLHKNOTVVDVAVLTSFLQDEKVKESYV 2261
Db 2221 AKDQSDDDLKDLSLHKNOTVVDVAVLTSFLQDEKVKESYV 2261

RESULT 10
AAB31367
ID AAB31367 standard; Protein: 2261 AA.
XX
AC AAB31367;
XX
DT 20-APR-2001 (first entry)
XX
DE Amino acid sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT MISC-difference 567 /note="this is changed from Arg to Trp in Tangier
FT FT disease"
XX
PN MO200078971-A2.
XX
PD 28-DEC-2000.
XX
PE 16-JUN-2000; 2000MO-US16591.
XX
PR 18-JUN-1999; 99US-0140264.
PR 14-SEP-1999; 99US-0153872.
PR 19-NOV-1999; 99US-0166573.
XX
XX (CVTH-) CV THERAPEUTICS INC.
XX (UNIW ) UNIV WASHINGTON.
XX
PI Lawn RM, Wade D, Oram JF, Garvin M;

```

XX WPI: 2001-137811/14.
 DR N-PSB: AAF24708.
 XX
 PT Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
 PT polynucleotides and polypeptides, useful for treatment of heart disease
 PT and other disorders associated with hypercholesterolemia and
 XX atherosclerosis -
 XX
 PS Claim 28: Page 172-187; 211pp: English.
 XX
 CC The present sequence represents a human adenosine triphosphate (ATP)
 CC binding cassette protein (ABC) 1 polypeptide, and is isolated from
 CC a Tangier disease patient. ABC1 resides in cell membranes and utilises
 CC ATP hydrolysis to transport a wide variety of substrates across the
 CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
 CC mobilisation of intracellular cholesterol stores. ABC1 is defective in
 CC Tangier disease, a genetic disorder characterised by abnormal
 CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
 CC 9q22-9q31. The ABC1 genes and proteins are useful for developing
 CC pharmaceutical agents for the treatment of heart disease and other
 CC disorders associated with hypercholesterolemia and atherosclerosis. The
 CC genes are useful for developing screening assays to screen for compounds
 CC that regulate the expression of genes associated with cholesterol
 CC transport. The genes and proteins are also useful for are also useful
 CC as diagnostic indicators of cardiovascular disease and other disorders
 CC associated with hypercholesterolemia.
 CC
 XX Sequence 2261 AA:
 Query Match 99.9%; Score 11789; DB 22; Length 2261;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 541 lcpgslejphhvkkykizmdidnvertunkikdgywdppradpfedmyvwvgfaylqdv 600
 QY 601 FOAIRVLVLTGKTKGVMQMOQPYPCYVDLFEIWMRSRSMPLFMTLAWITSVAVITKGY 660
 Db 601 egaqirvlrlygtekkgvymqmpjpcyvdfltrvmrsmplfmlclawlysvavllkgy 660
 QY 661 YEKEARLEKTMKIMGLDINSILWFWSFISLIPDLVSAGLLVILKGLNLPYSDPSVFEV 720
 Db 661 yekearlketmrimglinsilwfwfisslilplvsagllvllkgnllpydspsvfev 720
 QY 721 ELISFAVYTIIOGCEIISLFSRANLAAACGITYFTLYLPVLCVAMQDYVGTTLKIPAS 780
 Db 721 flsvaavlllqcllslfslsranaaacgilyfllylpvltcvaqdyvgtllkifas 780
 QY 781 ILSVPAFGCEYFALFEEDGIGVOMDNLFESEPEEDGFNLITISISMLPDTFLYGVMM 840
 Db 781 llsvpa fgcey falfeeg igyqwn l fespveed fnl tssim l fdl tlygvmm 840
 QY 841 YLEAFPGQYIIPRWYPCIKSTWFEGBESDEKSHPSNOKRMESEICMEEPHKLIGVS 900
 Db 841 yleafpgqyilprwyfpcklkywfeesdeksbpsnqkrmseicmeeephkligvs 900
 QY 901 IONLVKVRDGMKYAVDGLALNFEQITSPFGHNGAGTTMSILGLFPPSTGAYTL 960
 Db 901 ignlvkvyrdgmkyavdgla n fteeg it s fignagk t tms il t g l f p p s t g a y t l 960
 QY 961 GKDIRSEKSTIRONLGYCPOHNVLEDMITVEBHITWYARLKLSEKHVAEMOMALDVG 1020
 Db 961 gkdirseks t i r o n l g y c p o h n v l e d m i t v e b h i t w y a r l k l s e k h v a e m o m a l d v g 1020
 QY 1021 LPSSKLKSKTSQLSGQMOKRISVALAVGSKSVYIIDEFPAGVDPYSRSGIEMELLKRYQ 1080
 Db 1021 lpsklksktsq l s g q m k r i s v a l a v g s k s v y i i d e f p a g v d p y s r g i e m e l l k r y q 1080
 QY 1081 GRTIILSTHMDADVLDGRITAIISHGKLCQVSSFLKNQLOTGYTLTVKKDVSSLS 1140
 Db 1081 g r t i i l s t h m d e a d v l g d r i t a i i s h g k l c q v s s f l k n o l o t g y t l t v k k d v s s l s 1140
 QY 1141 SCRNSSSTVSLKKEPDSVSSSSSDAGIGSDHEDTLITIVSAISNLIRKHVSEARLVEDI 1200
 Db 1141 s c r n s s s t v s l k k e p d s v s s s s d a g i g s d h e d t l i t i v s a i s n l i r k h v s e a r l v e d i 1200
 QY 1201 GHELTIVLYPEAAKEGAFVLEFHEIDRLSDLGISYGISETTLIEIFLAKVEESGVDAE 1260
 Db 1201 g h e l t i v l y p e a a k e g a f v l e f h e i d r l s d l g i s y g i s e t t l i e i f l a k v e e s g v d a e 1260
 QY 1261 TSDGTLPARNRRAFGDKOSCLRPFTEDDAADPNDSIDPESRETDLLSGMDGKGSYGVK 1320
 Db 1261 t s d g t l p a r n r r a f g d k o s c l r p f t e d d a a d p n d s i d p e s r e t d l l s g m d g k s y g v k 1320
 QY 1321 GMLTJOOQFVALLMKRLIARRSRKGFPAOTYLPANFVCIALVESLIYPPRGKYSLELO 1380
 Db 1321 g m l t j o o q f v a l l m k r l i a r r s r k g f p a o t y l p a n f v c i a l v e s l i y p p r g k y s l e l o 1380
 QY 1381 PMWYNEQYFVSNDABEDTGTELLNALTKDPGFCGRMEGNPIPDTCQAGEEEMWTAP 1440
 Db 1381 p m w y n e q y f v s n d a b e d t g t e l l n a l t k d p g f c g r m e g n p i p d t c q a g e e e m w t a p 1440
 QY 1441 VPQTIMDLFQNGWMTWQNSPACQSSDKIKMLFVCPGAGLPPPOKRONATDILODL 1500
 Db 1441 v p q t i m d l f q n g w m t w q n s p a c q s s d k i k m l f v c p g a g l p p p o k r o n a t d i l o d l 1500
 QY 1501 TGRNISDYLVKTYVOITIASLKNKIMVNEFRYGSLSVSNQALPPOEYNDVAKOMK 1560
 Db 1501 t g r n i s d y l v k t y v o i t i a s l k n k i m v n e f r y g s l s v s n q a l p p o e y n d v a k o m k 1560
 QY 1561 HUKLAOSSADRLNSLGEFTGLDTRNNVKKWFNNKGMHAISFLVYNNAIIRANLOK 1620
 Db 1561 h u k l a o s s a d r l n s l g e f t g l d t r n n v k k w f n n k g m h a i s f l v y n n a i i r a n l o k 1620
 QY 1621 GENPSHYGITAFNHPPLNLTKOOLSEVALMTYSVYVNSICYIFAMSVYPASFVYFLQER 1680
 Db 1621 g e n p s h y g i t a f n h p p l n l t k o o l s e v a l m t y s v y v n s i c y i f a m s v y p a s f v y f l q e r 1680

```

QY 1681 VSKAKHLQFISGVKPYIYWLNFVDMQNVVYPATLVIIIFICFOOKSVSSTNLPVIAL 1740
    |||||||
Db 1681 VSKAKHLQFISGVKPYIYWLNFVDMQNVVYPATLVIIIFICFOOKSVSSTNLPVIAL 1740
QY 1741 LLLVGSWSTPLMPYASVEFKIPSTAYVYVLSVNFIFIGINSVAFFVIELFDNKLNNIN 1800
    |||||||
Db 1741 LLLVGSWSTPLMPYASVEFKIPSTAYVYVLSVNFIFIGINSVAFFVIELFDNKLNNIN 1800
QY 1801 DLKSVLELFPKCLGRGLIDWKNQAMADALREGENEFVPLSMIDLGRMLFMAVAG 1860
    |||||||
Db 1801 DLKSVLELFPKCLGRGLIDWKNQAMADALREGENEFVPLSMIDLGRMLFMAVAG 1860
QY 1861 VVEFLITVLIOYREFTRPPVNAKLSPLNDEDEDVARERORILDDGGONDLEIKELTKI 1920
    |||||||
Db 1861 VVEFLITVLIOYREFTRPPVNAKLSPLNDEDEDVARERORILDDGGONDLEIKELTKI 1920
QY 1921 YRRKKRPAYDRICVGIPECECGILGVNAGKSSFTFKMLTGPTVYRGDAFLNKSILSN 1980
    |||||||
Db 1921 YRRKKRPAYDRICVGIPECECGILGVNAGKSSFTFKMLTGPTVYRGDAFLNKSILSN 1980
QY 1981 IHEVHOMGXCPOFDAITELTGREHVEFFALRGVPEKEVGKVGEMATRKLGKYGK 2040
    |||||||
Db 1981 IHEVHOMGXCPOFDAITELTGREHVEFFALRGVPEKEVGKVGEMATRKLGKYGK 2040
QY 2041 YAGNYSGKNRKLSTAMALIGPPVFLDEPTTGMDPKARRFLMNCALSVEKGRSVLT 2100
    |||||||
Db 2041 YAGNYSGKNRKLSTAMALIGPPVFLDEPTTGMDPKARRFLMNCALSVEKGRSVLT 2100
QY 2101 SHMECEALCTMAIMVNRFCGLSVOLKRRFGDGTIVYRIGSNPDLPVDFG 2160
    |||||||
Db 2101 SHMECEALCTMAIMVNRFCGLSVOLKRRFGDGTIVYRIGSNPDLPVDFG 2160
QY 2161 LAEPGSLYKKEHNNMLQYOLPSSLSLARLSILSOSKKRLIEDYVSQGTILDQVFN 2220
    |||||||
Db 2161 LAEPGSLYKKEHNNMLQYOLPSSLSLARLSILSOSKKRLIEDYVSQGTILDQVFN 2220
QY 2221 AKQOSDDHLKDLISLKNQNVVAVYTSPLQDEKYESYV 2261
    |||||||
Db 2221 AKQOSDDHLKDLISLKNQNVVAVYTSPLQDEKYESYV 2261

```

RESULT 11

AAB38111 standard; protein: 2261 AA.

AAB38111;

29-JAN-2001 (first entry)

Human ABC1 cholesterol transporter mutant, V771M.

Human ABC1 cholesterol transporter; chromosome 9q31.

ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;

Tangier disease; TD; familial HDL deficiency; FHD; polymorphism;

cardiovascular disease; coronary artery disease; coronary restenosis;

cerebrovascular disease; peripheral vascular disease;

Alzheimer's disease; Niemann-Pick disease; Huntington's disease;

X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;

prognosis; prophylaxis; drug screening; transgenic animal; mutant;

muteln.

Homo sapiens.

WO200055318-A2.

21-SEP-2000.

15-MAR-2000; 2000WO-IB00532.

15-MAR-1999; 99US-0124702.

08-JUN-1999; 99US-0138048.

17-JUN-1999; 99US-0139600.

01-SEP-1999; 99US-0151977.

(XBR-) UNIV BRITISH COLUMBIA.

(XEN-) XENON BIORESEARCH INC.

Hayden MR, Wilson AR, Pamstone SN;

WPI: 2000-587528/55.

New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's disease and cancer -

Examples; Page -: 229pp; English.

The invention relates to the human ABC1 cholesterol transporter protein (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol efflux from the cell. The gene encoding ABC1 is located on chromosome 9q31, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders, Tangier disease (TD) and familial HDL deficiency (FHD). These diseases are distinguishable in that TD is an autosomal recessive disorder, while FHD is inherited as an autosomal dominant trait. Low levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular disease, particularly coronary artery disease, but also cerebrovascular disease, coronary restenosis, and peripheral vascular disease. Conversely, a high level of HDL has protective effects against cardiovascular disease. The invention provides genetic constructs and transgenic cells and non-human animals comprising human ABC1 nucleic acids, and methods of gene therapy for the treatment or prevention of cardiovascular disease, comprising the administration of an expression vector encoding ABC1 or an active fragment thereof. The invention also encompasses compounds which mimic ABC1 activity, compounds which stimulate ABC1 expression and methods of screening for such compounds. It further relates to methods for determining whether a patient has an increased risk for cardiovascular disease due to polymorphisms in the ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or prevent cardiovascular disease, especially coronary artery disease, cerebrovascular disease, coronary restenosis or peripheral vascular disease. They may also be used in the treatment of diseases associated with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer. The invention specifically excludes proteins with the exact amino acid sequences of Genbank Accession No: CAA10005.1 and X75926, and the nucleic acid with the exact sequence as Genbank Accession No: A7012376.1. The present sequence represents a mutant human ABC1 cholesterol transporter associated with an altered cholesterol level and therefore an altered risk of cardiovascular disease.

Note: The present sequence is not shown in the specification, but is derived from the native human ABC1 shown on pages 152-157.

Sequence 2261 AA:

Query Match 99.9%; Score 11786; DB 21; Length 2261;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2257; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MACWPQLRLILKMLNLFRRQTCQLLEVAWPLIFILILISVRLSPVPEOHCHEPNKA 60
    |||||||
Db 1 MACWPQLRLILKMLNLFRRQTCQLLEVAWPLIFILILISVRLSPVPEOHCHEPNKA 60
QY 61 MPSAGTLPWVOGIIICANNPCFRYPPTGEPAGVGVGNFNKSIYARLFSDARRLLYSQKDT 120
    |||||||
Db 61 MPSAGTLPWVOGIIICANNPCFRYPPTGEPAGVGVGNFNKSIYARLFSDARRLLYSQKDT 120
QY 121 SMKDMRKVRLTLOQIKSSNKLQDFVDNTEFSGFLYHNLSLPKSYDKNLRADVILH 180
    |||||||
Db 121 SMKDMRKVRLTLOQIKSSNKLQDFVDNTEFSGFLYHNLSLPKSYDKNLRADVILH 180

```

QY 181 KVFLOGLYHLTSLCNGSKSEEMTOLGDOVESELCLPKRKLAAREVYLRSMNDILKPTL 240
 |||||
 Db 181 kvflqyqjhltslcnsgskeemqjldgdevselcglprekllaavevrlrsmndllkptl 240
 QY 241 RTLNSTSPSPSKELAEATKTLHLSTGLAOLEFSMRSMDSMDROVMFLNVNSSSTOTI 300
 |||||
 Db 241 rrlnstspfskselaetkllhslgllaqel fsmrswdsmdrmvflnvnsstotl 300
 QY 301 YQAVSRIVCGHPGGGKIKTSIMWYEDNNKALFGNGTBEDEATRYDNTTFCMDLAK 360
 |||||
 Db 301 yqavsrivcghppeggkiktslmwedydnnykalfgngtbeedaetrydnttfcmdlak 360
 QY 361 NLESSLRLIWKALKPLVGLTLYTPDTPATQVAAEVNKKRPOELAVFPHDEGMEELS 420
 |||||
 Db 361 nlespsrlrlwkalplvlgklltlypdtpatqvaevnkkrtqelavfhfdlegmeels 420
 QY 421 PKIWTFMENQEMDLYRMLDSDNDHFWEQOLDGLDWTADIVAFLAHHPEDVOSSNGS 480
 |||||
 Db 421 pkltwmensqemdlvrmldsdndhfweqoldglwtadivaflahhpedsngs 480
 QY 481 VYTWREAFNETNOAIRTISRFMECVNLNKLPEIATEVNLINSMELDERKFMAGIVFTG 540
 |||||
 Db 481 vytwreafeinetnqairtisrfmecnlnklepiatevnlinsmellderkfmagivftg 540
 QY 541 ITPGSIELPHHVYKLRMDIDNVERTNKIKDGYWDPGRADPFEDMRVWGGFAYLQDYV 600
 |||||
 Db 541 itpgsielphhvkykirmidnvertnkikdgywdpgradpfedmrwywggfaylqdyv 600
 QY 601 EOAIIIVLTGTEKKGTVYQOQMPYPCYVDIFLRVWSRSMPLFPLTAMTYSVAVITKGLV 660
 |||||
 Db 601 eoaillvltgtekkgvnyqompypcyvdi flrvwsrsmplfpltlamtysvavitkglv 660
 QY 661 YEKEARLKEETRMIMGDINSILWFSFISSLRPLVASGLVYLKLGNLPLSDSYVAV 720
 |||||
 Db 661 yekearlketrmimgdinsilwfsfisslrplvasaglvyllkgnlplsdsyvav 720
 QY 721 ELISVAVVITLQCFILISTLFSRANLAACGGITFTLYLPLVYLCAWODVYFTLKIRAS 780
 |||||
 Db 721 elisvavviltqcfilistlfsranlaacggitftlylpyvlcawodymgftlkiras 780
 QY 781 LLSPVAFGGECEFFALFEEOGIGVOMDNLFSPEVEDGPNLTTSIMMLFDFILGVMTW 840
 |||||
 Db 781 llsprafggecfalfeeqigvqmdnlfspevedgpnlttsvmmldfilygmwtw 840
 QY 841 YLEAVFPGQYIPRPWYFPCCKSYWFGESDEKSHPGSNOKRMSFECMEEPETHLKLVS 900
 |||||
 Db 841 yleavfpgqyiprpwyfpccksywfgesdekshpgsnqkriseimeeepthklklys 900
 QY 901 IONLKVYVGDGKVAVDGLALMFYEGOTTSPGLGHGACKTTMTSLTGLFPPTSGTAYTL 960
 |||||
 Db 901 ionlkvvyrdgmkvavdglaalmfyegottspglghgackttmtsltglfpptsqta 960
 QY 961 GKDISEMSTIRONLGVCPQHNVLFDMLTVEEHIMFVARLKGISEKHAKAMEQALDVG 1020
 |||||
 Db 961 gkdiseemstirqlnlyvcqphnvlfdmltveehimfvarlkgisekhvkaemeqaldvg 1020
 QY 1021 LPSSLKTKTQSLSGMGKRLSVALAFAVGGSKVYLDEPTAGVDPYSRGGTWELLKTRQ 1080
 |||||
 Db 1021 lpslksktqslsgmgkrlsvalaafavggskvyldeptagvdpysrrggtwellktrq 1080
 QY 1081 GRTIILSTHMHDEADVLDRIAIITSHGKLCVGSSTFLKNLGGYLYTLVKKXVESTLS 1140
 |||||
 Db 1081 gtrtllsthhmdeadvldriaaitshgklccvgsstflknlggylytlvkkxvestls 1140
 QY 1141 SCRNSSTSVYLRKEDSVQSSDAGLGSDESDTLTIDVSAISNLRKHVSEARLVEDI 1200
 |||||
 Db 1141 scrnsstsvylrkedsyqssdaglgsdeshdtltdvsaaisnlrkhvsearlvedi 1200
 QY 1201 GHELTLYVLPYAAKGAFFVELFHEIDRLSDLGISYSIGISTTTEELFLKVAESGVDAE 1260
 |||||
 Db 1201 gheltlyvlypyaakegaffvelfheidrlsdlgisysigisttteeelflkvaesgvdae 1260
 QY 1261 TSDGTLPARNRRAFGDKOSCLRPFTEDDAADPNDSIDIPESRFTDLISGMDGGSYQVK 1320

|||||
 Db 1261 tsdgtlparnrarafgdkosclrpfteddaadpnosidipesretdlisgmddgksyqvk 1320
 QY 1321 GWKLTQOQFVALLMWRLLIARSRKGFPAQOIVLPVFCIALVSLTVPBPKXPSEIQ 1380
 |||||
 Db 1321 gwkltgqgfvallwrrlliarstrkgffaqivlpvfcialvsltlvpbpgkxpselq 1380
 QY 1381 PMWNEQYTFVNSDAPEDDTGLELLNALTKDPGFGTRCMGNPJPDPQOAGEEEMTAP 1440
 |||||
 Db 1381 pmwneqytfvnsdapeddtglllnaltdkpgfgtrcmegnppdpdpqageeewtap 1440
 QY 1441 VPQITMDLFOGNNMTMQNPSPACOCSSDKIKKMLPVCPBPGAGLPBPQKONTADITIDL 1500
 |||||
 Db 1441 vpgitmdlfgnngnmtnqnpaspacocssdkikkmlpvcpbpgaglpbpqkqntaditidl 1500
 QY 1501 TGRNISDYLVTYVOYLKSLKNKIWVEEFYGGFSLGVSMTQALPPSOEVDNADIKOMK 1560
 |||||
 Db 1501 tgrnisdylvtkyooyllkslknkiwveefyggfslgvsmtqalppsoevdnadikgmkk 1560
 QY 1561 HLKIAKDSADREFLNSLGRFMTGLDTRNNKAVWFNNKGWHAISSEFLVNNAILRANLQK 1620
 |||||
 Db 1561 hlkiakdsadrflnslgrfmgtdtrnnkvwnnkgwhaissseflvnnailranlqk 1620
 QY 1621 GENPSHYGITAFNPNLNTKQOLSEVALMTSVDVLVSIQVIFAMSPVASFVFLQER 1680
 |||||
 Db 1621 genpshtygitafnpnlntkqolsevalmtsvdvlvsiqvifamspvasfvflqer 1680
 QY 1681 VSAKHLQFISGVKPVYIWSLNFVWDMCNVVPATVLIIFICPOKSYSSNTLPVLA 1740
 |||||
 Db 1681 vsakhlqfsgvkpvylwslnfvwdmcnvvpatlviifcpgoksyssntlpvlat 1740
 QY 1741 LLLLYGMSITPPLMPASFPVKRIPSTAVVLTSVNLFGINGSAVTFVLELFTDNKLNIN 1800
 |||||
 Db 1741 llllygmsitpplmpasfpvkripstavvltsvnlfgingsavtfvlelftdnklnin 1800
 QY 1801 DILKSVLEIPHFCLRGGLIDMVKNOAMADALEFEGENRFPVPLSMOVLVRNLFAVAE 1860
 |||||
 Db 1801 dilksvleiphfclrgglidmvrknqamadalerefgenrfrvpplsmovlvrnlfavae 1860
 QY 1861 VVFFLITVLIOYREFIRPRVNAKLSPLNDEDEDERRERORILDDGGQNDILEIKELTKI 1920
 |||||
 Db 1861 vvfflitvlioyrefirprvnaaklsplndeedererorilddggqndileikeltki 1920
 QY 1921 YRRKRPAVDRICVGPBGCGFLGYNAGKSGSTFRMLTGDTTVRGAFLKNKSLN 1980
 |||||
 Db 1921 yrrkrpavdricvpgbgcflgynagksgstfrmltgdttvrgaflknksln 1980
 QY 1981 IHEVHQMGYCPOFDATTELLTGREHEVFPALLRGVPEKEVGKVGWMAIRKILVYGEK 2040
 |||||
 Db 1981 ihevqumgycpqfdaitelltgreheffallrgvpekevkvvgewairklglvygek 2040
 QY 2041 YAGNYSGGNRKRLSTAMALIGSPVYVFLDEPTGMDPPKARRPLMNCALSVYKGSVILT 2100
 |||||
 Db 2041 yagnysggnrkrlstamallgspvvfldeptgmdppkarrplmncalsvykgsvilt 2100
 QY 2101 SHSMECEALCTPMAIMVNGREFCLGSVOHLKKNRFGDGTIVIRIAGSNPDJLKVODFG 2160
 |||||
 Db 2101 shsmecealctrmalmvngrefclgsvohlkknrfgdgtivirriagsnpdlkvodfg 2160
 QY 2161 LAFPGSVLRKKNHNMIOYQLPSSLARIFSLQSSKRLHIEDYSVSQTTLDQVFN 2220
 |||||
 Db 2161 lafpgsvlrkknhnmioyqlpsslarifslqsskrlhiedysvsqttldqvfn 2220
 QY 2221 AKQSDDDHLKDLSTLKNQTVDVANLTSEFLDDEKYESYV 2261
 |||||
 Db 2221 akqsdaddhlkdlstlknqtvdvavnltsfldekvesyv 2261

RESULT 12
 AAB38114
 ID AAB38114 standard; Protein: 2261 AA.
 XX
 AC AAB38114;

XX 29-JAN-2001 (first entry)

DE Human ABC1 cholesterol transporter mutant, E1172D.

XX Human ABC1 cholesterol transporter; chromosome 9q31.

KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;

KW Tangier disease; TD; familial HDL deficiency; FHD; polymorphism;

KW cardiovascular disease; coronary artery disease; coronary restenosis;

KW cerebrovascular disease; peripheral vascular disease;

KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;

KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;

KW prognosis; prophylaxis; drug screening; transgenic animal; mutant;

KW mutant.

OS Homo sapiens.

XX WO200055318-A2.

PN 21-SEP-2000.

PD 15-MAR-2000; 2000WO-IB00532.

XX 15-MAR-1999; 99US-0124702.

PR 08-JUN-1999; 99US-0138048.

PR 17-JUN-1999; 99US-0139600.

PR 01-SEP-1999; 99US-0151977.

XX (UYBR-) UNIV BRITISH COLUMBIA.

PA (XEN0-) XENON BIORESEARCH INC.

XX Hayden MR, Wilson AR, Pimstone SN;

PI WPI; 2000-587528/55.

DR New ABC1 polypeptide is useful for treating diseases associated with

PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's

PT disease and cancer -

PS Examples: Page -; 229pp; English.

XX The invention relates to the human ABC1 cholesterol transporter protein

CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is

CC a member of the ATP-binding cassette (ABC transporter) superfamily of

CC proteins, and plays a crucial role in cholesterol transport, particularly

CC intracellular cholesterol trafficking in monocytes and fibroblasts, being

CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is

CC located on chromosome 9q31, and mutations in this gene are associated

CC with two genetic HDL (high density lipoprotein) deficiency disorders,

CC Tangier disease (TD) and familial HDL deficiency (FHD). These diseases

CC are distinguishable in that TD is an autosomal recessive disorder, while

CC FHD is inherited as an autosomal dominant trait. Low levels of HDL ("good

CC cholesterol") in the blood correlate with a high risk of cardiovascular

CC disease, particularly coronary artery disease, but also cerebrovascular

CC disease, coronary restenosis, and peripheral vascular disease.

CC Conversely, a high level of HDL has protective effects against

CC cardiovascular disease. The invention provides genetic constructs and

CC transgenic cells and non-human animals comprising human ABC1 nucleic

CC acids, and methods of gene therapy for the treatment or prevention of

CC cardiovascular disease comprising the administration of an expression

CC vector encoding ABC1 or an active fragment thereof. The invention also

CC encompasses compounds which mimic ABC1 activity, compounds which

CC stimulate ABC1 expression and methods of screening for such compounds.

CC It further relates to methods for determining whether a patient has an

CC increased risk for cardiovascular disease due to polymorphisms in the

CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat

CC or prevent cardiovascular disease, especially coronary artery disease,

CC cerebrovascular disease, coronary restenosis or peripheral vascular

CC disease. They may also be used in the treatment of diseases associated

CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick

CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.

CC The invention specifically excludes proteins with the exact amino acid

CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic

CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The

CC present sequence represents a mutant human ABC1 cholesterol transporter

CC associated with an altered cholesterol level and therefore an altered

CC risk of cardiovascular disease.

CC Note: The present sequence is not shown in the specification, but is

CC derived from the native human ABC1 shown on pages 152-157.

XX Sequence 2261 AA:

QY Query Match 99.9%; Score 11786; DB 21; Length 2261;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2257; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

1 MACWPQLRLIMKNTFFRRRCOLLLEVPMLFPLILISRLSPYPPEOHCHEPNKA 60

1 macwpqlrlilwnkntffrrrcqlllevpmlfplilislsvrlyspypgehehfnka 60

61 MPASGTLPMWQGIICNANPCFRYPTEGAPGVGNFNKSIVARLFSRARLLYSQDT 120

61 mpasagtlpmwqgiicnannpcfrypptegeapgvgnfnksivarlfadarrlllysqdt 120

121 SMKDMRKVLRTIQOTKKSSNKLDDFLVDNFTSGEFLYHMLSPKSYVCKMLRADVILH 180

121 smkdmrkvlrtlqotkkssnklldqdlvndfetsgfllyhmlslpkstlvckmlradvilh 180

181 KVFLOGYOLHLISLNGSKSEMIOLGDOEVSELCGLPKREKLAARLRNSMDILKPIIL 240

181 kvflogyohlhlislngsksemiolgdoevselcglpkreklaarlrnsmdilkpil 240

241 RTLNSTSPFSSKELAEATYTLTLHSLSGTLAQELFSMRSDMKRQEVMLTNNSSSSSTQI 300

241 rltnstspfskelaeatktilhsisgltlaqelfsmrsmkrmqevmltnnsssstqi 300

301 YQAVSRIVCGHPRGGGLKTKSLMWYEDNNYKALFGCGNEDEAFETYNSTTPPCNDIMK 360

301 yqavsrivcghprggglktkslmwylednnykalfgcngnedeaefetynsttpcndimk 360

361 NLESSPISRLIRWALKPLLVGKILYPPDPATROYMAEVNKTFOELAVFHDLEGMWELS 420

361 nlesspisrlirwalkplllvgkilyppdpatroymaevnktfoglavfhdllegmwels 420

421 PKIWTFWENSQENDLYRMLDSDNDHFEOQLDGDWTAQDITVAFIAKHPEDVSSNGS 480

421 pkltwfwensqendlyrmldsrdndhfewqldgdwtaqdivafiakhpedvssngs 480

481 VYIMREAFNETNOAIRTISFMFCVNLKLEPATEVWMLINKSMELDERKFWAGIVFTG 540

481 vyimreafnetnoairtisfmfcvnlklepatevwmlinksmelderkfwagivftg 540

541 ITPGSIELPHRVYKXKIRMDIDNVERTNKIKDGYWDPGRADPPEDMRYVWGFAYLDQV 600

541 itpgsielphrvykykirmdidnvertnkikdgywdpgradppeedmryvwgfyayldqv 600

601 EQAIRRVLTGTEKTYGVYMQOMPCYVDIFLRVRSRMPFLTAWTVSAVYIRKIV 660

601 eqairrvltgtektygvymqompcyvdiflrvsrmpfltlawtvsvayirkiiv 660

661 YEKEARLKETMRIMGDINSILMFSSFTSLIPLVSAGLVLILKGNLLPYSDPSVVFV 720

661 yekearlketmrimgdinsilwfsstslipllvsagllvlilkgnllypsdpsvvfv 720

721 FLVSFAVVTIAGFLISTLFSRANLAACGGIIYFTLVPYVLCAVMDYVGFYTLKIRAS 780

721 flvsfavvtiagflistlfsranlaacggillyftlpyvlcvawdyvgfytlkiras 780

781 LLSVAAGFCGCFEALFEEDGIGVOMDNLFESPVEEDGNLTSSMMLFDFFELGWMTW 840

781 llsvaagfcgcfefaleedgigvomdnlfespedgnltssmmlfdffelgwmtw 840

841 YIEAVPFGOYGIPIPWYFPTCKSYGEESEDEKSHPGSNOKRMSLECMDEEPTHLKGV 900

841 yieavpfgoygipipywfpctksygeesedeskshpgsnqrmslecmeepthlkgyv 900

QY 901 IONLVKVRDGMKVAVDGLANFEGQITSLFNGAGKTTTMSILTELPPTSGATIL 960
 DB 901 Iqnlvkvrdgmkvavdgla nlfegqit slfngagktttmsil telpptsgatyl 960
 QY 961 GKDIRSMSTIRQLGVCPCPHNTYFDMLJYVEBHIFARLKGISEKHVKEMEQMALDVG 1020
 DB 961 gkdirsmstirqlgvcpcphntyfdmljyvebhifarlkgisekhvkemeqmaldv 1020
 QY 1021 LPSSKLKSTQSOLSGMQRKLSVALAFVGGSKVYLDEPTAGVDPYSRRIQWELLYKRG 1080
 DB 1021 lpskklkstqsolsgmqrklsvalafvgsksvyldeptagvdpysrriqwel lkyrg 1080
 QY 1081 GRTIILSTHMDPADVLDGDAIATISHGKCLCCVSSSLFLKNQJLGTGYLFLVKKDVSSLS 1140
 DB 1081 grt iilsthmdpadvldgdaiatishgkclccvssslflknqjlgtyylflvkkdvssls 1140
 QY 1141 SCRRSSSTVSLKKEDESVSSSSDAGLSDHESDTLTIDVSAISNLIRKHVSARLVEDI 1200
 DB 1141 scrrssstvsylkkesdsvssssdaglsdhesdtltidvsa isnlirkhvsarlved i 1200
 QY 1201 GHELTIVLPYEAKEGAFVFLFHEIDRLSDLGISSYGISSETTLEELFLKVAEESGVDAE 1260
 DB 1201 gheltivlpyeakegafvelfheidrlsdlgissygissettleeiflkvaeesgvdae 1260
 QY 1261 TSDGTLPARNRRAFGDKOSCLRPTEDDAADPNDSIDPESEEDLISGMOKGSGYQK 1320
 DB 1261 tsdgtlparnrarafgdkosclrp teddaadpn dsidpe seeldisgmokgsgyvk 1320
 QY 1321 GMLTQOQVVALIKRLLIARRSRKGFPAQIVLPAFVFCIALVFLVPEFGKYSLEIQ 1380
 DB 1321 gmltqgfvallwkrllia rsrk gfpavfvcialvflvpefgkysleiq 1380
 QY 1381 PMYNYQCYFVNSDAEDGTLELINALTKDGFGRKHEGNPIPTPOQAESEETAP 1440
 DB 1381 pmynyqcyfvnsdaedgtlelinaltkd gfg rkh egnp i ptpoqae seetap 1440
 QY 1441 VPQITMDLFQNGNMTQMNPSPACOCSSDKIKKMLPVCPPGAGLPPPOKQMTADILQDL 1500
 DB 1441 vpqitmdlfqngnmtqmnp spacocssdk i kmlpvcppgag lpppokmtadilqdl 1500
 QY 1501 TGRNISDYLVKTYVOTIASKLNKIMVNEFRGSGSLGVSNTQALPPSOEVDIAIKOMK 1560
 DB 1501 tgrnisdylvktyvotiasklnk imvnefrgsgslgvsntqalpps oevdiaikomk 1560
 QY 1561 HUKLAKDSADREFLNSLGRFMTGLDTRNNVKKVFNKNGMHAISFLNNTNNAILKANLQK 1620
 DB 1561 huklaksadreflnslgrfmgtdtrnnvkkvfnkngmha isflnntnna ilkanlqk 1620
 QY 1621 GENPSHYGITTANNHPLNLTQOOLSEVALMTTSVDVLSICVIFAMSEVPASFEVLQER 1680
 DB 1621 genpshygit tannhplnltqoolsevalmttsvdvlsicvifamsevpasfevlqer 1680
 QY 1681 VSKANHLQFISGVKPVYIWLNFVMDMKNVYVPAVLVIIIFCFQOKSYVSSSTNLPVAL 1740
 DB 1681 vskahlqf isgvkpv yiwlnfvmdmknvyvpa vlvi i fcfqoksyvssstnlpval 1740
 QY 1741 LLLLYGMSITPLMAYASFEKIPSTAYVLTISVNLFIGINSVATFELETFDNKLNIN 1800
 DB 1741 llllygmsitplmayasfe k i psta yvltisvnlfiginsvatfele tfdnklnin 1800
 QY 1801 DILKSVFLIFPHFCGRGLIDVKNQAMADALERGENRFPSPISMDVGNLFRAMAVEG 1860
 DB 1801 dilksvflifphfcgrglidvknqamadergenr f pspismdvgnlframaveg 1860
 QY 1861 VVEFLITVLQYREFIRBPVNAKLSPLNDEDEDERERQRILDGGGONDILLETIKELTKI 1920
 DB 1861 vveflitvlqyrefirbpvna k l s p l n d e d e r e r q r i l d g g o n d i l l e t i k e l t k i 1920
 QY 1921 YRRKKRPVDRICVIGIPGEGFGLGVNGAKSSFFKMLTDITVTYRKDALKNKNSILSN 1980
 DB 1921 yrrkkrpvdr icvigipge g fglgvngakssffkmltditvt y rkdal knknsilsn 1980

QY 1981 THEVHONMGYCHPOFATITELLTGREHVEFPALLRGVPEKGVKXGEMAIRKLGLVKGEK 2040
 DB 1981 thevhonmgyc h p o f a t i t e l l t g r e h v e f p a l l r g v p e k g v k x g e m a i r k l g l v k g e k 2040
 QY 2041 YAGNYSGNKRRKLSAMALIGGPVFLDEPTTGMDPKARFELMNCALSVKESRYLT 2100
 DB 2041 yagnysgnkrrklsamalig g p v f l d e p t t g m d p k a r f e l m n c a l s v k e s r y l t 2100
 QY 2101 SHSMECEALCTRMAIMNNGRRCIGSVQHLKNRGGDGTITVRIAGSNPDLKRVODEFG 2160
 DB 2101 shsmecealctrmaimnngrrcigsvqhlknr ggdgtitvri agsnpdlkrvodefg 2160
 QY 2161 IAFPGSVLKEKHNNMLQYQLPSSLSLARIFSIQSOKKRRIHEDYSVQRTTLOVFNF 2220
 DB 2161 iafpgsvlkekhnnmlqyqlpssls larifsiqsokkrrih edysvqrttlovfnf 2220
 QY 2221 AKDQSDDDLKDLSLHKNQYVDAVLTSPLODEKVESYV 2261
 DB 2221 akdqsddhldkdlshknqyvda v l t s p l o d e k v e s y v 2261

RESULT 13

ID AAB38115 standard; Protein: 2261 AA.

AC AAB38115;

DT 29-JAN-2001 (first entry)

DE Human ABC1 cholesterol transporter mutant, R1587K.

KW Human ABC1 cholesterol transporter; chromosome 9q31;

KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;

KW Tangier disease; TD; familial HDL deficiency; FHL; polyomorphism;

KW cardiovascular disease; coronary artery disease; coronary restenosis;

KW cerebrovascular disease; peripheral vascular disease;

KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;

KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;

KW prognosis; prophylaxis; drug screening; transgenic animal; mutant;

KW mutln.

OS Homo sapiens.

PN WC20005318-A2.

XX 21-SEP-2000.

PF 15-MAR-2000; 2000MO-IB00532.

XX 15-MAR-1999; 99US-0124702.

PR 08-JUN-1999; 99US-0138048.

PR 17-JUN-1999; 99US-0139600.

PR 01-SEP-1999; 99US-0151977.

XX (UYBR-) UNIV BRITISH COLUMBIA.

PA (XENO-) XENON BIORESEARCH INC.

XX Hayden MR, Wilson AR, Pimstone SN;

DR WPI; 2000-587528/55.

XX New ABC1 polypeptide is useful for treating diseases associated with

PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's

PT disease and cancer -

XX Examples: Page -: 229pp: English.

CC The invention relates to the human ABC1 cholesterol transporter protein

CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is

CC a member of the ATP-binding cassette (ABC transporter) superfamily of

CC proteins, and plays a crucial role in cholesterol transport, particularly

CC intracellular cholesterol trafficking in monocytes and fibroblasts, being

CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is

located on chromosome 9q31, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders, Tangier disease (TD) and familial HDL deficiency (FHD). These diseases are distinguishable in that TD is an autosomal recessive disorder, while FHD is inherited as an autosomal dominant trait. Low levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular disease, particularly coronary artery disease, but also cerebrovascular disease, coronary restenosis, and peripheral vascular disease. Conversely, a high level of HDL has protective effects against cardiovascular disease. The invention provides genetic constructs and transgenic cells and non-human animals comprising human ABC1 nucleic acids, and methods of gene therapy for the treatment or prevention of cardiovascular disease comprising the administration of an expression vector encoding ABC1 or an active fragment thereof. The invention also encompasses compounds which mimic ABC1 activity, compounds which stimulate ABC1 expression and methods of screening for such compounds. It further relates to methods for determining whether a patient has an increased risk for cardiovascular disease due to polymorphisms in the ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or prevent cardiovascular disease, especially coronary artery disease, cerebrovascular disease, coronary restenosis or peripheral vascular disease. They may also be used in the treatment of diseases associated with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer. The invention specifically excludes proteins with the exact amino acid sequences of GenBank Accession No: CA11005.1 and X75926, and the nucleic acid with the exact sequence as GenBank Accession No: AJ012376.1. The present sequence represents a mutant human ABC1 cholesterol transporter associated with an altered cholesterol level and therefore an altered risk of cardiovascular disease.

Note: The present sequence is not shown in the specification, but is derived from the native human ABC1 shown on pages 152-157.

XX Sequence 2261 AA:

Query Match 99.9%; Score 11786; DB 21; Length 2261;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2257; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACWPQRLRLMKNLFRROTCQLLEVAWPLFIFILISVRLSPYEQHECHPNKA 60
Db 1 macwpqrlllwnlfrfrrtcqllelvawplfifilislrvlspyyeqhechfnka 60
QY 61 MPASGTPWVGITICANNNCFRPTGEPAGVGNFNKSTVARLPSDARRILLISQKOT 120
Db 61 mpsagtlpwvgiticanncpfrptgepagvgnfnksivarllisdarrillllysqkdt 120
QY 121 SMKMRVRLTLOQIRKSSNLKLDPLVNEFPFGFLYNLSPKSTVDMKLRAVDILH 180
Db 121 smkdmrvrltlqoirkssnllkldplvnefpfgflynlslpkstvdmlradvilnh 180
QY 181 KVLQGYQLHLTSLCNGSKSEEMIQLDQEVSEICGLPKREKLAARVLRNSMDILKPL 240
Db 181 kvlqgyqlhltslcnsgskseemiqldqevselcglpreklaaervlrsnmllkpll 240
QY 241 RLTAISTSPFPEKLEAATKTLILSLGLTAELEFMSRSMQMRQWMLTLVNVNSSSTOI 300
Db 241 rltastspfpeskelaaatktilslgltaelefmsrswdmrgevmlltnvnssstci 300
QY 241 RLTAISTSPFPEKLEAATKTLILSLGLTAELEFMSRSMQMRQWMLTLVNVNSSSTOI 300
Db 241 rltastspfpeskelaaatktilslgltaelefmsrswdmrgevmlltnvnssstci 300
QY 301 YQAVSRIVCGHPGEGGLIKISLAWYEDNNYKALFGNGTEDEATFYDNSTTPYCNLDMK 360
Db 301 yqavsrivcghpeggglkikslawyednnykalfgngteedactfydnsttpeycnldmk 360
QY 361 NLESSPSRIITWAKILKPLLVKILYTPDTPATROVMAEVNKTFOELAVFHDLEGMWEELS 420
Db 361 nlesspsrliitwakilpllvkilytpdtpatrgvmaevnktfoelavfhdlegmweels 420
QY 421 PKITFMFNSQMDLVRLRLSDRNDHFWEQOOLGDMTADDIYAFLAKHEDVQSSNGS 480
Db 421 pkivfmsnsqmdlvrlslsdndhfwegqlgldwtacddiayflakhpdedvqssngs 480
QY 481 VYTWREAFENETQAIKRTISREMECVNLKLEPIATEVWLINLKMELLDERKFMAGIVFTG 540

Db 481 vylwreafeneqtlrtisrfmecvnlklepiatevwlilnksmellderkfwagivftg 540
QY 541 ITPGSIELPHVKKIKIMDDINVERTKIKIGYNDPPRPADPFEDMKVWVGAFYIADYV 600
Db 541 itpgsielephvkkikimddinvertkikigyndpprpadpfedmkvwyvgafyayidvv 600
QY 601 BOAIRRVLTGTEKTKGYVMQMPYCYVDIDFLRWMSRMLFMTLAMIYSAVITIGIV 660
Db 601 boairrvltgtektkgyvmqmpycyvdidflrwmsrmlfmtlamiysavlitgiv 660
QY 661 YEKEARLEKTRKIMGLDNLILMFSWISSLIPLVSAGLVYILKGNLPLSPSVYFV 720
Db 661 yekearlektkrmglndnlilmfswisslipllvsaqlvylkgnllpyspsvfv 720
QY 721 FLISAVAVTITQCLISLIFSRANLAAAGGIIFTYTLPLVLCVAMODYGFLLKIFAS 780
Db 721 flisavavtllqclisllfstranlaaaggilftlylplvlcvaodgygflklifas 780
QY 781 ILSPVAFGFGCEYFALFEEOGIGVQMDNLFPSPVEDGFNLTTISIIMLFDFTLYGWTW 840
Db 781 ilspvafgfgceyfalfeegigvqmdnlfspveedgfnlttsvsmllfdtlygwtw 840
QY 841 YTEAVFPGQYCIIPRWYTPCTKSTYFGESEDEKSHPSGNOKRMSFCHEEPTHLKIGVS 900
Db 841 yteavfpgqyqiprwytpctkstyfgeedekshpsngdriselmeepthlkigvs 900
QY 901 IONLVKVVYRDGKVVAVDGLALNFYEGQITSPFGHNGACKTTMTSTLTGLFPPTSGTAYIL 960
Db 901 ionlvkvvyrdgkvavdglaalnfyegqitspfghngackttmtstltglfpptsgtayil 960
QY 961 GMDIRSEMSTIQNLGVCPOHNVLFDMLTVEEHIFVARKGLSEKHVKAEMQALDVG 1020
Db 961 gmdirsemstiqnlgvcpohnvlfdmllveehifvarkglsekhvkaemqaldvg 1020
QY 1021 LPSSKLKSTQSOLSGMOKKLSVALAFVGGSKVYVILDEPTAGVDYPSRGIWELLKXRO 1080
Db 1021 lpsklkstqsolsgmqkksvalafvggskvyllddeptagvdypsrgiwellkxyr 1080
QY 1081 GTTILSTHMHMEDADVIGRIRAITSHGKLCYSSSLFLKNQGTGYTLTVLKKDESSLS 1140
Db 1081 gttilsthmedadvigriraitshgkcyssslflknqgtgytltlvkkdssls 1140
QY 1141 SCRNSSSTVYLKEDSVQSSSDAGLGSDBESDRLTIDVSAISMLIRKHVSEARLVEDI 1200
Db 1141 scnssstvsylkedsvqsssdaglgdhesdrltdvsaismllrkhssearlvedi 1200
QY 1201 GHELYVLDPEAKKAGAYELFHEIDRLSDIGISYGISSETTLBEIPLKVAEBSGVNAE 1260
Db 1201 ghelyvldpeaakegafelheidrlsdigisysgissettleelkvaeesgvdae 1260
QY 1261 TSDGTLPARRRNRPFCDDKQSLRPFTEDADPNDSIDIPESRETDLSGMDGKSSYQVK 1320
Db 1261 tsdgtlparrrnrrpfcddkqslrpfteadaadpnidipesretdllsgmdgkssyqvk 1320
QY 1321 GWKLTQOQFVALMKRLRLIARRSRKGFQAQIVLPAVFCIALVFSILYPPFGKYSLELO 1380
Db 1321 gwkltgqfvallwkrlllarrsrkffaqivlpavfcialvfsilypfgkyslelq 1380
QY 1381 PMWYNDQYTFVNSDAPEDTGTELELNAALTKDQFGTRCMEGNPIDPTPCQAQEEETNAP 1440
Db 1381 pmwyndqytfvnsdapedtgtelelnaaltkdqfgtrcmegnpidptpcqaqeeetnap 1440
QY 1441 VPQITMDLPONGMWYQWNSPACQSSDKIKKMLPVCPPGAGIAPPQKQKQNTADILODL 1500
Db 1441 vpgitmdlpngmwqwnspacqssdkikmlpvcppgaggipppqkqkntadilqdl 1500
QY 1501 TGRNISDYLVKTYVQIITANSLSKNK IWNNEFRYGGFSLGVSNTOALPPSOEVDALIKOKK 1560
Db 1501 tgrnisdylvktyvqiitanslsknk iwnnefr yggsfslgvsn toalppsoevdalikokk 1560
QY 1561 HKLAKDSSADRLNLSIGRMTGLDTRNNYKWFNNKGWHAISSFLVNNALIRANLQK 1620


```

Db 1561 hllakassadrfinslgrfmgldtknnykvwfnkqwhalsfjlnvlnaallranlqk 1620
QY 1621 GENPSHGITAFNHNPLNLTFRQOLSEVALMTSTVDLVSTICVIFAMSPVPAFVFLIOER 1680
Db 1621 genpshtgitaftnplnltdtqglsevalmtstvdvlsicvifamsfvpasfvflqger 1680
QY 1681 VSRKAKHOFISGVKPVYIWTLSNFVWDMCNVVPATLVIIIFICFOOKSVYSTNLPVAL 1740
Db 1681 vsrkakhofisgvkpvwyiwtlsnfvmcnyvvpatlviifcfoqsksvystnlpval 1740
QY 1741 LLLLYGWSITPLMYPASVFKIPSTAVVLTSTNLTGINSVATFVLETFEONTKLNIN 1800
Db 1741 llllygwsitplmypasfvfkpstatvvtltsnltfginsvatfvtlftdnklnln 1800
QY 1801 DILKSVLIRPHHCLGRLIDVYKKNQAMADALERFGENRFPVSLMDVGRNLFAMAVRG 1860
Db 1801 dilksvllrphhclgrlildvynkqamadalrfgentfsvplswdlvgrnlfamavrg 1860
QY 1861 VVFLITVLIOYRPFIRPRPVNAKLSPINDEDEDVRERORITLDGGGNDILEIKELTKI 1920
Db 1861 vvflitvlioyrpfirprpvnaklspindededvrrerqrlldgggndileikeltki 1920
QY 1921 YRRKRKPAVDRIICVGIIPGECFGLGVNGAKSSTFKMLTGDITVTRGDAFLNKNLSIN 1980
Db 1921 yrrkrkpavdrlicvgiippgescfgllgvngakstfkmltgdltvtrgdaflnknlsin 1980
QY 1981 IHEVHOMGVCPOPDATITELLTGREHVEFPALLRGVPEKEVGKVGWMAIRKLGVLVYGER 2040
Db 1981 ihvghomgvcppdattelltgrehveftallrgvpekevgkvgwmairklgvlvyger 2040
QY 2041 YAGNYSGNRKRLSTAMALIGBPVYFLDEPTTGMDPKARREPLMNCALSYVEGRSVLT 2100
Db 2041 yagnysgnrkrlstamalligbpvvyfldepttgmdpkarrplmncalsvvegrsvlt 2100
QY 2101 SHSMECEALCTEMALIMVNRFRCLGSVQHLKMRPDDGTTIYRIAGSNPDLPKPVDFPG 2160
Db 2101 shsmeecealctemalimvnrfrclgsvqhlkmrpdggttiyriagsnpdlpkpvdfpg 2160
QY 2161 LAFPGSVLKKRHRNMLQOYLPSLSLSIARIFSLISQSKRLHTEQSVSQTLLDOGVNF 2220
Db 2161 lafpgsvllkkrhrnmlyolpsslsislarifslisqskrlhedyvsqtlldgvfnf 2220
QY 2221 AKQSGDDHKKDLSLKNQTVDVAVLTSLDDEKVESTY 2261
Db 2221 akqsgddhkkdlslnkqtlvdvavltslldekvkesyv 2261

```

RESULT 14

AAB38105 ID AAB38105 standard; Protein; 2261 AA.

AC AAB38105;

DT 29-JAN-2001 (first entry)

DE Human ABC1 cholesterol transporter TD-2 mutant protein (Q597R).

KM Human ABC1 cholesterol transporter; chromosome 9q31;

KM ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;

KM Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;

KM cardiovascular disease; coronary artery disease; coronary stenosis;

KM cerebrovascular disease; peripheral vascular disease;

KM Alzheimer's disease; Niemann-Pick disease; Huntington's disease;

KM X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;

KM prognosis; prophylaxis; drug screening; transgenic animal; mutant;

KM mutant.

```

PF 15-MAR-2000; 2000MO-IB00532.
XX
PR 15-MAR-1999; 9905-0124702.
PR 08-JUN-1999; 9905-0138046.
PR 17-JUN-1999; 9905-0139600.
PR 01-SEP-1999; 9905-0151977.
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (XENO-) XENON BIORESEARCH INC.
XX
PI Hayden MR, Wilson AR, Plimstone SN:
XX WPI; 2000-587528/55.
DR N-PSDB; AAC69386.
XX
PT New ABC1 polypeptide is useful for treating diseases associated with
PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
PT disease and cancer -
XX
PS Examples; Page -: 229pp; English.
XX
CC The invention relates to the human ABC1 cholesterol transporter protein
CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
CC a member of the ATP-binding cassette (ABC transporter) superfamily of
CC proteins, and plays a crucial role in cholesterol transport, particularly
CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC located on chromosome 9q31, and mutations in this gene are associated
CC with two genetic HDL (high density lipoprotein) deficiency disorders,
CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
CC are distinguishable in that TD is an autosomal recessive disorder, while
CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ('good
CC cholesterol') in the blood correlate with a high risk of cardiovascular
CC disease, particularly coronary artery disease, but also cerebrovascular
CC disease, coronary stenosis, and peripheral vascular disease.
CC Conversely, a high level of HDL has protective effects against
CC cardiovascular disease. The invention provides genetic constructs and
CC transgenic cells and non-human animals comprising human ABC1 nucleic
CC acids, and methods of gene therapy for the treatment or prevention of
CC cardiovascular disease comprising the administration of an expression
CC vector encoding ABC1 or an active fragment thereof. The invention also
CC encompasses compounds which mimic ABC1 activity, compounds which
CC stimulate ABC1 expression and methods of screening for such compounds.
CC It further relates to methods for determining whether a patient has an
CC increased risk for cardiovascular disease due to polymorphisms in the
CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
CC or prevent cardiovascular disease, especially coronary artery disease,
CC cerebrovascular disease, coronary stenosis or peripheral vascular
CC disease. They may also be used in the treatment of diseases associated
CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC The invention specifically excludes proteins with the exact amino acid
CC sequences of GenBank Accession No: CAA10005.1 and X75926.1. The
CC acid with the exact sequence as GenBank Accession No: A012376.1. The
CC present sequence represents a mutant human ABC1 cholesterol transporter
CC associated with an altered cholesterol level and therefore an altered
CC risk of cardiovascular disease.
CC Note: The present sequence is not shown in the specification, but is
CC derived from the native human ABC1 shown on pages 152-157.
XX
SQ Sequence 2261 AA:

```

Query Match 99.9%; Score 11785; DB 21; Length 2261;

Best Local Similarity 99.8%; Pired. No. 0;

Matches 2257; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACWPQLRLIMKNNLTERRRQTCOLLEAVAMPFLILITISVRLSYPEQEHCPNKA 60
 Db 1 macwpqlrlimknnltfrrrrtcqlllevawpflifllisvrlsyppqechcpnka 60
 QY 61 MPSAGTLPWQGIICNANNPCFRYPGGAAGVGNKSTVARLFSRARLLYSQKDT 120
 |||

Db 61 mpsadclpwwvgjllonannpcfrytpcpaepgvvgnfnksivarllfadarllllysgkdt 120
Qy 121 SMKDKRKALRLTLOQIKKSSNLKQDPLVNETPSSGLYHNLSPKSTVDKMLRADVILH 180
Db 121 smkdmrkvrltqlqksssnlkldqdlvdnetisgilyhnlslpkstvdcmradvllh 180
Qy 181 KVPLOGYOHLHLSLONKSGSEEMOLQDOEVESELGLPKREKLAEAERLRSNMDILPIL 240
Db 181 kvllfgyqylhltslcnqskseemlqldqevselcglprekilaaeavylismndllkplil 240
Qy 241 RLNSTSPSPSKELAEATKTLHSLGLTALQELFSMRKSDMRQOEVMPLTVNVSSTSTOI 300
Db 241 rllnstspfspeklaeaetkllhslgltaqelfsmrswdmrgvmflltnvssststql 300
Qy 301 QOANSRIVCGHPREGGLKIKSLNMYEDNNYKALFGGNTEDDATFTFDNSTTPPCNOLMK 360
Db 301 yqavsrlvcghpeggglkikslmwyednnkalfgngteedaeflydnstltpcndlmk 360
Qy 361 NLESSPLRIITMKALPLLVGKIITYPTPATROVMAEVNKTFOELAFVHDLGEMWELLS 420
Db 361 nlessplriitwkalpllvgkilyptpatrtymaevnktfqlavfndlegmwelss 420
Qy 421 PKIWTFMENSQEMDLVRMLLDSRDNDHFEQOQDLGDLMTAODIVAFLAKHPEDVQSSNGS 480
Db 421 pkltwfmsngemdlvrmlldsrndhfwegqldglwtadqivaflakhpdevqssngs 480
Qy 481 VYTWEAENETNOARTISRMECVNLKLEPIATEVVLINKSMELDERKFMAGIVTGT 540
Db 481 vyltweaenetaartlsrimecvnlklepiatevvllinksmellderkfmgagivltg 540
Qy 541 ITPGSEILPHHKYKIRMDIDNVERTNKIKDGYMDPGRADPFEDMRVVMGFAILOVY 600
Db 541 itpgseilphnhkykirmidnvertnkikdgywpgpradpfedmrvvvgfaylilvv 600
Qy 601 EQAIIRLVLTGTEKKTGYVMQMPYCYVDIIFLRVMSRSMPLFMTLAMIYSAVILKISIV 660
Db 601 eqaillrvltgtekktgyvmqmpcyvddiflrvmrsmpflmtlamiysavilkgiv 660
Qy 661 YKKEARLEKTRIMGLDMSIIMFSWFISSLIPPLVSAQLVILKLGMLRYSOPSYVYFV 720
Db 661 ykkaarlektrimgldmsiimfswfisslpllvsaqlilvvlkignlpydspsvfv 720
Qy 721 FLSVAFAVVTILOCFLISTFESRANLAACGIIYFTLPLVLYCYAOMDYVGTFLKIFAS 780
Db 721 flsvaavvtllqcfllstfstranlaaacgiiyftlplvlycyawdyvgtflkifas 780
Qy 781 LLSVAFGFCGYFALFEBOGIGVOMDLFESSVEDEGNLTTSISKMLFDTFLGYMTW 840
Db 781 llsvafgfcgyfalfebogigvomdlfessveedgnlttsiskmlfdtflgyvmtw 840
Qy 841 YLEAVPPOGYGIPRMYPRCTKSYWFGESDEKSHPGSNOKRMSRICMEEPTHLKLGVS 900
Db 841 yleavppogygiprmyprctksywfgesdeksphpsnqrtselcmeeptchlkivs 900
Qy 901 IONLVKYNDDGKAVAVDGLALNFYEGQITSPFLHNGAGKTTMTSILTGLFPTSGTAYIL 960
Db 901 ionlvkynddgkavavdglaalnfyegqitspflhngagktmtstlglfptsgtayil 960
Qy 961 GKDINSEMTIRONTGVCPOHNVLFDMLTVEEHIMFYARLKGLSKRYAKAEQNALDVG 1020
Db 961 gkdinsemtirontgvcpohnvlfdmaltveehimfyarlkglsekryakaemegnalavg 1020
Qy 1021 LPSRSKSTKSTOLSGGMOKSLVALAFVGSVVVLIDPTAGVDVSRGIMELLKTKRO 1080
Db 1021 lpsrskstksqslsggmqklsvalafvgsvvvlidptagvdystrigwellkkyrq 1080
Qy 1081 GRTIILSTHHMDEADVLGDRIAIISHGKLCYGVSSILFKNLQGTGYTLTVLKKEDEVSSLS 1140
Db 1081 grtiilsthmdeadvlgrtialishgklcvgssilfknlqgtgytltlvkkevssls 1140
Qy 1141 SCRNSSTYVYLKEDSVSQSSDAGLGDHSDTLTIVSAISNLIRKHSEARLVEDI 1200
Db 1141 scrnsstlvylkedsvsqssdaglgsdhesdtltdvsaisnlirkhsearlvdi 1200

Qy 1201 GHELTIVLPEAKEGAFVELFHEIDRLSDLGISSYGISSETTLEIFLKAEEGVDAE 1260
Db 1201 gheiltvlylpeaakegafvelfheidrrlsdligissygslettleelkveeesgvdae 1260
Qy 1261 TSDGTLPARNRRAFGDKOSCLRPTEDDAADPNDSIDIPESRETDLSGMDGKSYQVK 1320
Db 1261 tsdgtlparnrrafgdkgscrlrpteedaadpndsidpresretallsgmdgksgyvk 1320
Qy 1321 GMLTQOQFALLMKRLTLARRSRKGFPAQIYLPAYFVCIATVFSIYVPPFGYPSLEIO 1380
Db 1321 gmltqgfavallwkrlltarrsrkgfpaqiyvapvfcialvflsvppfgkypslleiq 1380
Qy 1381 PMMYNEQYTFVNSDADPDTLEILNALATDPGFGTRCMEGNPIPDTPCOAGEEWTAP 1440
Db 1381 pmyneqytfvnsdapedtletlelnalatdkpgfgrcmeagnpdpdtpqageewtap 1440
Qy 1441 VPQTIMDLFQNGMWTMONPSPACQSSDKIKKMLPVCPEGAGLPPPOKONTADILQDL 1500
Db 1441 vpqtimdlfqngwmtmonpspacqssdklkmllpvcppagglpppqkqntadillqdl 1500
Qy 1501 TGRNISYLVKTYVOIITAKSLKMKIWNERRVGFSLGVSNTQALPPSOEVNDAIKOMK 1560
Db 1501 tgrnisdylvktyvoitakslkmkiwnerrvgfslgvsntqalppsoevndaikomk 1560
Qy 1561 HLKLAQSSADRFUNSLGRFMTGIDTERRNKKVFNKNGWHAISSFLNVLINAILRANLQK 1620
Db 1561 hlklakssadrfunslgrfmgtdttrnnkvfnkngwhaissflnvlinalranlqk 1620
Qy 1621 GENPSHYGTAFFNHPLMLTKOOLEVALMTSVDLVLSICVIFAMSGVPSFVFLIOER 1680
Db 1621 genpshygtafahplmltkqglevalmtsvdlvlsicvifamsfvpsfvflioger 1680
Qy 1681 VSKAKHLQFISGKAPVLYWLSNFWMDCNVYVATVLIIFICFOQKSYSSNTLVYAL 1740
Db 1681 vskakhlqfissgkpvlywlsnfwmdcnvyvatvliiflfcfoqksyssntlvyal 1740
Qy 1741 LLLLYGMSITPLMPASFEVFKISTAYVLTSNLFLIGINGSVATFVLELTDNKLNIN 1800
Db 1741 llllygmsitplmpasfevfkistayvltsnlfligingsvatfvlldtnklnin 1800
Qy 1801 DIKSVFLIPHPCLRGCLIDMKVKNQADALBERFGENRVSPISMDVGRNLPMAAVEG 1860
Db 1801 diksvfliphpclrgclidmkvknqadalerfgenrvspiswldvgrnlfmaaveg 1860
Qy 1861 VVEFLTVLLOYREFIRPRVNAKLSPLNDEDEVRERORILIDGGGONILFETKELTKI 1920
Db 1861 vvfltlvlylloyrefirprvnaklsplndedevrrerqllidgggondilelkeltki 1920
Qy 1921 YRRRKRAVDRIKCIIPPECFGILGYNAGKSSFTFKMLTGDTTVTRGDAFLKNKSTILSN 1980
Db 1921 yrrrkrapvdricyippecfgilgynagkssftfkmlltgdtvttrgdaflknksilsn 1980
Qy 1981 IHEVHONMGVCPOFDAITELLTGREHVEFALLRGVEKEVYGEWAIRKGLGYKGEK 2040
Db 1981 ihevhomngvcpoftdaitealltgrehvefallrgvkekygawairkglgykgek 2040
Qy 2041 YAGNYSGGNKRKLSSTAALIGGPPVFLDEPTTGMDKARRFLMNCALSYVKEGRSVLT 2100
Db 2041 yagnysggnkrklsstaaaliggppvfldepttgmdkarrflmncalsvykegrsvlt 2100
Qy 2101 SHSMECEALCTRAAIWNGFRCLGSOHLKRNFGDGYTIVRIAGSNBCLKPVODFG 2160
Db 2101 shsmeecealctraaimngfrclgsvghknrfgygtclivragsnplkpvodfg 2160
Qy 2161 LAFPGSVLKEKHRMLOLYOLPSSLSLARIFSILSOKSKRLHIEDYVSQTTIDQVYVNF 2220
Db 2161 lafpgsvlkekhrmlolyolpsslsstarifsilsokskrlhiedyvsqttldqvynf 2220
Qy 2221 AKDOSDDPHLKDLSLHKNOTVVDVAVLTSPLODEKVESYV 2261
Db 2221 akdosddphlkdlslhknotvvdvavltsplodekvesyv 2261

RESULT	15	
AB38110		
ID	AB38110	standard; Protein; 2261 AA.
XX		
AC	AB38110;	
XX		
DT	29-JAN-2001	(first entry)
XX		
DE	Human ABC1 cholesterol transporter mutant, V399A.	
XX		
KW	Human ABC1 cholesterol transporter; chromosome 9q31.	
KW	ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;	
KW	Tangier disease; TD; familial HDL deficiency; FHD; polymorphism;	
KW	cardiovascular disease; coronary artery disease; coronary restenosis;	
KW	cardiovascular disease; peripheral vascular disease;	
KW	Alzheimer's disease; Niemann-Pick disease; Huntington's disease;	
KW	X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;	
KW	prognosis; prophylaxis; drug screening; transgenic animal; mutant;	
KW	mutin.	
XX		
OS	Homo sapiens.	
XX		
PN	WO20005318-A2.	
XX		
PD	21-SEP-2000.	
XX		
PF	15-MAR-2000; 2000WO-1B00532.	
XX		
PR	15-MAR-1999; 99US-0124702.	
PR	08-JUN-1999; 99US-0138048.	
PR	17-JUN-1999; 99US-0139600.	
PR	01-SEP-1999; 99US-0151977.	
XX		
PA	(UYBR-) UNIV BRITISH COLUMBIA.	
PA	(XENO-) XENON BIORESEARCH INC.	
XX		
PI	Hayden MR, Wilson AR, Pimstone SN;	
XX		
DR	WPI: 2000-587528/55.	
XX		
PT	New ABC1 polypeptide is useful for treating diseases associated with	
PT	ABC1 biological activity, e.g. Alzheimer's disease, Huntington's	
PT	disease and cancer -	
XX		
PS	Examples: Page -: 229pp; English.	
XX		

```

|||||:|||||
Db 11spafgfcyefalfieegiygvwnlifesveedgfnlttsvnmldtflywmtv 840
QY YIEAVFPGQVIGIRPWPYPCPKSYWFGESDEKSHPSNOKRMEIOMEPEPTLTKGVs 900
Db YIEAVFPGQVIGIRPWPYPCPKSYWFGESDEKSHPSNOKRMEIOMEPEPTLTKGVs 900
QY YIEAVFPGQVIGIRPWPYPCPKSYWFGESDEKSHPSNOKRMEIOMEPEPTLTKGVs 900
Db YIEAVFPGQVIGIRPWPYPCPKSYWFGESDEKSHPSNOKRMEIOMEPEPTLTKGVs 900
QY IONLVKVRDGMKVAVVGALALNFYEGQITTSFLGHNGAGKTTTMSILTGLEPPTSGTAYIL 960
Db IONLVKVRDGMKVAVVGALALNFYEGQITTSFLGHNGAGKTTTMSILTGLEPPTSGTAYIL 960
QY IONLVKVRDGMKVAVVGALALNFYEGQITTSFLGHNGAGKTTTMSILTGLEPPTSGTAYIL 960
Db IONLVKVRDGMKVAVVGALALNFYEGQITTSFLGHNGAGKTTTMSILTGLEPPTSGTAYIL 960
QY 961 GKDIREKSTIRONLGVCPQHNIVFDMITVEEHTMFWARLKGLEKHYKAKMEQMALDVG 1020
Db 961 GKDIREKSTIRONLGVCPQHNIVFDMITVEEHTMFWARLKGLEKHYKAKMEQMALDVG 1020
QY 961 GKDIREKSTIRONLGVCPQHNIVFDMITVEEHTMFWARLKGLEKHYKAKMEQMALDVG 1020
Db 961 GKDIREKSTIRONLGVCPQHNIVFDMITVEEHTMFWARLKGLEKHYKAKMEQMALDVG 1020
QY 1021 LPSKSKSTKTSOLSGQMORKLSVALAFVGSKVYLDEPTGVPYSPRGIMETLLKYRQ 1080
Db 1021 LPSKSKSTKTSOLSGQMORKLSVALAFVGSKVYLDEPTGVPYSPRGIMETLLKYRQ 1080
QY 1021 LPSKSKSTKTSOLSGQMORKLSVALAFVGSKVYLDEPTGVPYSPRGIMETLLKYRQ 1080
Db 1021 LPSKSKSTKTSOLSGQMORKLSVALAFVGSKVYLDEPTGVPYSPRGIMETLLKYRQ 1080
QY 1081 GRTIILSTHMDADVIGDRIAIISHGKLCVSSSLFLKNOLGTGYVTLTKVDVSSLS 1140
Db 1081 GRTIILSTHMDADVIGDRIAIISHGKLCVSSSLFLKNOLGTGYVTLTKVDVSSLS 1140
QY 1081 GRTIILSTHMDADVIGDRIAIISHGKLCVSSSLFLKNOLGTGYVTLTKVDVSSLS 1140
Db 1081 GRTIILSTHMDADVIGDRIAIISHGKLCVSSSLFLKNOLGTGYVTLTKVDVSSLS 1140
QY 1141 SCRNSSTSVYILKEDSVSSQSSDAGLSDHESDTITDVAISNLRKHVSEARLYVEDI 1200
Db 1141 SCRNSSTSVYILKEDSVSSQSSDAGLSDHESDTITDVAISNLRKHVSEARLYVEDI 1200
QY 1141 SCRNSSTSVYILKEDSVSSQSSDAGLSDHESDTITDVAISNLRKHVSEARLYVEDI 1200
Db 1141 SCRNSSTSVYILKEDSVSSQSSDAGLSDHESDTITDVAISNLRKHVSEARLYVEDI 1200
QY 1201 GHELYVLPYEAKEGAVELEFHEIDRLSDLGISSTYISSTTLEELFLKVAEESGVDAE 1260
Db 1201 GHELYVLPYEAKEGAVELEFHEIDRLSDLGISSTYISSTTLEELFLKVAEESGVDAE 1260
QY 1201 GHELYVLPYEAKEGAVELEFHEIDRLSDLGISSTYISSTTLEELFLKVAEESGVDAE 1260
Db 1201 GHELYVLPYEAKEGAVELEFHEIDRLSDLGISSTYISSTTLEELFLKVAEESGVDAE 1260
QY 1261 TSDGTLPARNRRAFQKOSCLRPTEBDADPNDSIDIPESRETDLLSGMDKGSYQV 1320
Db 1261 TSDGTLPARNRRAFQKOSCLRPTEBDADPNDSIDIPESRETDLLSGMDKGSYQV 1320
QY 1261 TSDGTLPARNRRAFQKOSCLRPTEBDADPNDSIDIPESRETDLLSGMDKGSYQV 1320
Db 1261 TSDGTLPARNRRAFQKOSCLRPTEBDADPNDSIDIPESRETDLLSGMDKGSYQV 1320
QY 1321 GWKLTQOQFVALLMKRLIARSRKGFPAQIYLPVAFVCIALVFSIIVPPFGKYPSLEQ 1380
Db 1321 GWKLTQOQFVALLMKRLIARSRKGFPAQIYLPVAFVCIALVFSIIVPPFGKYPSLEQ 1380
QY 1321 GWKLTQOQFVALLMKRLIARSRKGFPAQIYLPVAFVCIALVFSIIVPPFGKYPSLEQ 1380
Db 1321 GWKLTQOQFVALLMKRLIARSRKGFPAQIYLPVAFVCIALVFSIIVPPFGKYPSLEQ 1380
QY 1381 PMWYNEQYTFVSNDEPDTGTELLNALTKDPFGSTRCEMGNPDPTRPCQAGEEWTAP 1440
Db 1381 PMWYNEQYTFVSNDEPDTGTELLNALTKDPFGSTRCEMGNPDPTRPCQAGEEWTAP 1440
QY 1381 PMWYNEQYTFVSNDEPDTGTELLNALTKDPFGSTRCEMGNPDPTRPCQAGEEWTAP 1440
Db 1381 PMWYNEQYTFVSNDEPDTGTELLNALTKDPFGSTRCEMGNPDPTRPCQAGEEWTAP 1440
QY 1441 VQGITMDLFONGNMTMONSPACOCSSDKIKMLPVCPPGAGLPPOROKONTADILDD 1500
Db 1441 VQGITMDLFONGNMTMONSPACOCSSDKIKMLPVCPPGAGLPPOROKONTADILDD 1500
QY 1441 VQGITMDLFONGNMTMONSPACOCSSDKIKMLPVCPPGAGLPPOROKONTADILDD 1500
Db 1441 VQGITMDLFONGNMTMONSPACOCSSDKIKMLPVCPPGAGLPPOROKONTADILDD 1500
QY 1501 TGRNISDYLVKTYVOIIAKSLKNKIWVNEFRYGFSLGVSNTQALPPSOEVNDATKOMKK 1560
Db 1501 TGRNISDYLVKTYVOIIAKSLKNKIWVNEFRYGFSLGVSNTQALPPSOEVNDATKOMKK 1560
QY 1501 TGRNISDYLVKTYVOIIAKSLKNKIWVNEFRYGFSLGVSNTQALPPSOEVNDATKOMKK 1560
Db 1501 TGRNISDYLVKTYVOIIAKSLKNKIWVNEFRYGFSLGVSNTQALPPSOEVNDATKOMKK 1560
QY 1561 HUKLAOSSADRFNLNGLGRFMTGLDTRNNVXYWENNNKWHAISSFLNVTNNAILRANLQK 1620
Db 1561 HUKLAOSSADRFNLNGLGRFMTGLDTRNNVXYWENNNKWHAISSFLNVTNNAILRANLQK 1620
QY 1561 HUKLAOSSADRFNLNGLGRFMTGLDTRNNVXYWENNNKWHAISSFLNVTNNAILRANLQK 1620
Db 1561 HUKLAOSSADRFNLNGLGRFMTGLDTRNNVXYWENNNKWHAISSFLNVTNNAILRANLQK 1620
QY 1621 GENPSHYGTATFHPNLNFKOOLSEVALMTTSYDVLSICVIFAMSEVPASFFVFLQER 1680
Db 1621 GENPSHYGTATFHPNLNFKOOLSEVALMTTSYDVLSICVIFAMSEVPASFFVFLQER 1680
QY 1621 GENPSHYGTATFHPNLNFKOOLSEVALMTTSYDVLSICVIFAMSEVPASFFVFLQER 1680
Db 1621 GENPSHYGTATFHPNLNFKOOLSEVALMTTSYDVLSICVIFAMSEVPASFFVFLQER 1680
QY 1681 VSKAKHLQETSGVKPVYIWLNSNFVWDMCNVVPATLVIIIFICFOOKSYVSSTNLPLVAL 1740
Db 1681 VSKAKHLQETSGVKPVYIWLNSNFVWDMCNVVPATLVIIIFICFOOKSYVSSTNLPLVAL 1740
QY 1681 VSKAKHLQETSGVKPVYIWLNSNFVWDMCNVVPATLVIIIFICFOOKSYVSSTNLPLVAL 1740
Db 1681 VSKAKHLQETSGVKPVYIWLNSNFVWDMCNVVPATLVIIIFICFOOKSYVSSTNLPLVAL 1740
QY 1741 LLLLGMSTPLMYPASFYFKIPSTAYVVLTSYNLFIGINGSAPFVLELFTDNKLNNIN 1800
Db 1741 LLLLGMSTPLMYPASFYFKIPSTAYVVLTSYNLFIGINGSAPFVLELFTDNKLNNIN 1800
QY 1741 LLLLGMSTPLMYPASFYFKIPSTAYVVLTSYNLFIGINGSAPFVLELFTDNKLNNIN 1800
Db 1741 LLLLGMSTPLMYPASFYFKIPSTAYVVLTSYNLFIGINGSAPFVLELFTDNKLNNIN 1800
QY 1801 DILKSVFLJPFHPCIRGLGLDMYKNOAMADALERFGENRFVSPLSMDLGVRLFAMAVEG 1860
Db 1801 DILKSVFLJPFHPCIRGLGLDMYKNOAMADALERFGENRFVSPLSMDLGVRLFAMAVEG 1860
QY 1801 DILKSVFLJPFHPCIRGLGLDMYKNOAMADALERFGENRFVSPLSMDLGVRLFAMAVEG 1860
Db 1801 DILKSVFLJPFHPCIRGLGLDMYKNOAMADALERFGENRFVSPLSMDLGVRLFAMAVEG 1860
QY 1861 VFEFLITVLIOYRFFIRPREVNAKLSPLNDEDEVRERORIIDGGQNDILEIKELTKI 1920
Db 1861 VFEFLITVLIOYRFFIRPREVNAKLSPLNDEDEVRERORIIDGGQNDILEIKELTKI 1920

```

```

Db 1861 vffllitvllyqrrfirprpvnaklsplndedvrrergrilldgggqndlleikeltki 1920
QY 1921 YRRRRKPAVDRLICVGIPEBCEGLGVNGAKSSTFKMLTGDTVTYRGDAFLNKSIIISN 1980
Db 1921 YRRRRKPAVDRLICVGIPEBCEGLGVNGAKSSTFKMLTGDTVTYRGDAFLNKSIIISN 1980
QY 1921 YRRRRKPAVDRLICVGIPEBCEGLGVNGAKSSTFKMLTGDTVTYRGDAFLNKSIIISN 1980
Db 1921 YRRRRKPAVDRLICVGIPEBCEGLGVNGAKSSTFKMLTGDTVTYRGDAFLNKSIIISN 1980
QY 1981 IHEVHONMGCPQFQDAITELLTGREHVEFPALLRGVPEKEVGKGEWMAIRKGLVYGEK 2040
Db 1981 IHEVHONMGCPQFQDAITELLTGREHVEFPALLRGVPEKEVGKGEWMAIRKGLVYGEK 2040
QY 1981 IHEVHONMGCPQFQDAITELLTGREHVEFPALLRGVPEKEVGKGEWMAIRKGLVYGEK 2040
Db 1981 IHEVHONMGCPQFQDAITELLTGREHVEFPALLRGVPEKEVGKGEWMAIRKGLVYGEK 2040
QY 2041 YAGNYSGNRKRLSTAMALIGBPVVFLEPTTGMDPKARFLMNCALSVKEGRSVLT 2100
Db 2041 YAGNYSGNRKRLSTAMALIGBPVVFLEPTTGMDPKARFLMNCALSVKEGRSVLT 2100
QY 2041 YAGNYSGNRKRLSTAMALIGBPVVFLEPTTGMDPKARFLMNCALSVKEGRSVLT 2100
Db 2041 YAGNYSGNRKRLSTAMALIGBPVVFLEPTTGMDPKARFLMNCALSVKEGRSVLT 2100
QY 2101 SHSMECEALCTMAIMVNGREFCLGVHUKRFGDGTIYVIRINGSNPDLKPVQDFRG 2160
Db 2101 SHSMECEALCTMAIMVNGREFCLGVHUKRFGDGTIYVIRINGSNPDLKPVQDFRG 2160
QY 2101 SHSMECEALCTMAIMVNGREFCLGVHUKRFGDGTIYVIRINGSNPDLKPVQDFRG 2160
Db 2101 SHSMECEALCTMAIMVNGREFCLGVHUKRFGDGTIYVIRINGSNPDLKPVQDFRG 2160
QY 2161 IAPPGSVLKKEHNNMLQYOLPSSLSLARIFSLISQSKRLHIEDYSVSQTTLDQFVNF 2220
Db 2161 IAPPGSVLKKEHNNMLQYOLPSSLSLARIFSLISQSKRLHIEDYSVSQTTLDQFVNF 2220
QY 2161 IAPPGSVLKKEHNNMLQYOLPSSLSLARIFSLISQSKRLHIEDYSVSQTTLDQFVNF 2220
Db 2161 IAPPGSVLKKEHNNMLQYOLPSSLSLARIFSLISQSKRLHIEDYSVSQTTLDQFVNF 2220
QY 2221 AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKYESYV 2261
Db 2221 AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKYESYV 2261

```

Search completed: September 15, 2002, 12:59:42
 Job time: 331 sec

Mon Sep 16 10:20:20 2002

us-09-595-526b-2.rag

Page 26

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2002, 07:48:35 ; Search time 1589.81 Seconds

(without alignments)
7347.976 Million cell updates/sec

Title: US-09-595-526b-1_COPY_291_7094

Perfect score: 6804
Sequence: 1 atggctgtgtggcctcagct.....gaagaatcctgtcctacagg 6804

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802.*

- 1: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1980.DAT.*
- 2: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT.*
- 3: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT.*
- 4: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT.*
- 5: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1984.DAT.*
- 6: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1985.DAT.*
- 7: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1986.DAT.*
- 8: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1987.DAT.*
- 9: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1988.DAT.*
- 10: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1989.DAT.*
- 11: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1990.DAT.*
- 12: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1991.DAT.*
- 13: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1992.DAT.*
- 14: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1993.DAT.*
- 15: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1994.DAT.*
- 16: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1995.DAT.*
- 17: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1996.DAT.*
- 18: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT.*
- 19: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT.*
- 20: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT.*
- 21: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT.*
- 22: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT.*
- 23: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT.*
- 24: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6804	100.0	10442	22	AAF24680
2	6804	100.0	10442	22	AAF24702
3	6802.4	100.0	10474	22	AAF24686
4	6802.4	100.0	10474	22	AAF24686
5	6802.4	100.0	10474	22	AAF24707
6	6802.4	100.0	10474	22	AAF24708
7	6796	99.9	7860	22	AAF92835
8	6792.8	99.8	7860	22	AAF83826
9	6788	99.8	7260	22	AA213326

10	6788	99.8	7260	22	AA170315	Human ATP binding
11	6784.8	99.7	9741	22	AA506120	Human ABC1 DNA seq
12	6784.8	99.7	9854	22	AA506121	Human ABC1 DNA seq
13	6783.2	99.7	7281	22	AAK51683	Human polynucleoti
14	6762.2	99.4	7086	22	ABA09200	Human ABCA1 homolo
15	6762.2	99.4	7086	22	AAK52667	Human polynucleoti
16	6762	99.4	7864	21	AAK59130	Human ABC1 choles
17	6760.4	99.4	7864	21	AAK59385	Human ABC1 choles
18	6760.4	99.4	7864	21	AAK59386	Human ABC1 choles
19	6760.4	99.4	7864	21	AAK59387	Human ABC1 choles
20	6746	99.1	7861	21	AAK59387	Human ABC1 choles
21	6738	99.0	7857	21	AAK59388	Human ABC1 choles
22	6728	98.9	6880	21	AA294734	Human ABC1 choles
23	6728	98.9	6880	22	AA170314	Human ABC1 choles
24	6724.8	98.8	6880	22	AA21325	Human ABC1 choles
25	1926.8	28.3	7323	21	AA294746	Human ABC1 choles
26	1926.8	28.3	7784	19	AAV33392	Human ABC1 choles
27	1922.8	28.3	5097	22	AA193913	Human ABC1 choles
28	1922.8	28.3	5097	22	AAH18233	Human ABC1 choles
29	1735.8	25.5	6522	22	AA508706	Human ABC1 choles
30	1596	24.9	6607	22	AA54812	Human ABC1 choles
31	1531.6	22.5	5762	22	AA54792	Human ABC1 choles
32	1528.8	22.5	5811	22	AA505626	Human ABC1 choles
33	1465	21.5	5669	22	AA508707	Human ABC1 choles
34	985	14.5	8040	22	AA57452	Human ABC1 choles
35	985	14.5	8195	22	AAH75187	Human ABC1 choles
36	953.6	14.0	3437	22	AA502722	Human ABC1 choles
37	949.2	14.0	3437	23	AA573965	Human ABC1 choles
38	949.2	14.0	4413	23	AA583715	Human ABC1 choles
39	872.6	12.8	2911	21	AA294751	Human ABC1 choles
40	870.8	12.8	3635	22	AA56389	Human ABC1 choles
41	716.2	10.5	1556	22	AAH18606	Human ABC1 choles
42	625.4	9.2	669	22	AAH08356	Human ABC1 choles
43	598	8.8	2740	24	AA562249	Human ABC1 choles
44	430.8	6.3	5894	18	AA785474	Human ABC1 choles
45	430.8	6.3	5894	19	AAV16307	Human ABC1 choles

ALIGNMENTS

RESULT	1	
AAF24680	standard; DNA; 10442 BP.	
ID	AAF24680	
AC	AAF24680;	
XX		
DT	20-APR-2001 (first entry)	
XX		
DE	Nucleotide sequence of a human ABC1 polypeptide.	
XX		
KW	Human: adenosine triphosphate binding cassette protein 1; ABC1;	
KW	apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;	
KW	chromosome 9q22-9q31; heart disease; hypercholesterolemia;	
KW	atherosclerosis; cholesterol transport; ss.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	291..7076
FT		/*tag= a
FT		/product= "ABC1 polypeptide"
PN	WO200078972-A2.	
XX		
PD	28-DEC-2000.	
XX		
PF	16-JUN-2000; 2000WO-US16765.	
XX		
PR	18-JUN-1999; 99US-0140264.	
PR	14-SEP-1999; 99US-0153872.	
PR	19-NOV-1999; 99US-0166573.	
XX		

PA (CVTH-) CV THERAPEUTICS INC.

XX Lawn RM, Wade D, Garvin M;

XX WPI; 2001-137812/14.

PT Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT useful for the development of agents for the treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -

PS Disclosure; Page 122-128; 215pp; English.

XX The present sequence encodes a human adenosine triphosphate (ATP)
XX binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
XX membranes and utilizes ATP hydrolysis to transport a wide variety of
XX substrates across the plasma membrane. ABC1 is a pivotal protein in
XX the apolipoprotein-mediated mobilisation of intracellular cholesterol
XX stores. ABC1 is defective in Tangier disease, a genetic disorder
XX characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
XX localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
XX useful for developing pharmaceutical agents for the treatment of heart
XX disease and other disorders associated with hypercholesterolemia and
XX atherosclerosis. The genes are useful for developing screening assays to
XX screen for compounds that regulate the expression of genes associated
XX with cholesterol transport. The genes and proteins are also useful for
XX are also useful as diagnostic indicators of cardiovascular disease and
XX other disorders associated with hypercholesterolemia.

Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match 100.0%; Score 6804; DB 22; Length 10442;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 6804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggtctgttgctcgaagctgagtggtctgtctgtgtgaagaacctcacttcagaagaaga 60
DB 291 atggtctgttgctcgaagctgagtggtctgtctgtgtgaagaacctcacttcagaagaaga 350
QY 61 caaactatgcagctgttactggaagtgtgctgtgctcctattatcttctctatctgctatc 120
DB 351 caaactatgcagctgttactggaagtgtgctgtgctcctattatcttctctatctgctatc 410
QY 121 tctgttcggtgagctaccaccactatgaacaacatgaatgacatcttcccaataaagcc 180
DB 411 tctgttcggtgagctaccaccactatgaacaacatgaatgacatcttcccaataaagcc 470
QY 181 atgacctctgaggaacacttctggtgttgaaggatattactgtatgccaacaacccc 240
DB 471 atgacctctgaggaacacttctggtgttgaaggatattactgtatgccaacaacccc 530
QY 241 tgttcctgtaaccgactcctctggtggaagctcccgagttgttgaagaacttaacaatcc 300
DB 531 tgttcctgtaaccgactcctctggtggaagctcccgagttgttgaagaacttaacaatcc 590
QY 301 atttgggtgcctggttctcagatgctcggaggtcttcttatacagccagaagaacacc 360
DB 591 atttgggtgcctggttctcagatgctcggaggtcttcttatacagccagaagaacacc 650
QY 361 agcatgaagacatgcgcaaaagtctcagaaacatctacagcatcaagaagaatccagctca 420
DB 651 agcatgaagacatgcgcaaaagtctcagaaacatctacagcatcaagaagaatccagctca 710
QY 421 aacttgaagctcaagattctcctgtgtggaacaatgaacactctctgtgttccatatac 480
DB 711 aacttgaagctcaagattctcctgtgtggaacaatgaacactctctgtgttccatatac 770
QY 481 aactctctctcccaaaagtctcagaaagatgtctgaggggtgtgtgtcatcttccac 540
DB 771 aactctctctcccaaaagtctcagaaagatgtctgaggggtgtgtgtcatcttccac 830
QY 541 aaggtattttgcaagctacagctacatttgacaagctgtgtgcaatgcatcaaatca 600

DB 831 aaggtattttgcaagctacagctacatttgacaagctgtgtgcaatgcatcaaatca 890
QY 601 gaagagatgatcaactgtgtgacccaagaagtcttctgagcttctggtcctccaaagag 660
DB 891 gaagagatgatcaactgtgtgacccaagaagtcttctgagcttctggtcctccaaagag 950
QY 661 aactggtctgacgaagcagagatctctgtccacaatgacatccctgaagaacatccctg 720
DB 951 aactggtctgacgaagcagagatctctgtccacaatgacatccctgaagaacatccctg 1010
QY 721 agaactaactaactcactcctccctcccgaggaagagctgtgtgagccaacaaca 780
DB 1011 agaactaactaactcactcctccctcccgaggaagagctgtgtgagccaacaaca 1070
QY 781 ttgtgtcatttcttggactctgtgccaagagctgttcacgacatgagaagctgtgtgac 840
DB 1071 ttgtgtcatttcttggactctgtgccaagagctgttcacgacatgagaagctgtgtgac 1130
QY 841 atgcagacagagtgatgttcttgaacatgtgaacagctccagctctccaccaccatc 900
DB 1131 atgcagacagagtgatgttcttgaacatgtgaacagctccagctctccaccaccatc 1190
QY 901 taccagagctgtgtctgtatgtctgtcgggacatcccgaggaggggtgagatcaag 960
DB 1191 taccagagctgtgtctgtatgtctgtcgggacatcccgaggaggggtgagatcaag 1250
QY 961 tctctcaactgtgtatgtgagcaacaactataaagcctcttggaggcaatgtgactgag 1020
DB 1251 tctctcaactgtgtatgtgagcaacaactataaagcctcttggaggcaatgtgactgag 1310
QY 1021 gaagatgctgaacactctatgaacactcactcactcactgacatgatttgatgag 1080
DB 1311 gaagatgctgaacactctatgaacactcactcactcactgacatgatttgatgag 1370
QY 1081 aattgagctgtgtctctcttcccgatattctggaagctctgagcgcgtcgtt 1140
DB 1371 aattgagctgtgtctctcttcccgatattctggaagctctgagcgcgtcgtt 1430
QY 1141 gggagaagctctgtatatacacttgacactccagccaagaagctgtgctgagtgac 1200
DB 1431 gggagaagctctgtatatacacttgacactccagccaagaagctgtgctgagtgac 1490
QY 1201 aagaccttcaggaactcgtgtgttccatgactctggaagcattgtggaggaactcagc 1260
DB 1491 aagaccttcaggaactcgtgtgttccatgactctggaagcattgtggaggaactcagc 1550
QY 1261 cccaagatctgacactctcacttgaggaacagccaagaatgacacttccggatgtgtg 1320
DB 1551 cccaagatctgacactctcacttgaggaacagccaagaatgacacttccggatgtgtg 1610
QY 1321 gacagcagaggaacatgacactcttgggaacagcagctgtgagctttagatggacagcc 1380
DB 1611 gacagcagaggaacatgacactcttgggaacagcagctgtgagctttagatggacagcc 1670
QY 1611 gaagcagaggaacatgacactcttgggaacagcagctgtgagctttagatggacagcc 1670
QY 1381 caagacatcgtgtgttcttggccaagcaccagagagatgctcagctgaatgtgttct 1440
DB 1671 caagacatcgtgtgttcttggccaagcaccagagagatgctcagctgaatgtgttct 1730
QY 1441 ggtgtacactgtgaggaagacttcaacagagactcaacaggaatcccggaacatctcgc 1500
DB 1731 ggtgtacactgtgaggaagacttcaacagagactcaacaggaatcccggaacatctcgc 1790
QY 1501 ttcatgagtggttcaactctgacaagctcagagacatgacagaagaagctcgtgtctc 1560
DB 1791 ttcatgagtggttcaactctgacaagctcagagacatgacagaagaagctcgtgtctc 1850
QY 1561 aacaagtcacatgagagctgtgagatgagagaggtctgtgagctgtatgttcaactgga 1620
DB 1851 aacaagtcacatgagagctgtgagatgagagaggtctgtgagctgtatgttcaactgga 1910
QY 1621 attactcagagagatgagctgtgagctcactatgacatgacatgacatgacatgacat 1680

Db 1911 attactcagcagcattgagctgcgccatcatgtcaagtacaaagatccgaatgagacatt 1970
QY 1681 gacaaatgtgagagagacaaataaaatcaaggatggtactgagagccctggtcccgagct 1740
Db 1971 gacaaatgtgagagagacaaataaaatcaaggatggtactgagagccctggtcccgagct 2030
QY 1741 gaccccttgagagacatgctgtagctgctggggggtcttcgctctctgagagatggtg 1800
Db 2031 gaccccttgagagacatgctgtagctgctggggggtcttcgctctctgagagatggtg 2030
QY 1801 gacgagacacatcatcaagggtgctgtagcggcgcccgagaaagaaatggtgtctatagtcaa 1860
Db 2091 gacgagacacatcatcaagggtgctgtagcggcgcccgagaaagaaatggtgtctatagtcaa 2150
QY 1861 cagatgcccctacccctgttaacgttgaatgacatcttctgcggtgtagagccggtcaatg 1920
Db 2151 cagatgcccctacccctgttaacgttgaatgacatcttctgcggtgtagagccggtcaatg 2210
QY 1921 cccctcttcatgacgtctgagcctggatcttactcaagtggctgtagatcatcaaggagcatggtg 1980
Db 2211 cccctcttcatgacgtctgagcctggatcttactcaagtggctgtagatcatcaaggagcatggtg 2270
QY 1981 tatgagaagaagagcagcgtctgtagaagacacatgtagcatcatgtagccttgagacaagcata 2040
Db 2271 tatgagaagaagagcagcgtctgtagaagacacatgtagcatcatgtagccttgagacaagcata 2330
QY 2041 ctctggtttagcgtgttcaatgtagcctcatctcctctctgtgtgagcgtgagcctgcta 2100
Db 2331 ctctggtttagcgtgttcaatgtagcctcatctcctctctgtgtgagcgtgagcctgcta 2390
QY 2101 gtagtcatcctgaagttaagaaacccgtgctcactcaagtgaatcccgagcgtgtgtgtgtc 2160
Db 2391 gtagtcatcctgaagttaagaaacccgtgctcactcaagtgaatcccgagcgtgtgtgtgtc 2450
QY 2161 ttccgtgctgctgttctgctgtgtgtagaatacctgtagcgtcttccctgattagacaactctc 2220
Db 2451 ttccgtgctgctgttctgctgtgtgtagaatacctgtagcgtcttccctgattagacaactctc 2510
QY 2221 tccagagacaaactgtagcagcagcctgtgggggagatcatctacttcaacgtgtgaactgtccc 2280
Db 2511 tccagagacaaactgtagcagcagcctgtgggggagatcatctacttcaacgtgtgaactgtccc 2570
QY 2281 taagcttcgtgtgtgtagcagcagcctgtgggggagatcatctacttcaacgtgtgaactgtccc 2340
Db 2571 taagcttcgtgtgtgtagcagcagcctgtgggggagatcatctacttcaacgtgtgaactgtccc 2630
QY 2341 ctgctgctcctctgtgagccttlttggtctgtgagtaactgtgccccttlttgaggagagca 2400
Db 2631 ctgctgctcctctgtgagccttlttggtctgtgagtaactgtgccccttlttgaggagagca 2690
QY 2401 ggcattgagatgtagcagcagcctgtgtgagatccctgtgtagaagaatggtcttcaat 2460
Db 2691 ggcattgagatgtagcagcagcctgtgtgagatccctgtgtagaagaatggtcttcaat 2750
QY 2461 ctcaacacatcagatcctcaatgtagcgttlttgagacacttccctcatgtgggtgtagaactgt 2520
Db 2751 ctcaacacatcagatcctcaatgtagcgttlttgagacacttccctcatgtgggtgtagaactgt 2810
QY 2521 tacattgagcgtgtcttccagagccagtaacggaattcccaagccctgtatttccctgtc 2580
Db 2811 tacattgagcgtgtcttccagagccagtaacggaattcccaagccctgtatttccctgtc 2870
QY 2581 accaagtccttaactgttctgtagaggaagatgtagaagaagcacaactgtgttcccaacag 2640
Db 2871 accaagtccttaactgttctgtagaggaagatgtagaagaagcacaactgtgttcccaacag 2930
QY 2641 aagagaatgtagaagaatcgtatgtagaggaagaaacccaactgtgaagctggcggtgtcc 2700
Db 2931 aagagaatgtagaagaatcgtatgtagaggaagaaacccaactgtgaagctggcggtgtcc 2990
QY 2701 attcagaacctgtgtaaaagtctacccgagatgtagaggtgtaggtgtgtcgtatgtagcctgtgca 2760
Db 2991 attcagaacctgtgtaaaagtctacccgagatgtagaggtgtaggtgtgtcgtatgtagcctgtgca 3050
QY 2761 ctgaatttltatgaaggccagatcatcactcctctctgtagccacaatgtagcggggagagcg 2820
Db 3051 ctgaatttltatgaaggccagatcatcactcctctctgtagccacaatgtagcggggagagcg 3110
QY 2821 accacatgtcaactcctgaacgggtgtgttcccccagactctgggacacgcctcatatctcg 2880
Db 3111 accacatgtcaactcctgaacgggtgtgttcccccagactctgggacacgcctcatatctcg 3170
QY 2881 ggaagaagaatcgtctcgtgagatgtagcacaatcccgagaaacccgtggggtctgtcccaag 2940
Db 3171 ggaagaagaatcgtctcgtgagatgtagcacaatcccgagaaacccgtggggtctgtcccaag 3230
QY 2941 cataagctgtctgtgagatgtagcactgtcgaagaacaacatctgtgtctatgtcccgcttg 3000
Db 3231 cataagctgtctgtgagatgtagcactgtcgaagaacaacatctgtgtctatgtcccgcttg 3290
QY 3001 aaagggtctctgagaagaacgtgtagagcggagatgtagcagacatggccctggatgtgtgt 3060
Db 3291 aaagggtctctgagaagaacgtgtagagcggagatgtagcagacatggccctggatgtgtgt 3350
QY 3061 ttagcacaagaagaatgtagaagaacaaacaaagccagctgtcaagtgtgagatgtagagaag 3120
Db 3351 ttagcacaagaagaatgtagaagaacaaacaaagccagctgtcaagtgtgagatgtagagaag 3410
QY 3121 ctactgtgagccttgagccttltgtaggagatcctaaggtgtgtcaatctgtgatgaaaccca 3180
Db 3411 ctactgtgagccttgagccttltgtaggagatcctaaggtgtgtcaatctgtgatgaaaccca 3470
QY 3181 gctgtgtgtagaaccttaactcccgagggagataatgtagagcgtgtgtgtaataatccgagaa 3240
Db 3471 gctgtgtgtagaaccttaactcccgagggagataatgtagagcgtgtgtgtaataatccgagaa 3350
QY 3241 ggcgcgaacacatcttctcttaac 3300
Db 3531 ggcgcgaacacatcttctcttaac 3590
QY 3301 atgacatcatctccacatggaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3360
Db 3591 atgacatcatctccacatggaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3650
QY 3361 caagctggaacaggtctactaactcctgagcctgtgtcaagaagaatgtagaactccctccag 3420
Db 3651 caagctggaacaggtctactaactcctgagcctgtgtcaagaagaatgtagaactccctccag 3710
QY 3421 tccctgagaaacaggttagcactgtgtcatcactgtgaaagaaagagagacagtggttctcag 3480
Db 3711 tccctgagaaacaggttagcactgtgtcatcactgtgaaagaaagagagacagtggttctcag 3770
QY 3481 agcagttctatgtctgtgctgtgtagcagacacatgtagagatgtagacagctgtagcatgtgtc 3540
Db 3771 agcagttctatgtctgtgctgtgtagcagacacatgtagagatgtagacagctgtagcatgtgtc 3830
QY 3541 tctgtcatctccaaactcactcaagaagatgtgtctggaagcccggtgtgtgtgaaagacata 3600
Db 3831 tctgtcatctccaaactcactcaagaagatgtgtctggaagcccggtgtgtgtgaaagacata 3890
QY 3601 gggcatagcgtgacatgtgtgtgtagcatalgtagagcgtctcaagaagagagacacttltgtgaa 3660
Db 3891 gggcatagcgtgacatgtgtgtgtagcatalgtagagcgtctcaagaagagagacacttltgtgaa 3950
QY 3661 ctcttcatgagatltgtagcagcgtctcagacactgtggcatcttctagatgtgtagcatctaa 3720
Db 3951 ctcttcatgagatltgtagcagcgtctcagacactgtggcatcttctagatgtgtagcatctaa 4010
QY 3721 gaggcagccctggagaagaatattcctcaaggtgtgtagcgaagaaggtgtgtgtgtgtgtgtg 3780
Db 4011 gaggcagccctggagaagaatattcctcaaggtgtgtagcgaagaaggtgtgtgtgtgtgtgtg 4070
QY 3781 accatagatgtgtactgtgtgtagcagaagaagaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3840
Db 4071 accatagatgtgtactgtgtgtagcagaagaagaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4130

QY 3841 tgccttcgcccgttccactgagatgtagtgcctgcatcccaatgattctcgaatagacca 3900
|||||
Db 4131 tgccttcgcccgttccactgagatgtagtgcctgcatcccaatgattctcgaatagacca 4190
QY 3901 gaatccagagagacagactgtcagtgagtgatgcatgacgaaggtccctacacgggagaa 3960
|||||
Db 4191 gaatccagagagacagactgtcagtgagtgatgcatgacgaaggtccctacacgggagaa 4250
QY 3961 ggttggaactttacacagcaacaggttctgccccttcttggaagagactgtcaattgccc 4020
|||||
Db 4251 ggttcggaactttacacagcaacaggttctgccccttcttggaagagactgtcaattgccc 4310
QY 4021 agacggagtggaagagattttgtctcagatgtcttcacggctgtgtcttcgcatc 4080
|||||
Db 4311 agacggagtggaagagattttgtctcagatgtcttcacggctgtgtcttcgcatc 4370
QY 4081 ggccttggttccagctgtatcggtgcaccccttggcaagtaacccagccttggaattcag 4140
|||||
Db 4371 ggccttggttccagctgtatcggtgcaccccttggcaagtaacccagccttggaattcag 4430
QY 4141 cccctgagttaacacgaaacagtaacatttgtcaagaatgagtcctctgagacacggga 4200
|||||
Db 4431 cccctgagttaacacgaaacagtaacatttgtcaagaatgagtcctctgagacacggga 4490
QY 4201 accctggaactcttaaacgcctccacaaagacccctgctcgaggacccgctgtatgga 4260
|||||
Db 4491 accctggaactcttaaacgcctccacaaagacccctgctcgaggacccgctgtatgga 4550
QY 4261 ggaacacccatcccaacacgcctcgcaagcgaggggaggaagatggaacccctccca 4320
|||||
Db 4551 ggaacacccatcccaacacgcctcgcaagcgaggggaggaagatggaacccctccca 4610
QY 4321 gtccccaagacatcatgagacctctccagaatgggaactggaacatgcaagaacccctca 4380
|||||
Db 4611 gtccccaagacatcatgagacctctccagaatgggaactggaacatgcaagaacccctca 4670
QY 4381 cctgcatgccaagtgtagacgagcgacaaatcaagaagatgctgcctgtgtgtccccaagg 4440
|||||
Db 4671 cctgcatgccaagtgtagacgagcgacaaatcaagaagatgctgcctgtgtgtccccaagg 4730
QY 4441 gcaagggggctgcctcccaacaaagaacaaacactgcaagatactcccaagacctg 4500
|||||
Db 4731 gcaagggggctgcctcccaacaaagaacaaacactgcaagatactcccaagacctg 4790
QY 4501 acaaggaagaacattctggattatctgtgtgaagacgtatgtgcagatacgaacaaagc 4560
|||||
Db 4791 acaaggaagaacattctggattatctgtgtgaagacgtatgtgcagatacgaacaaagc 4850
QY 4561 ttaagaagaacagatctgggtgaatgatttagatgtagcgctttccctgggtgtcagt 4620
|||||
Db 4851 ttaagaagaacagatctgggtgaatgatttagatgtagcgctttccctgggtgtcagt 4910
QY 4621 aatctcaagcattctcctcagtgcaagaagttaatgtagcattcaacaaacaaatgaagaa 4680
|||||
Db 4911 aatctcaagcattctcctcagtgcaagaagttaatgtagcattcaacaaacaaatgaagaa 4970
QY 4681 caccctaaagctggccaagagagatcttgcagatctgcagattcttcccaacagcttggaagatt 4740
|||||
Db 4971 caccctaaagctggccaagagagatcttgcagatctgcagattcttcccaacagcttggaagatt 5030
QY 4741 atgacagactggaacacagaatlaatgtcaaggtgtgttcaataacaaagggtgcat 4800
|||||
Db 5031 atgacagactggaacacagaatlaatgtcaaggtgtgttcaataacaaagggtgcat 5090
QY 4801 gcaatcagcttcttccgtgaatgtcatcaacaatgccaattctccggcgcaacccctgcaaaag 4860
|||||
Db 5091 gcaatcagcttcttccgtgaatgtcatcaacaatgccaattctccggcgcaacccctgcaaaag 5150
QY 4861 ggaagagacccctagccatttgaatgaattacgcttcaatccctggaatctcaacaaag 4920
|||||
Db 5151 ggaagagacccctagccatttgaatgaattacgcttcaatccctggaatctcaacaaag 5210
QY 4921 cagcagcttcaaggtgtgctctgatgacacatcagtgatgtctctgtgtccatctgt 4980
|||||
Db 5211 cagcagcttcaaggtgtgctctgatgacacatcagtgatgtctctgtgtccatctgt 5270
QY 4981 gtcattcttgaatgtctctgtcccgacgacttctgtatctcctgcatccagagcg 5040
|||||
Db 5271 gtcattcttgaatgtctctgtcccgacgacttctgtatctcctgcatccagagcg 5330
QY 5041 gtcagcaagcaaaacacactgcaattcactagtgagtgagagctgtcatctactgtctc 5100
|||||
Db 5331 gtcagcaagcaaaacacactgcaattcactagtgagtgagagctgtcatctactgtctc 5390
QY 5101 tctaatcttgcctgagatgtgcaatgaatgtgtccctgcacactgtcatatcatc 5160
|||||
Db 5391 tctaatcttgcctgagatgtgcaatgaatgtgtccctgcacactgtcatatcatc 5450
QY 5161 ttcactgtctccacgagaaatctctatgtgtccctccacacactgcctgtgtagccctt 5220
|||||
Db 5451 ttcactgtctccacgagaaatctctatgtgtccctccacacactgcctgtgtagccctt 5510
QY 5221 ctacttctgtctatggtgtgcaatcaacacttcaatgtaacccagctctctgtgttc 5280
|||||
Db 5511 ctacttctgtctatggtgtgcaatcaacacttcaatgtaacccagctctctgtgttc 5570
QY 5281 aagatcccccagcacagcctatgtgtgtcaacagcggtgaaccccttcatatgcatat 5340
|||||
Db 5571 aagatcccccagcacagcctatgtgtgtcaacagcggtgaaccccttcatatgcatat 5630
QY 5341 ggcagcgtgacacacttctgtctgagcgtgtcaacgcaataagctgaataatcat 5400
|||||
Db 5631 ggcagcgtgacacacttctgtctgagcgtgtcaacgcaataagctgaataatcat 5690
QY 5401 gataccttgaaagctgcgttcttgatcttccacatcttctgtctggaagagagctcatc 5460
|||||
Db 5691 gataccttgaaagctgcgttcttgatcttccacatcttctgtctggaagagagctcatc 5750
QY 5461 gacatggtgtaaaaacacagcgcaatgctgtcatgaccttggaagagcttgggagaaatcgctt 5520
|||||
Db 5751 gacatggtgtaaaaacacagcgcaatgctgtcatgaccttggaagagcttgggagaaatcgctt 5810
QY 5521 gttgtcaacattactcttggagcctgtgtggaacgaacccctctgcacatggtggaagag 5580
|||||
Db 5811 gttgtcaacattactcttggagcctgtgtggaacgaacccctctgcacatggtggaagag 5870
QY 5581 gtgtgtctctccatlaactgtctcgaatccagtaacagattcttcaacggcccaacct 5640
|||||
Db 5871 gtgtgtctctccatlaactgtctcgaatccagtaacagattcttcaacggcccaacct 5930
QY 5641 gtaatgcaaaagctatctcctctgaatgtagaagatgtagaagtgtagcggaagacag 5700
|||||
Db 5931 gtaatgcaaaagctatctcctctgaatgtagaagatgtagaagtgtagcggaagacag 5990
QY 5701 agaatcttgaatgtggaagcggaatgtagatcttagaatacgaagagtgtagcgaagata 5760
|||||
Db 5991 agaatcttgaatgtggaagcggaatgtagatcttagaatacgaagagtgtagcgaagata 6050
QY 5761 tatagaaggaagcggaagcctgtgtgacagagattgtgtggaattctcctcctgtag 5820
|||||
Db 6051 tatagaaggaagcggaagcctgtgtgacagagattgtgtggaattctcctcctgtag 6110
QY 5821 tgccttgggtcctcctggaattaaatgggctggaataatcaacttcaagaatgttaaca 5880
|||||
Db 6111 tgccttgggtcctcctggaattaaatgggctggaataatcaacttcaagaatgttaaca 6170
QY 5881 ggaatagcaactgttagccggaagagatgcttcttcaacaaatagatattatcaaac 5940
|||||
Db 6171 ggaatagcaactgttagccggaagagatgcttcttcaacaaatagatattatcaaac 6230
QY 5941 atccatgaaatgacatcagaacatggtgctacgtccctcagatttgatgcatcacaagatgt 6000
|||||
Db 6231 atccatgaaatgacatcagaacatggtgctacgtccctcagatttgatgcatcacaagatgt 6290
QY 6001 ttgactgggaggaacacgtgagattcttgcctttagaagagatccagagaagaa 6060
|||||


```

Db 6291 ttgactggagagaaacagtgagttcttgccttcttgagagagatcccaagaagaa 6350
Qy 6061 gttggcaaggttggtagagcgtatccgaaactggcctcgtagatcaggaagaa 6120
Db 6351 gttggcaaggttggtagagcgtatccgaaactggcctcgtagatcaggaagaa 6410
Qy 6121 tatgtgttaactaatagtagaggaacaaagcaagctctctacagcattgcttgc 6180
Db 6411 tatgtgttaactaatagtagaggaacaaagcaagctctctacagcattgcttgc 6470
Qy 6181 ggcggggccctctgtgttcttgatgaaccaccacagagatgattcccaagcccg 6240
Db 6471 ggcggggccctctgtgttcttgatgaaccaccacagagatgattcccaagcccg 6530
Qy 6241 cgttcttgtagaactgtgcccataagtggttgcagaagaggagagatcagtagtgc 6300
Db 6531 cgttcttgtagaactgtgcccataagtggttgcagaagaggagagatcagtagtgc 6590
Qy 6301 tctcatagtagaagaaatgtagagctcttgcactagatgtagcaatcattgcaatg 6360
Db 6591 tctcatagtagaagaaatgtagagctcttgcactagatgtagcaatcattgcaatg 6650
Qy 6361 aggttcaagtgcttgtagcaggttccagcactcaaaaataggtttggagatggtata 6420
Db 6651 aggttcaagtgcttgtagcaggttccagcactcaaaaataggtttggagatggtata 6710
Qy 6421 atagttgtagaataagcaaggttccacccgagcctgtagagccttcttgg 6480
Db 6711 atagttgtagaataagcaaggttccacccgagcctgtagagccttcttgg 6770
Qy 6481 ctgtgcttcccggaaggttctcaaaaggaacacccggaatgtagaataacagctt 6540
Db 6771 ctgtgcttcccggaaggttctcaaaaggaacacccggaatgtagaataacagctt 6830
Qy 6541 ccatcttcattatctctctcgtgcaggaatattcagatcctctccagagcaaaagc 6600
Db 6831 ccatcttcattatctctctcgtgcaggaatattcagatcctctccagagcaaaagc 6890
Qy 6601 ctccacatagaagaactactctgttctcagacaacaccttgaccagatttggactt 6660
Db 6891 ctccacatagaagaactactctgttctcagacaacaccttgaccagatttggactt 6950
Qy 6661 gccaaggaacaaagtatagatgacacacttaaaagacctcattacacaaaacagaca 6720
Db 6951 gccaaggaacaaagtatagatgacacacttaaaagacctcattacacaaaacagaca 7010
Qy 6721 gtagtggagcttgagttctacacatcttctacagagatgagaagtgaaagaagctat 6780
Db 7011 gtagtggagcttgagttctacacatcttctacagagatgagaagtgaaagaagctat 7070
Qy 6781 gtagtggagcttgagttctacacatcttctacagagatgagaagtgaaagaagctat 7070
Db 7071 gtagtggagcttgagttctacacatcttctacagagatgagaagtgaaagaagctat 7094

```

RESULT 2

AAF24702 standard; DNA: 10442 BP.

AAF24702:
20-APR-2001 (first entry)

DE Nucleotide sequence of a human ABC1 polypeptide.

KX Human: adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KM chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

```

FT CDS 291..7076
FT /tag= a
FT /product= "ABC1 polypeptide"
PN WO200078971-A2.
XX 28-DEC-2000.
PD 16-JUN-2000; 2000MO-US16591.
PE 18-JUN-1999; 99US-0140264.
PR 14-SEP-1999; 99US-0153872.
PR 19-NOV-1999; 99US-0166573.
XX (CVTH-) CV THERAPEUTICS INC.
PA (UNIW ) UNIV WASHINGTON.
PI Lawn RM, Wade D, Oram JF, Garvin M;
DR MPI: 2001-137811/14.
DR P-PSDB; AAB31365.
XX
XX Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT polynucleotides and polypeptides, useful for treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX
XX Claim 3; Page 117-123; 211pp; English.
PS
XX
XX The present sequence encodes a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
CC membranes and utilises ATP hydrolysis to transport a wide variety of
CC substrates across the plasma membrane. ABC1 is a pivotal protein in
CC the apolipoprotein-mediated mobilisation of intracellular cholesterol
CC stores. ABC1 is defective in Tangier disease, a genetic disorder
CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
CC useful for developing pharmaceutical agents for the treatment of heart
CC disease and other disorders associated with hypercholesterolemia and
CC atherosclerosis. The genes are useful for developing screening assays to
CC screen for compounds that regulate the expression of genes associated
CC with cholesterol transport. The genes and proteins are also useful for
CC are also useful as diagnostic indicators of cardiovascular disease and
CC other disorders associated with hypercholesterolemia.
XX
SQ Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other:
Query Match 100.0%; Score 6804; DB 22; Length 10442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 atggtctgttgccctcagtagtgcgtgctgtagaagaacctcacttcagaaga 60
Db 291 atggtctgttgccctcagtagtgcgtgctgtagaagaacctcacttcagaaga 350
Qy 61 caaatgcaagctgttactggaagtgacctgacctattatctctcgtatcgtc 120
Db 351 caaatgcaagctgttactggaagtgacctgacctattatctctcgtatcgtc 410
Qy 121 tctgttgagctagctaccaccctatgaaacaaatgaaatgcaattccaaataagcc 180
Db 411 tctgttgagctagctaccaccctatgaaacaaatgaaatgcaattccaaataagcc 470
Qy 181 atgacctgcaggaacacctcttgggttcaggggattatctgtaatgccaacacc 240
Db 471 atgacctgcaggaacacctcttgggttcaggggattatctgtaatgccaacacc 530
Qy 241 tgttcgttaaccgacctctcgggagagctcccggaagtgttggaaactttaacaatcc 300
Db 531 tgttcgttaaccgacctctcgggagagctcccggaagtgttggaaactttaacaatcc 590
Qy 301 atgtgtcgcgcctgttctcagatgctcggagagcttcttatacagccagaagaacc 360

```

Db 591 atgtgctgcgcctgtctcagatgctcggagctctctttatcacgcggaagaagacc 650
QY 361 agcttgaagacatgcgcaagtlcttgaagacatlaacagacatacaagaaatccagctca 420
Db 651 agcttgaagacatgcgcaagtlcttgaagacatlaacagacatacaagaaatccagctca 710
QY 421 aacttgaagcttcaagaatcttcctgttgaagacataaagcttctgtgttccatatac 480
Db 711 aacttgaagcttcaagaatcttcctgttgaagacataaagcttctgtgttccatatac 770
QY 481 aacctctctcccaagcttactatgttgaagacataaagcttctgtgttccatatac 540
Db 771 aacctctctcccaagcttactatgttgaagacataaagcttctgtgttccatatac 830
QY 541 aagttattttgcaagcttccagcttacttgaagacataaagcttctgtgttccatatac 600
Db 831 aagttattttgcaagcttccagcttacttgaagacataaagcttctgtgttccatatac 890
QY 601 gaagagatgatacacttggtagcacaagaagtlcttgaagcttctgtgttccatatac 660
Db 891 gaagagatgatacacttggtagcacaagaagtlcttgaagcttctgtgttccatatac 950
QY 661 aacttgcctgcgcaagcagagagatcttcttccacatggaatccctgaagccaatctgt 720
Db 951 aacttgcctgcgcaagcagagagatcttcttccacatggaatccctgaagccaatctgt 1010
QY 721 agaacataaactatacctccctcccgagagagagctgttgaagccaataaaca 780
Db 1011 agaacataaactatacctccctcccgagagagagctgttgaagccaataaaca 1070
QY 781 ttgtctcatagtlcttggagctctgcccagagagctgttgaagcagagctgtgagac 840
Db 1071 ttgtctcatagtlcttggagctctgcccagagagctgttgaagcagagctgtgagac 1130
QY 841 atgcgcag 900
Db 1131 atgcgcag 1190
QY 901 taacagagctgttctcgtatcttctgcgagacatcccgagagagagagagagagagagag 960
Db 1191 taacagagctgttctcgtatcttctgcgagacatcccgagagagagagagagagagagag 1250
QY 961 tctcttaactgtatgagagac 1020
Db 1251 tctcttaactgtatgagagac 1310
QY 1021 gaagatgctgaaacctctatgacacactatacactccttacttgaagatgttgaag 1080
Db 1311 gaagatgctgaaacctctatgacacacactatacactccttacttgaagatgttgaag 1370
QY 1081 aatttggagctagtcctcttcccgacatlaacttgaagagcttgaagagcgtgctgct 1140
Db 1371 aatttggagctagtcctcttcccgacatlaacttgaagagcttgaagagcgtgctgctgct 1430
QY 1141 gggagagatcctgtatatacacttgaacatccagacacacacacacacacacacacacac 1200
Db 1431 gggagagatcctgtatatacacttgaacatccagacacacacacacacacacacacacac 1490
QY 1201 aagaccttccaggaactgctgttcatatgactggaagagcagatgttgaaggaatacagc 1260
Db 1491 aagaccttccaggaactgctgttcatatgactggaagagcagatgttgaaggaatacagc 1550
QY 1261 cccaagatcctgagactgctgttcatatgactggaagagcagatgttgaaggaatacagc 1320
Db 1551 cccaagatcctgagactgctgttcatatgactggaagagcagatgttgaaggaatacagc 1610
QY 1321 gacacagagagacatgacacacttcttggagaagacagatgttgaaggaatacagc 1380
Db 1611 gacacagagagacatgacacacttcttggagaagacagatgttgaaggaatacagc 1670
QY 1381 caagacatcgttgcgttcttggcagacacacacacacacacacacacacacacacacacac 1440
Db 1671 caagacatcgttgcgttcttggcagacacacacacacacacacacacacacacacacacac 1730
QY 1441 gtgtacacacttgaagagagagcttcaacagacatacagagacatcccgacacatcttgcg 1500
Db 1731 gtgtacacacttgaagagagagcttcaacagacatacagagacatcccgacacatcttgcg 1790
QY 1501 ttcatgtgagtgatgtaacactgaacagagctgaacccaatagacaagaagtlctgtctatc 1560
Db 1791 ttcatgtgagtgatgtaacactgaacagagctgaacccaatagacaagaagtlctgtctatc 1850
QY 1561 aacaagcttcaagctgtctgtatgagagagagagagagagagagagagagagagagagag 1620
Db 1851 aacaagcttcaagctgtctgtatgagagagagagagagagagagagagagagagagagagag 1910
QY 1621 attactcagagacagatgagagctgcccacatagatgaagacatccgaatgagacat 1680
Db 1911 attactcagagacagatgagagctgcccacatagatgaagacatccgaatgagacat 1970
QY 1681 gacaaatgttggag 1740
Db 1971 gacaaatgttggag 2030
QY 1741 gacctcttgaagacatgctgttactgttggagagagagagagagagagagagagagagagag 1800
Db 2031 gacctcttgaagacatgctgttactgttggagagagagagagagagagagagagagagagag 2090
QY 1801 gagcagagacatcacaagagtgctgacgagagacagagagagagagagagagagagagagag 1860
Db 2091 gagcagagacatcacaagagtgctgacgagagacagagagagagagagagagagagagagag 2150
QY 1861 cagatgcccatacctctgttgaagtgacatcttctgtggagagagagagagagagagagagag 1920
Db 2151 cagatgcccatacctctgttgaagtgacatcttctgtggagagagagagagagagagagagag 2210
QY 1921 cccctcttcaatgacagctgagcctgagattactcagtgctgtgacatcaagagcagctgtg 1980
Db 2211 cccctcttcaatgacagctgagcctgagattactcagtgctgtgacatcaagagcagctgtg 2270
QY 1981 tatagaag 2040
Db 2271 tatagaag 2330
QY 2041 ctctgttgaagctgttcatatgagcctatccctctctcttcttgaagcgtgagcgtgagta 2100
Db 2331 ctctgttgaagctgttcatatgagcctatccctctctcttcttgaagcgtgagcgtgagta 2390
QY 2101 gtgttcatctcgtgaagatgaagaaacgtgctgcttcaagtgatcccgagcgtgtgtgtc 2160
Db 2391 gtgttcatctcgtgaagatgaagaaacgtgctgcttcaagtgatcccgagcgtgtgtgtc 2450
QY 2161 ttccgttccgtgttgt 2220
Db 2451 ttccgttccgtgttgt 2510
QY 2221 tccagagcacaacctgagcagagcctgttgggggacatcatctacttcaacgcgtgtaacatgccc 2280
Db 2511 tccagagcacaacctgagcagagcctgttgggggacatcatctacttcaacgcgtgtaacatgccc 2570
QY 2281 taagctcgt 2340
Db 2571 taagctcgt 2630
QY 2341 ctgctgttccctgt 2400
Db 2631 ctgctgttccctgt 2690
QY 2401 ggcattggagtgagtgagagac 2460
Db 2691 ggcattggagtgagtgagagac 2750
QY 2461 ctcaacacttgcattcctatgagcagctgttgaacacacttccctatgaggggtgagcctgg 2520
Db 2751 ctcaacacttgcattcctatgagcagctgttgaacacacttccctatgaggggtgagcctgg 2810

QY 2521 tacattgagcgtctcttccagcgcaatgaaatcccaagcccttgatatttccctgc 2580
|||||
Db 2811 tacattgagcgtctcttccagcgcaatgaaatcccaagcccttgatatttccctgc 2870
QY 2581 accaagctcctactggttctgaggaagatgaatgaagaagcaacctgttccaacag 2640
|||||
Db 2871 accaagctcctactggttctgaggaagatgaatgaagaagcaacctgttccaacag 2930
QY 2641 aagaagaatgctcaaatctgcatgaggaagaaacccccccttgaaagcggtgtcc 2700
|||||
Db 2931 aagaagaatgctcaaatctgcatgaggaagaaacccccccttgaaagcggtgtcc 2990
QY 2701 attcgaacctgttaaaagctctaccgagatgagatgaagctgtctcgatgagcgca 2760
|||||
Db 2991 attcgaacctgtgtaaaagctctaccgagatgagatgaagctgtctcgatgagcgca 3050
QY 2761 ctgaattttatgagggcgcaagatcaacctctctctctgagcccaatgagagcggaagagc 2820
|||||
Db 3051 ctgaattttatgagggcgcaagatcaacctctctctgagcccaatgagagcggaagagc 3110
QY 2821 accacatgtcaatctcaacgggtgttccccccgacctgagggcaacgctatactctg 2880
|||||
Db 3111 accacatgtcaatctcaacgggtgttccccccgacctgagggcaacgctatactctg 3170
QY 2881 ggaagaagacatctcgctctgagatgaagcaacatccgcaagaaacctgagggtctgtcccaag 2940
|||||
Db 3171 ggaagaagacatctcgctctgagatgaagcaacatccgcaagaaacctgagggtctgtcccaag 3230
QY 2941 cataaagctctgtttgacatgctgactgtctgaaagaaacatctggtttctatgcccgccttg 3000
|||||
Db 3231 cataaagctctgtttgacatgctgactgtctgaaagaaacatctggtttctatgcccgccttg 3290
QY 3001 aaagggctctctgaggaagacagctgaagcgagatgagcaagatgagccctgagatgtgtg 3060
|||||
Db 3291 aaagggctctctgaggaagacagctgaagcgagatgagcaagatgagccctgagatgtgtg 3350
QY 3061 ttgcatcaagcaagctgaaagaacaaagaacacagctgttcaggtgagatgcaaggaag 3120
|||||
Db 3351 ttgcatcaagcaagctgaaagaacaaagaacacagctgttcaggtgagatgcaaggaag 3410
QY 3121 ctctctgtgacctgtgacctgtgtcgaggagatctgaagttgtcatctctgatatgaaccaca 3180
|||||
Db 3411 ctctctgtgacctgtgacctgtgtcgaggagatctgaagttgtcatctctgatatgaaccaca 3470
QY 3181 gctgtgtgtggaaccttaactccgcaagggaataatgagagctgtctgtgaataaccgaca 3240
|||||
Db 3471 gctgtgtgtggaaccttaactccgcaagggaataatgagagctgtctgtgaataaccgaca 3530
QY 3241 ggcgcgcacatatttctctctacacacacatgagatgagcggaagctctctgaggagacag 3300
|||||
Db 3531 ggcgcgcacatatttctctctacacacacatgagatgagcggaagctctctgaggagacag 3590
QY 3301 attgcacatctctcccatgaggaagctgtgtgtgtgagctctccctgtttctgaagaac 3360
|||||
Db 3591 attgcacatctctcccatgaggaagctgtgtgtgtgagctctccctgtttctgaagaac 3650
QY 3361 cagctgtggaacagctctactacccctgacctgtgtcaagaagaatgtggaatccctcccaag 3420
|||||
Db 3651 cagctgtggaacagctctactacccctgacctgtgtcaagaagaatgtggaatccctcccaag 3710
QY 3421 tctcgcgaaacagtaagtaagctgtgtcaatctgaanaaagaaagacagtttctccag 3480
|||||
Db 3711 tctcgcgaaacagtaagtaagctgtgtcaatctgaanaaagaaagacagtttctccag 3770
QY 3481 agcagttctgagctgtgacctgtgagcgacatgagatgaaacgctgtgacatcgatgtcc 3540
|||||
Db 3771 agcagttctgagctgtgacctgtgagcgacatgagatgaaacgctgtgacatcgatgtcc 3830
QY 3541 tctgtctctccaaacctcaagaagaacatgtctgtcaagcccgctgtgtggaagacata 3600
|||||
Db 3831 tctgtctctccaaacctcaagaagaacatgtctgtcaagcccgctgtgtggaagacata 3890

QY 3601 gggcatgagcgtgacctatgtctgcatatgaagctgtcaaggaggaagccttctgaa 3660
|||||
Db 3891 gggcatgagcgtgacctatgtctgcatatgaagctgtcaaggaggaagccttctgaa 3950
QY 3661 cctctctatgagatgagatgagacggcctctcagaacctgtgacattctgaatgaatcaca 3720
|||||
Db 3951 cctctctatgagatgagatgagacggcctctcagaacctgtgacattctgaatgaatcaca 4010
QY 3721 gagaagacctgtgaaagaatatctccaaagtgagcggaagaagatgtgtgtgtgtcgtgag 3780
|||||
Db 4011 gagaagacctgtgaaagaatatctccaaagtgagcggaagaagatgtgtgtgtgtcgtgag 4070
QY 3781 acctgaagatgtaacctgttcagcaagacgaacgaacgggacctctgaggaacagcagagc 3840
|||||
Db 4071 acctgaagatgtaacctgttcagcaagacgaacgaacgggacctctgaggaacagcagagc 4130
QY 3841 tgtcttcgcccgtctcactgaagaatgagctgtctgcatccaaatgattctgacatagacca 3900
|||||
Db 4131 tgtcttcgcccgtctcactgaagaatgagctgtctgcatccaaatgattctgacatagacca 4190
QY 3901 gaatccagagaagacgactgtgtctcagtgagatgagatgagcaagggtctcaccagtgaa 3960
|||||
Db 4191 gaatccagagaagacgactgtgtctcagtgagatgagatgagcaagggtctcaccagtgaa 4250
QY 3961 ggtctgaaatctacacacagcaagcttctgtgaccttctgtgaagagagctgtaattgac 4020
|||||
Db 4251 ggtctgaaatctacacacagcaagcttctgtgaccttctgtgaagagagctgtaattgac 4310
QY 4021 agacggagctcgaaagaattttgtctcagatgtctgtccagctgtgtgtgtgtcatc 4080
|||||
Db 4311 agacggagctcgaaagaattttgtctcagatgtctgtccagctgtgtgtgtgtcatc 4370
QY 4081 ggcctgtgttgaagcctgt 4140
|||||
Db 4371 ggcctgt 4430
QY 4141 cctctgagtgatcacacagaaagatatacatctgtcagaatgagatgtctctgaggaacagga 4200
|||||
Db 4431 cctctgagtgatcacacagaaagatatacatctgtcagaatgagatgtctctgaggaacagga 4490
QY 4201 accctggaactctttaaagccctcaccaagaacccctgtgtgtgtgtgtgtgtgtgtgtgt 4260
|||||
Db 4491 accctggaactctttaaagccctcaccaagaacccctgtgtgtgtgtgtgtgtgtgtgtgt 4550
QY 4261 ggaaccccaatcccaagacagccctctgcaagcgagggaggaagctggaacatgtcccca 4320
|||||
Db 4551 ggaaccccaatcccaagacagccctctgcaagcgagggaggaagctggaacatgtcccca 4610
QY 4321 gtccccaagacatcatgagacctcttccagaatgtggaactgtgaaacatgtcagaaccccttca 4380
|||||
Db 4611 gtccccaagacatcatgagacctcttccagaatgtggaactgtgaaacatgtcagaaccccttca 4670
QY 4381 cctgtcatgcaagtgtagcagcgaacaaatcaagaagaatgtctgtgtgtgtgtgtgtgtgt 4440
|||||
Db 4671 cctgtcatgcaagtgtagcagcgaacaaatcaagaagaatgtctgtgtgtgtgtgtgtgtgt 4730
QY 4441 gcaagggt 4500
|||||
Db 4731 gcaagggt 4790
QY 4501 acagaagaagaacattctgt 4560
|||||
Db 4791 acagaagaagaacattctgt 4850
QY 4561 ttaagaagaagaatctgt 4620
|||||
Db 4851 ttaagaagaagaatctgt 4910
QY 4621 aatactcaagcactctctccgagtgcaagaagtttaagatgagatgagatgagatgagatgag 4680
|||||
Db 4911 aatactcaagcactctctccgagtgcaagaagtttaagatgagatgagatgagatgagatgag 4970
|||||
QY 4681 caactaaagctgtgcaaggaagctgtgtgagatcagatcttctcaacagctgtggaagatct 4740

|||||
Db 4971 caccataagctggcgaagcagcttcgcagatccgatttctcaacgcttggaagattt 5030
OY 4741 atgacagagctggacacacgaataatgltcaagtgltgttcaataacaaggctggcat 4800
Db 5031 atgacagagctggacacacgaataatgltcaagtgltgttcaataacaaggctggcat 5090
OY 4801 gcaatcagctcttcctggaatgltcatcaacaatgcattctccgggccaactcgcaaaag 4860
Db 5091 gcaatcagctcttcctggaatgltcatcaacaatgcattctccgggccaactcgcaaaag 5150
OY 4861 ggcaggaacccctagccattatggaattactgcttcaatccctctgatatccacaag 4920
Db 5151 ggcaggaacccctagccattatggaattactgcttcaatccctctgatatccacaag 5210
OY 4921 cagcagctctcagagtgctgctcgtgacacacacagtgatgctctgttccatctgt 4980
Db 5211 cagcagctctcagagtgctgctcgtgacacacacagtgatgctctgttccatctgt 5270
OY 4981 gtaatcttgcaatgtcctcgtccagcagccttgctgattcttcctgatacagagcg 5040
Db 5271 gtaatcttgcaatgtcctcgtccagcagccttgctgattcttcctgatacagagcg 5330
OY 5041 gtcagcaaaagcaaaacacctgcagtcatcagtgagtgaaagcctgtcatctacgctc 5100
Db 5331 gtcagcaaaagcaaaacacctgcagtcatcagtgagtgaaagcctgtcatctacgctc 5390
OY 5101 tctaatcttgctggagatgtgcaattacgttcccccgccacacactgtgcatatc 5160
Db 5391 tctaatcttgctggagatgtgcaattacgttcccccgccacacactgtgcatatc 5450
OY 5161 ttcacatgctccacagaagaagtcctatgtgtctccacacacatctgcctgtgtagccct 5220
Db 5451 ttcacatgctccacagaagaagtcctatgtgtctccacacacatctgcctgtgtagccct 5510
OY 5221 ctactcttgctgattgggggtgcaatcaacctctccatgtaacacagcctcctgtgttc 5280
Db 5511 ctactcttgctgattgggggtgcaatcaacctctccatgtaacacagcctcctgtgttc 5570
OY 5281 aagatcccccagacacagcctatgtgtgtcacaacagcgtgaaacctctcatgtgcatat 5340
Db 5571 aagatcccccagacacagcctatgtgtgtcacaacagcgtgaaacctctcatgtgcatat 5630
OY 5341 ggcagcgtggcgaaccttctgtgtgtgagctgtgtcacacgaataaagctgataatacaat 5400
Db 5631 ggcagcgtggcgaaccttctgtgtgtgagctgtgtcacacgaataaagctgataatacaat 5690
OY 5401 gatacctggaagctcgtgtctgtgtctccacacatttctcctgggagcgaggtcatc 5460
Db 5691 gatacctggaagctcgtgtgtctgtgtctccacacatttctcctgggagcgaggtcatc 5750
OY 5461 gacatggtggaataaacacaggaatgtgtgtgtccctggaaggtttggggaagatcgcttt 5520
Db 5751 gacatggtggaataaacacaggaatgtgtgtgtccctggaaggtttggggaagatcgcttt 5810
OY 5521 gttgacacattatctcttggaactgtgtggaggaacacctctgcgcacatggcgtggaagg 5580
Db 5811 gttgacacattatctcttggaactgtgtggaggaacacctctgcgcacatggcgtggaagg 5870
OY 5581 gttggtgtctctcctcaatctactgtctctgatacagatcagatctctcatcagcgccagcct 5640
Db 5871 gttggtgtctctcctcaatctactgtctctgatacagatcagatctctcatcagcgccagcct 5930
OY 5641 gtaaatcaaaagctatctcctctgaaatgataaagatgtgagcgagggaagacag 5700
Db 5931 gtaaatcaaaagctatctcctctgaaatgataaagatgtgagcgagggaagacag 5990
OY 5701 agaatcttgatgttgagagcgacgaatgacatcttagaataccaagaggttgacgaagata 5760
Db 5991 agaatcttgatgttgagagcgacgaatgacatcttagaataccaagaggttgacgaagata 6050
OY 5761 tataagaaggaagcgagcctgtctgtgacaggaattgctggtgcatctcctcgtgtgag 5820
|||||

Db 6051 tataagaaggaagcgagcctgtctgtgacaggaatttgcgtgggcatctcctcgtgtgag 6110
OY 5821 tgccttgggctcccttgagggttaatgagggtctggaataatcatcaacttcaagaatttaca 5880
Db 6111 tgccttgggctcccttgagggttaatgagggtctggaataatcatcaacttcaagaatttaca 6170
OY 5881 ggaataaccactgttaccagaagagatgtcttctcttaacaaaataaglatatcttaacaac 5940
Db 6171 ggaataaccactgttaccagaagagatgtcttctcttaacaaaataaglatatcttaacaac 6230
OY 5941 atccatgagatcacatcaagaatggtgctactgacctgaatttggatccatcaacagagctg 6000
Db 6231 atccatgagatcacatcaagaatggtgctactgacctgaatttggatccatcaacagagctg 6290
OY 6001 ttgactgggagagaacacgttgagatctcttggcctttttgagagagagctcccaaggaagaa 6060
Db 6291 ttgactgggagagaacacgttgagatctcttggcctttttgagagagagctcccaaggaagaa 6350
OY 6061 gttggcaaggttggtgagtgagtgagcgatccgaaactgggctcgtgaaagatgagaaanaa 6120
Db 6351 gttggcaaggttggtgagtgagtgagcgatccgaaactgggctcgtgaaagatgagaaanaa 6410
OY 6121 tatgctgtaactatagtgagaggaacaacaacgagctctctacagcagatgcttgatc 6180
Db 6411 tatgctgtaactatagtgagaggaacaacaacgagctctctacagcagatgcttgatc 6470
OY 6181 ggcgggctccctgtgtgtctcgtgataaaccacacacaggaatggaatcccaagccgg 6240
Db 6471 ggcgggctccctgtgtgtctcgtgataaaccacacacaggaatggaatcccaagccgg 6530
OY 6241 cggctcttgaggaaatgtgtgcctaaagtgtgtgaaggaaggagagatgagatgcatca 6300
Db 6531 cggctcttgaggaaatgtgtgcctaaagtgtgtgaaggaaggagagatgagatgcatca 6590
OY 6301 tctcaatagatggaagaaatgtgaaagctcttgcactagagatggaatggaatggaatgga 6360
Db 6591 tctcaatagatggaagaaatgtgaaagctcttgcactagagatggaatggaatggaatgga 6650
OY 6361 aggttcaaggtgctctggcagatgtccagcatctaaataataggtttgagatggttataca 6420
Db 6651 aggttcaaggtgctctggcagatgtccagcatctaaataataggtttgagatggttataca 6710
OY 6421 atagttgtaagaaatgaaaggttccaaacccggaacctgaagcctgtccaggaattcttga 6480
Db 6711 atagttgtaagaaatgaaaggttccaaacccggaacctgaagcctgtccaggaattcttga 6770
OY 6481 ctggcaattctccttggaagtggttcttaaaagagaacacccggaacatgctacaatacagctt 6540
Db 6771 ctggcaattctccttggaagtggttcttaaaagagaacacccggaacatgctacaatacagctt 6830
OY 6541 ccatcttcaatctctctcgtgcagagatatacagatcctcccaaggccaanaagcga 6600
Db 6831 ccatcttcaatctctctcgtgcagagatatacagatcctcccaaggccaanaagcga 6890
OY 6601 ctccacaatagaagaactactcgttcttcagacaacacatgacaaagtatttggacttt 6660
Db 6891 ctccacaatagaagaactactcgttcttcagacaacacatgacaaagtatttggacttt 6950
OY 6661 gccaaaggacaaagtataatatacacaacttaaaagcctctcttcaacaaaaaacagaca 6720
Db 6951 gccaaaggacaaagtataatatacacaacttaaaagcctctcttcaacaaaaaacagaca 7010
OY 6721 gtagtgagcgttgcaagttctcacaatcttcttcaacaggaatgaaaggtgaaagagcgtat 6780
Db 7011 gtagtgagcgttgcaagttctcacaatcttcttcaacaggaatgaaaggtgaaagagcgtat 7070
OY 6781 gtaatgaagaatcctgttcaatcag 6804
Db 7071 gtaatgaagaatcctgttcaatcag 7094

RESULT 3
AAF24685

ID AAF24685 standard; DNA; 10474 BP.
 AC AAF24685;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
 XX
 KW Human: adenosine triphosphate binding cassette protein 1; ABC1;
 KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
 KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
 KW atherosclerosis; cholesterol transport; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 323..7108
 FT /tag= a
 FT /product= "defective ABC1 polypeptide"
 FT
 PN MO200078972-A2.
 XX
 XX 28-DEC-2000.
 XX
 PF 16-JUN-2000; 2000MO-US16765.
 XX
 XX 18-JUN-1999; 99US-0140264.
 PR 14-SEP-1999; 99US-0153872.
 PR 19-NOV-1999; 99US-0166573.
 XX
 PA (CVTH-) CV THERAPEUTICS INC.
 XX
 PT Lawn RM, Wade D, Garvin M;
 DR WPI; 2001-137812/14.
 XX
 PT Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
 PT useful for the development of agents for the treatment of heart disease
 PT and other disorders associated with hypercholesterolemia and
 PT atherosclerosis -
 PT
 PS Disclosure; Page 148-154; 215pp; English.
 XX
 CC The present sequence encodes a human adenosine triphosphate (ATP)
 CC binding cassette protein (ABC) 1 polypeptide, and is isolated from
 CC a Tangier disease patient. ABC1 resides in cell membranes and utilises
 CC ATP hydrolysis to transport a wide variety of substrates across the
 CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
 CC mobilisation of intracellular cholesterol stores. ABC1 is defective in
 CC Tangier disease, a genetic disorder characterised by abnormal
 CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
 CC 9q22-9q31. The ABC1 genes and proteins are useful for developing
 CC pharmaceutical agents for the treatment of heart disease and other
 CC disorders associated with hypercholesterolemia and atherosclerosis. The
 CC genes are useful for developing screening assays to screen for compounds
 CC that regulate the expression of genes associated with cholesterol
 CC transport. The genes and proteins are also useful for are also useful
 CC as diagnostic indicators of cardiovascular disease and other disorders
 CC associated with hypercholesterolemia.
 CC
 XX
 SO Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

Query Match 100.0%; Score 6802.4; DB 22; Length 10474;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 6803; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 atggttcttgagctgaagcttgctgctggaagaacccacttcagaagaaga 60
 Db 333 atggttcttgagctgaagcttgctgctggaagaacccacttcagaagaaga 382
 QY 61 caaacatgcagctgtactcgaagctgctgctcattatcttctgactgac 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 383 caaacatgcagctgtactcgaagctgctgctcattatcttctgactgac 442
 QY 121 tctgttcgctgaagcttacccaccctatgaaacacatgaatgcaatcttccaataaagcc 180
 Db 443 tctgttcgctgaagcttacccaccctatgaaacacatgaatgcaatcttccaataaagcc 502
 QY 181 atgccccttgaggaacaccttccttggttcgaaggatattatctgtaatgcaaacaccc 240
 Db 503 atgccccttgaggaacaccttccttggttcgaaggatattatctgtaatgcaaacaccc 562
 QY 241 tgttcctgtaacccgactcctctggtggaagctcccgagttgttgaacattacaatcc 300
 Db 563 tgttcctgtaacccgactcctctggtggaagctcccgagttgttgaacattacaatcc 622
 QY 301 atttggtctgcctgttcttcagatgctggaagctcttctatcagccagaagaacacc 360
 Db 623 atttggtctgcctgttcttcagatgctggaagctcttctatcagccagaagaacacc 682
 QY 361 agcatgaaggaatgcgaagaagttctggaacattacagcagatcaagaatccagctca 420
 Db 683 agcatgaaggaatgcgaagaagttctggaacattacagcagatcaagaatccagctca 742
 QY 421 aacttgaagcttcaagattctctgtggaacatgaacacctctctggttccatatac 480
 Db 743 aacttgaagcttcaagattctctgtggaacatgaacacctctctggttccatatac 802
 QY 481 aacctctctcccaagaatctactgtggaacagaatgctggaagctgagtatctctcac 540
 Db 803 aacctctctcccaagaatctactgtggaacagaatgctggaagctgagtatctctcac 862
 QY 541 aaggtattttgcaagctcagctacagttacattgcaacagcttctgtaatgtaataatca 600
 Db 863 aaggtattttgcaagctcagctacagttacattgcaacagcttctgtaatgtaataatca 922
 QY 601 gaagagaatgattcaactgtgtgacccaagaagttcttgagcttctggtcctacccaagag 660
 Db 923 gaagagaatgattcaactgtgtgacccaagaagttcttgagcttctggtcctacccaagag 982
 QY 661 aacttgctgcagcagagagagttactctgttccaacatgacatcctgaagccaatctg 720
 Db 983 aacttgctgcagcagagagagttactctgttccaacatgacatcctgaagccaatctg 1042
 QY 721 agaacactaaactctacatctccctcccgagcaaggagctgctggaagccaacaaaca 780
 Db 1043 agaacactaaactctacatctccctcccgagcaaggagctgctggaagccaacaaaca 1102
 QY 781 ttgtctcatagcttctggaagctctgcccagagctggttgaatgaagaagctggaagttgac 840
 Db 1103 ttgtctcatagcttctggaagctctgcccagagctggttgaatgaagaagctggaagttgac 1162
 QY 841 atgcgacgaagagttgatttcttgaccaaattggaacagctcagctcctccaccacaatc 900
 Db 1163 atgcgacgaagagttgatttcttgaccaaattggaacagctcagctcctccaccacaatc 1222
 QY 901 taccagctgtgtctctgtatgtctcgtgagcattcccgagggaggggctggaagatcaag 960
 Db 1223 taccagctgtgtctctgtatgtctcgtgagcattcccgagggaggggctggaagatcaag 1282
 QY 961 tctctcaactgtgataagagaacaactacaagccctcttggagggcaatgagcactgag 1020
 Db 1283 tctctcaactgtgataagagaacaactacaagccctcttggagggcaatgagcactgag 1342
 QY 1021 gaagatgctgaacactctctatgacaactctacaaccccttactgcaatatttgatgaag 1080
 Db 1343 gaagatgctgaacactctctatgacaactctacaaccccttactgcaatatttgatgaag 1402
 QY 1081 aatttgagctagctcctcttcccgatattctggaagctctggaagcgcgtgtctgtt 1140
 Db 1403 aatttgagctagctcctcttcccgatattctggaagctctggaagcgcgtgtctgtt 1462
 QY 1141 gggagaatctgtatatacactgacactcagccacagaagcagttatgctgagtgagac 1200
 Db 1463 gggagaatctgtatatacactgacactcagccacagaagcagttatgctgagtgagac 1522

QY	1201	aagaccttcagaagactgctgctgtgtccatglatctggaagagcattgtggaggaactcagc	1260
Db	1523	aaggaaccttcacaggaactgctgtgttccatglatctggaagagcattgtggaggaactcagc	1582
QY	1261	cccaagatctggaacttcatactgagaaagccaagaaatggacctgtccgagatcgtgtg	1320
Db	1583	cccaagatctggaacttcatactgagaaagccaagaaatggacctgtccgagatcgtgtg	1642
QY	1321	gacacgacgaggaacaaatgacacacttttggagacacagatgtagatgttgatattggacac	1380
Db	1643	gacacgacgaggaacaaatgacacacttttggagacacagatgtagatgttgatattggacac	1702
QY	1381	caagacatcgtgctgtgttttggccaagacccaagagatgtccagtlccagtaatgtctct	1440
Db	1703	caagacatcgtgctgtgttttggccaagacccaagagatgtccagtlccagtaatgtctct	1762
QY	1441	ggtacacacctggagagagagactttccaaagagacataacacagacatccgagacatattcc	1500
Db	1763	ggtacacacctggagagagagactttccaaagagacataacacagacatccgagacatattcc	1822
QY	1501	ttcatgtagctgtgttcaacctgaaacagcttgaacccatgtgcaacagagatctgtgctatc	1560
Db	1823	ttcatgtagctgtgttcaacctgaaacagcttgaacccatgtgcaacagagatctgtgctatc	1882
QY	1561	aacaaagtccacagagcgtcgtcgtgatalgtagagagaattctctgctcgtatctgttcaactg	1620
Db	1883	aacaaagtccacagagcgtcgtcgtgatalgtagagagaattctctgctcgtatctgttcaactg	1942
QY	1621	attaactccagacagacatctgacgtcgtcccaacatgltcaaatataaataatccgaatggacat	1680
Db	1943	attaactccagacagacatctgacgtcgtcccaacatgltcaaatataaataatccgaatggacat	2002
QY	1661	gacaaatgtgtagagagagaataataataacagagatgtagtactgtagacctgtctctcagct	1740
Db	2003	gacaaatgtgtagagagagaataataataacagagatgtagtactgtagacctgtctctcagct	2062
QY	1741	gacctccttgtagagacatgtagctgtccttgaggagcttcctgcactattgcaagatgtgtg	1800
Db	2063	gacctccttgtagagacatgtagctgtccttgaggagcttcctgcactattgcaagatgtgtg	2122
QY	1801	gagcagagacatcatcagagtgctgtgacggtgacccgagaaacactggtgtctatatacgaa	1860
Db	2123	gagcagagacatcatcagagtgctgtgacggtgacccgagaaacactggtgtctatatacgaa	2182
QY	1861	cagatgcacctatccctgttaactgttaagcattctctcgtgggtgtagatagacggttcaatg	1920
Db	2183	cagatgcacctatccctgttaactgttaagcattctctcgtgggtgtagatagacggttcaatg	2242
QY	1921	ccaccttcaatgtagcgtgtagctgtgatttcaactagtagctgtgcatcatcaagagagatcgtg	1980
Db	2243	ccaccttcaatgtagcgtgtagctgtgatttcaactagtagctgtgcatcatcaagagagatcgtg	2302
QY	1981	tatagaagaagagacacagctctgaaagagacacatgtagcatatgagctgtgagacaagcata	2040
Db	2303	tatagaagaagagacacagctctgaaagagacacatgtagcatatgagctgtgagacaagcata	2362
QY	2041	ctctgagtttagcgtgctcatctagtagacccatctctctcttctgtgtagcgtcgtgcgtgcta	2100
Db	2363	ctctgagtttagcgtgctcatctagtagacccatctctctcttctgtgtagcgtcgtgcgtgcta	2422
QY	2101	gttgatcatcctgaagttaggaacctgctgcaccttaacagtatcccaacgctgtgtgtgttc	2160
Db	2423	gttgatcatcctgaagttaggaacctgctgcaccttaacagtatcccaacgctgtgtgtgttc	2482
QY	2161	ttctcgtgcagtgattgtctgtgtgtgacaactcctgcaggtctccctcgtattagaacaactcttc	2220
Db	2483	ttctcgtgcagtgattgtctgtgtgtgacaactcctgcaggtctccctcgtattagaacaactcttc	2542
QY	2221	tccagagacaaacctgtagcagacagcctgtgtgggtgacatcatcattctcaagcgtgtacccgcc	2280
Db	2543	tccagagacaaacctgtagcagacagcctgtgtgggtgacatcatcattctcaagcgtgtacccgcc	2602

[illegible]

|||||
Db 3683 cagctggtggaagagctactaccctgctctggttcagaagaagtgtggaatacctccctcaagt 3742
QY 3421 tccctgagaagaagtagtagcaactgtgtcattacccttgnaaaaggagagcaggtttctcag 3480
Db 3743 tccctcagaanaacagtagtagcaactgtgtcattacccttgnaaaaggagagcaggtttctcag 3802
QY 3481 agcaagttcgaagctgagcctgagcagcagcattagagtagcaagcttgacacatcagatgtc 3540
Db 3803 agcagttcagatgagcctgagcctgagcagcagcattagagtagcaagcttgacacatcagatgtc 3862
QY 3541 tctgtattctccaaacctaatcagaagaacatgtgtctgnaagcccgctgtgtgagaacata 3600
Db 3863 tctgtattctccaaacctaatcagaagaacatgtgtctgnaagcccgctgtgtgagaacata 3922
QY 3601 gggcagagctgacacatgtgtctgacacataagagctgtcgaaggagagccttctgtgaa 3660
Db 3923 gggcagagctgacacatgtgtctgacacataagagctgtcgaaggagagccttctgtgaa 3982
QY 3661 ctcttcagagatgtatgtaccggtctcagaacctgagcattctagtatgacatccta 3720
Db 3983 ctcttcagagatgtatgtaccggtctcagaacctgagcattctagtatgacatccta 4042
QY 3721 gagaagacctggaagaataattctcagaagtgtgcccgaagagagtggtgtgagctgag 3780
Db 4043 gagaagacctggaagaataattctcagaagtgtgcccgaagagagtggtgtgagctgag 4102
QY 3781 acctcagatgtatcctctgccaagaagaacagcagcctctcgaggagacagaagagc 3840
Db 4103 acctcagatgtatcctctgccaagaagaacagcagcctctcgaggagacagaagagc 4162
QY 3841 tgtcttcgcccgttcactgnaagatgtatgtctgacaaatgattctgacataaccca 3900
Db 4163 tgtcttcgcccgttcactgnaagatgtatgtctgacaaatgattctgacataaccca 4222
QY 3901 gaatccgaagaagacagactgtgtcagtgagatgagatgagcagaggtccctacaagctgaa 3960
Db 4223 gaatccgaagaagacagactgtgtcagtgagatgagatgagcagaggtccctacaagctgaa 4282
QY 3961 ggtctgnaacttacaacagcacaagttgtgtgccccttctgtgnaagagactgttaattgc 4020
Db 4283 ggtctgnaacttacaacagcacaagttgtgtgccccttctgtgnaagagactgttaattgc 4342
QY 4021 agacgagctcggaaggaattttgtctcagaattgtcttcagactgtgtttgtctgcat 4080
Db 4343 agacgagctcggaaggaattttgtctcagaattgtcttcagactgtgtttgtctgcat 4402
QY 4081 ggccttgttccagctgacgtgtgcccaccttctggaagaatcccgagcctgtgactcag 4140
Db 4403 ggccttgttccagctgacgtgtgcccaccttctggaagaatcccgagcctgtgactcag 4462
QY 4141 cctctgtagtacaagaacagatcacatltgtcagaacatgtatcctcctgagaacagga 4200
Db 4463 cctctgtagtacaagaacagatcacatltgtcagaacatgtatcctcctgagaacagga 4522
QY 4201 acctgtgaaaccttaaacgcccctacaaagaacctgtgtctggaagcccttatggaa 4260
Db 4523 acctgtgaaaccttaaacgcccctacaaagaacctgtgtctggaagcccttatggaa 4582
QY 4261 ggaacccaatcccaagacagcctctgccaagcagggaggaagatgtgaaacctgtcccca 4320
Db 4583 ggaacccaatcccaagacagcctctgccaagcagggaggaagatgtgaaacctgtcccca 4642
QY 4321 gtccccaagacatcatgacacctctccagaatgtggaactgtggaacatgacgaacaccttca 4380
Db 4643 gtccccaagacatcatgacacctctctccagaatgtggaactgtggaacatgacgaacaccttca 4702
QY 4381 cctgtatgccagtgtagcagcgacacaaatcagaagaatgtgtcctgtgttcccccaggg 4440
Db 4703 cctgtatgccagtgtagcagcgacacaaatcagaagaatgtgtcctgtgttcccccaggg 4762
QY 4441 gcaaggggggtgtgctcctccacaagaagaacaaacactgtcagatattccttcaggactgt 4500
|||||

Db 4763 gcaaggggggtgtgctcctccacaagaagaacaaacactgtcagatattccttcaggactgt 4822
QY 4501 acaggaagaacatctcgattatcctgtgtgaagacgtatgtgcagatcatagccaagaagc 4560
Db 4823 acaggaagaacatctcgattatcctgtgtgaagacgtatgtgcagatcatagccaagaagc 4882
QY 4561 ttaagaagaacatctcgattatcctgtgtgaagacgtatgtgcagatcatagccaagaagc 4620
Db 4883 ttaagaagaacatctcgattatcctgtgtgaagacgtatgtgcagatcatagccaagaagc 4942
QY 4621 aatcactcaagcacttccctccgaagtcgaagaagttaattgtccatccacaacatgaagaaa 4680
Db 4943 aatcactcaagcacttccctccgaagtcgaagaagttaattgtccatccacaacatgaagaaa 5002
QY 4681 caactaaagctgtgccaagagacagctcgcagatcgaattcccaacagcttggagaagatt 4740
Db 5003 caactaaagctgtgccaagagacagctcgcagatcgaattcccaacagcttggagaagatt 5062
QY 4741 atgacagagctgacacccaagaataatgtcaaggtgtgttccaataacaaggctgtgcat 4800
Db 5063 atgacagagctgacacccaagaataatgtcaaggtgtgttccaataacaaggctgtgcat 5122
QY 4801 gcaatcagctcttccctgaatgtcatcaacaattgccattccctccgagccaacctgcaaaag 4860
Db 5123 gcaatcagctcttccctgaatgtcatcaacaattgccattccctccgagccaacctgcaaaag 5182
QY 4861 gggagagaaccttagccattatggaattactgtcttccaatccatccctgaatccacaag 4920
Db 5183 gggagagaaccttagccattatggaattactgtcttccaatccatccctgaatccacaag 5242
QY 4921 cagcagctcctcagaagtggtcctctgataccacaatcagtagatgtccctgtgtcactgt 4980
Db 5243 cagcagctcctcagaagtggtcctctgataccacaatcagtagatgtccctgtgtcactgt 5302
QY 4981 gtaactcttgcaatgtccctctgtcccaagcagcttgtgtatcttcctatccaagagcgg 5040
Db 5303 gtaactcttgcaatgtccctctgtcccaagcagcttgtgtatcttcctatccaagagcgg 5362
QY 5041 gtcagcaagaacaaacacacctcagcttcaatcagtgagtgaaacctgtcatcactgtctc 5100
Db 5363 gtcagcaagaacaaacacacctcagcttcaatcagtgagtgaaacctgtcatcactgtctc 5422
QY 5101 tctaatttgcctggaatgtatgtcgaattacgtgtccctgcgaacactgtgtcatcactc 5160
Db 5423 tctaatttgcctggaatgtatgtcgaattacgtgtccctgcgaacactgtgtcatcactc 5482
QY 5161 ttcatctgctccagcagaaggtccatagtgtcctccacaacatctgctgtgtaagccct 5220
Db 5483 ttcatctgctccagcagaaggtccatagtgtcctccacaacatctgctgtgtaagccct 5542
QY 5221 ctactttgtctgtatgtgtgtcatcatcacactcctcaatgtacccaagcctccttgtgtc 5280
Db 5543 ctactttgtctgtatgtgtgtcatcatcacactcctcaatgtacccaagcctccttgtgtc 5602
QY 5281 aagatccccaagcagcactatgtgtgtcctacaagcgttgaaacctcttcattgtgcatatt 5340
Db 5603 aagatccccaagcagcactatgtgtgtcctacaagcgttgaaacctcttcattgtgcatatt 5662
QY 5341 ggcagcgtgtgcacacttgtgtgtgagctgttcaacgaacataagctgtgaataatcaat 5400
Db 5663 ggcagcgtgtgcacacttgtgtgtgagctgttcaacgaacataagctgtgaataatcaat 5722
QY 5401 gatatccctgaagctcgtgttcttgatcctccacaattttgtcctgtggaagaggtccatc 5460
Db 5723 gatatccctgaagctcgtgttcttgatcctccacaattttgtcctgtggaagaggtccatc 5782
QY 5461 gacatgtgtgaaaaaacaggaatgtgctgtgagtcctctgnaaaggtttgtggaagatcgtct 5520
Db 5783 gacatgtgtgaaaaaacaggaatgtgctgtgagtcctctgnaaaggtttgtggaagatcgtct 5842
QY 5521 gtgtcaacattatcttggagactgtgtggaagcaaacctcttcgcaatgtgcgtgtgaagg 5580
Db 5843 gtgtcaacattatcttggagactgtgtggaagcaaacctcttcgcaatgtgcgtgtgaagg 5902
|||||

OY	5581	gtgggtcttctctcaactactgttcttcgtaccagacagattcttcaatccagcccaagct	5640
Db	5903	gtgtgtcttctctcctaactactgttctgtctccagacagattcttcaatccagcccaagct	5962
OY	5641	gttaatgcaaaactctctccctctgtaatgtaagaatgaagaatgtgaagcgggaaagacag	5700
Db	5963	gttaatgcaaaactctctccctctgtaatgtaagaatgaagaatgtgaagcgggaaagacag	6022
OY	5701	agaattcttgatgtgtgagcgccagaaatgacatcttaagaatcaagaagctgtgcgaagta	5760
Db	6023	agaattcttgatgtgtgagcgccagaaatgacatcttaagaatcaagaagctgtgcgaagta	6082
OY	5761	tataagaagaaacgggaacccgcgctgtgaacaagatttgctgtggaattcttccctgtgtag	5820
Db	6083	tataagaagaaacgggaacccgcgctgtgaacaagatttgctgtggaattcttccctgtgtag	6142
OY	5821	tgctttggctctccctgtggaagttaatgtyggcgctggaataatcatcaacttcaagaatgttaaca	5880
Db	6143	tgctttggctctccctgtggaagttaatgtyggcgctggaataatcatcaacttcaagaatgttaaca	6202
OY	5881	ggagatacacacactgttacacagagggagatgcttcttccaaacaaatagatatcttaacaac	5940
Db	6203	ggagatacacacactgttacacagagagatgcttcttccaaacaaatagatatcttaacaac	6262
OY	5941	atccatgtaagtacatcaagaacatbtggtactatgcctccagatttgatgycatcaacagagctg	6000
Db	6263	atccatgtaagtacatcaagaacatbtggtactatgcctccagatttgatgycatcaacagagctg	6322
OY	6001	ttgacctgggagagaaacacgctgagatctcttctgcccctttgagaagagctcccaagagaaagaa	6060
Db	6323	ttgacctgggagagagaaacacgctgagatctcttctgcccctttgagaagagctcccaagagaaagaa	6382
OY	6061	gttcggcaaggtctgtgtgagctgagcgcatctgcgaataactgycgctgtgaagtatagagaaataa	6120
Db	6383	gttcggcaaggtctgtgtgagctgagcgcatctgcgaataactgycgctgtgaagtatagagaaataa	6442
OY	6121	tatgtctgttaactatagtgtgaagcgacaacacgcgaactctctacaagcatgtgctttgac	6180
Db	6443	tatgtctgttaactatagtgtgaagcgacaacacgcgaactctctacaagcatgtgctttgac	6502
OY	6181	ggcggcgccctccctgtgaggtgttctctggtatggaaacccacacagagatgatacccaaaagcccg	6240
Db	6503	ggcggcgccctccctgtgaggtgttctctggtatggaaacccacacagagatgatacccaaaagcccg	6562
OY	6241	cggttctctgtggaattgtgtccctaaagtgtgttccaagagggagatcaagatgtgttaca	6300
Db	6563	cggttctctgtggaattgtgtccctaaagtgtgttccaagagggagatcaagatgtgttaca	6622
OY	6301	tctcaatgataggaagaatgtgaagctctcttgccttaagatgagaaatcatgtgtccaatgga	6360
Db	6623	tctcaatgataggaagaatgtgaagctctcttgccttaagatgagaaatcatgtgtccaatgga	6682
OY	6361	aggtctcaaggtgtcctgtgcaagtggtccaagatcttaaaaaaataaggttctggaatgtgtataca	6420
Db	6683	aggtctcaaggtgtcctgtgcaagtggtccaagatcttaaaaaaataaggttctggaatgtgtataca	6742
OY	6421	atagtgttaagaaatagcaaggtgtccaaacccggacccgtgaagcctgtgccagatcttcttgga	6480
Db	6743	atagtgttaagaaatagcaaggtgtccaaacccggacccgtgaagcctgtgccagatcttcttgga	6802
OY	6481	cttgcatcttccctggaagtgttcttaaaagagaacacccgaacatgctacataatccagctt	6540
Db	6803	cttgcatcttccctggaagtgttcttaaaagagaacacccgaacatgctacataatccagctt	6862
OY	6541	ccatcttcatatctctctctgtgccaagatatccagcatcctctcccaagacaaagacga	6600
Db	6863	ccatcttcatatctctctctgtgccaagatatccagcatcctctcccaagacaaagacga	6922
OY	6601	ctccacaataaagaactactctgttcttcaagaacaactgtgacaagaatttgtgaactt	6660
Db	6923	ctccacaataaagaactactctgttcttcaagaacaactgtgacaagaatttgtgaactt	6982

Accession	Sequence	Position
QY 6661	gccaaagcacaag tga tga tga cca tta aag ac ctt cta tta caca aac caa gca	6720
Db 6983	gccaaagcacaag tga tga tga cca tta aag ac ctt cta tta caca aac caa gca	7042
QY 6721	gtatggacgtttgacgtttccacatctttttctacagatgagaaagtgaagaagcat	6780
Db 7043	gtatggacgtttgacgtttccacatctttttctacagatgagaaagtgaagaagcat	7102
QY 6781	gtatgaagaatcctgtttacaag	6804
Db 7103	gtatgaagaatcctgtttacaag	7126

RESULT	4
AAEF24686	
ID	AAEF24686 standard; DNA; 10474 BP.
XX	
XX	
AC	AAEF24686;
XX	
DT	20-APR-2001 (first entry)
XX	
DE	Nucleotide sequence of ABC1 polypeptide from Tanglier disease patient.

KM Human; adenosine triphosphate binding cassette protein 1; ABC1;
 KM apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
 KM chromosome 9q22-q31; heart disease; hypercholesterolemia;
 KM atherosclerosis; cholesterol transport; ss.

OS Homo sapiens.

FH	Key	Location/Qualifiers
FT	CDS	323..7108

```

FT
.....
/product= "defective ABC1 polypeptide"

```

PN WO200078972-A2

PD 28-DEC-2000.

16-JUN-2000; 2000WO-US16765.

PR 18-JUN-1999: 99US-0140264

PR	14-SEP-1999;	99US-0153872.
PR	19-NOV-1999;	99US-0166573

XX
XX
PA (C/УМН -) ОУ ПИИДА ПЕРМОТАС ТУО

XX
PT

XX

XX

useful for the development of

PT atherosclerosis -

AA
PS Disclosure: Page 170-176. 21

The present authors would

CC blinding cassette protein (AB

ATP hydrolysis to transport

mobilisation of intracellular

HDL-cholesterol metabolism.

pharmacological agents for the

disorders associated with hyp

that regulate the expression

CC as diagnostic indicators of

Disclosure, Page 170-176; 215pp; English.

The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide, and is isolated from a Tangier disease patient. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders

Db 2363 ctcgggtttagcgtggttcattagtaagcttcaatctctctcttctgtgagcgtctgctca 2422
QY 2101 gtgtctccctcgaagttagaaccctgtctccttacagtgatccagcgtggtgttgc 2160
Db 2423 gtgtctccctcgaagttagaaccctgtctccttacagtgatccagcgtggtgttgc 2482
QY 2161 ttctgtcgtgttctgtctgtgtgtaacaatccctgcaagtgcttccctgtatagcaactctc 2220
Db 2483 ttctgtcgtgttctgtctgtgtgtaacaatccctgcaagtgcttccctgtatagcaactctc 2542
QY 2221 tccagaaaccaactgagcagcctgttgaggatcatcatcactcaacgtctgtacccgccc 2280
Db 2543 tccagaaaccaactgagcagcctgttgaggatcatcatcactcaacgtctgtacccgccc 2602
QY 2281 taagctcgtgtgtgagcagtgagcaactagctgaggtctcaactcaagaatctctgctagc 2340
Db 2603 taagctcgtgtgtgagcagtgagcaactagctgaggtctcaactcaagaatctctgctagc 2662
QY 2341 ctgctgtctcctgtggtcttctgtgtgtgtgagtgacttctgtcccttcttgagagcag 2400
Db 2663 ctgctgtctcctgtggtcttctgtgtgtgtgagtgacttctgtcccttcttgagagcag 2722
QY 2401 ggcattgagtgagtgagtgagcaaccctgttgagagtcctgttgagagagatgcttcaat 2460
Db 2723 ggcattgagtgagtgagtgagcaaccctgttgagagtcctgttgagagagatgcttcaat 2782
QY 2461 ctcaaccactctgactcccatgagtgtgtttgacaacctctctataggggtgagtacgtg 2520
Db 2783 ctcaaccactctgactcccatgagtgtgtttgacaacctctctataggggtgagtacgtg 2842
QY 2521 tacattgagtgctgtcttctccagccagtgacggaattcccaaggccctggtatttctctgc 2580
Db 2843 tacattgagtgctgtcttctccagccagtgacggaattcccaaggccctggtatttctctgc 2902
QY 2581 accaagtcctactggtgtgtgagagaaagtgaatgagaaagccacccctgttctcaaccag 2640
Db 2903 accaagtcctactggtgtgtgagagaaagtgaatgagaaagccacccctgttctcaaccag 2962
QY 2641 aagaagaatgtcagaatactgcatactgagagagaaaccaaccacttgaagctgtgcgttcc 2700
Db 2963 aagaagaatgtcagaatactgcatactgagagagaaaccaaccacttgaagctgtgcgttcc 3022
QY 2701 attcagaacctgtgtaaaagtctacagagatgagatgagatgtgctgctgactgtgca 2760
Db 3023 attcagaacctgtgtaaaagtctacagagatgagatgagatgtgctgctgactgtgca 3082
QY 2761 ctggaatttttaagagggccagatcacctcctcctgtggccacaatgagcgaggagaaagc 2820
Db 3083 ctggaatttttaagagggccagatcacctcctcctgtggccacaatgagcgaggagaaagc 3142
QY 2821 accacacatgtcaatcctgtgacgggtgtgttcccccagcactctgagacacgctcaactctg 2880
Db 3143 accacacatgtcaatcctgtgacgggtgtgttcccccagcactctgagacacgctcaactctg 3202
QY 2881 ggaaaaaagacattcgtctgagatgagcaaccatccggcagaaacctgtgggtctgttcccaag 2940
Db 3203 ggaaaaaagacattcgtctgagatgagcaaccatccggcagaaacctgtgggtctgttcccaag 3262
QY 2941 cataacgtgtgtgtgacatctgtctgtcgaagaacaactgtgttctatagcccgcttg 3000
Db 3263 cataacgtgtgtgtgacatctgtctgtcgaagaacaactgtgttctatagcccgcttg 3322
QY 3001 aaaaggtctctcagaaacagtgtaagcgagatgagcagatgagccttctgactgtgt 3060
Db 3323 aaaaggtctctcagaaacagtgtaagcgagatgagcagatgagccttctgactgtgt 3382
QY 3061 ttgcatcaagaacagctgtaaaagcaaaacagccagctgttcaagtgtgaatgcagagaag 3120
Db 3383 ttgcatcaagaacagctgtaaaagcaaaacagccagctgttcaagtgtgaatgcagagaag 3442
QY 3121 ctatctgtggtcgtcgtcttctgtcgggagatcaagtttgcattcttgatgaaccaca 3180
Db 3443 ctatctgtggtcgtcgtcttctgtcgggagatcaagtttgcattcttgatgaaccaca 3502
QY 3181 gctgtgtgtggaaccttactcccgaggggataatgagagctgtctgtgaataccagaca 3240
Db 3503 gctgtgtgtggaaccttactcccgaggggataatgagagctgtctgtgaataccagaca 3562
QY 3241 ggcgcacacattatctctctacacacacatgtagtaagcgagcgttccctgttgagagc 3300
Db 3563 ggcgcacacattatctctctacacacacatgtagtaagcgagcgttccctgttgagagc 3622
QY 3301 attgcatactctcccatgaggaaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3360
Db 3623 attgcatactctcccatgaggaaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3682
QY 3361 cagctgggaaagcgtactacatcctgtgacacctgtgtgcaagaagaatgtagaatccctcag 3420
Db 3683 cagctgggaaagcgtactacatcctgtgacacctgtgtgcaagaagaatgtagaatccctcag 3742
QY 3421 tctgtcagaacagtagtagcactgtgtlcatcctgaaaaaagagagacagtglttctcag 3480
Db 3743 tctgtcagaacagtagtagcactgtgtlcatcctgaaaaaagagagacagtglttctcag 3802
QY 3481 agcagttctgt 3540
Db 3803 agcagttctgt 3862
QY 3541 tctgtatctcccaacctcatcaggaagacatgtgtctgaagcccggtctgtgtgaagacata 3600
Db 3863 tctgtatctcccaacctcatcaggaagacatgtgtctgaagcccggtctgtgtgaagacata 3922
QY 3601 gggcattgagctgacactatgt 3660
Db 3923 gggcattgagctgacactatgt 3982
QY 3661 cctcttcattgagattgtatgacagcgtctccagacctctgagaccttcttctgtgtgtgtgt 3720
Db 3983 cctcttcattgagattgtatgacagcgtctccagacctctgagaccttcttctgtgtgtgtgt 4042
QY 3721 gagaagacctgtgagaataatctctcaagtgagtcgaaagagatgtgtgtgtgtgtgtgt 3780
Db 4043 gagaagacctgtgagaataatctctcaagtgagtcgaaagagatgtgtgtgtgtgtgtgt 4102
QY 3781 accctcagatgttaactctgtccagagaagcagaagcagcgtctctgtgtgtgtgtgtgtgtgt 3840
Db 4103 accctcagatgttaactctgtccagagaagcagaagcagcgtctctgtgtgtgtgtgtgtgtgt 4162
QY 3841 tgtcttcgaccttcaactgtagatgtatgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3900
Db 4163 tgtcttcgaccttcaactgtagatgtatgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4222
QY 3901 gaatccagagaagagacagctgtgtcagtgagatgagcagaaggtctctacagatgaa 3960
Db 4223 gaatccagagaagagacagctgtgtcagtgagatgagcagaaggtctctacagatgaa 4282
QY 3961 ggtctgaaacttacaacagcagatgt 4020
Db 4283 ggtctgaaacttacaacagcagatgt 4342
QY 4021 agacagagctggaagagatgt 4080
Db 4343 agacagagctggaagagatgt 4402
QY 4081 ggcctgt 4140
Db 4403 ggcctgt 4462
QY 4141 ccctgtgagtacacagcaagatcacatattgtcagaagaatgtgtgtgtgtgtgtgtgtgtgtgt 4200
Db 4463 ccctgtgagtacacagcaagatcacatattgtcagaagaatgtgtgtgtgtgtgtgtgtgtgtgt 4522
QY 4201 accctgtgaactcttaagcgtctccacaaagacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4260
Db 4523 accctgtgaactcttaagcgtctccacaaagacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4582

QY 4261 ggaacccaatccagacagccctgcccagggaggaagatgagccactgccca 4320
|||||
Db 4583 ggaacccaatccagacagccctgcccagggaggaagatgagccactgccca 4642
QY 4321 gtccccagaccatctatgagaccccttcaggatgggaactggaatgagaaccccttca 4380
4643 gtccccagaccatctatgagaccccttcaggatgggaactggaatgagaaccccttca 4702
QY 4381 cctgcacatgacgtatgacgcgcgaacaaatcaagaatgctgcctgtgctcccccagg 4440
|||||
Db 4703 cctgcacatgacgtatgacgcgcgaacaaatcaagaatgctgcctgtgctcccccagg 4762
QY 4441 gcaagggggctgctccctccacaagaacaaacacatgacagatctcctcagaagctg 4500
4763 gcaagggggctgctccctccacaagaacaaacacatgacagatctcctcagaagctg 4822
QY 4501 acagaggaacaaatcttcggaatctctgtggaagacgtatgtgagatctcaagcaaaagc 4560
4823 acagaggaacaaatcttcggaatctctgtggaagacgtatgtgagatctcaagcaaaagc 4882
QY 4561 ttaagacacagatctctggtggaatgaglttaagltatgagcgctcttccttggtgtcagt 4620
4883 ttaagacacagatctctggtggaatgaglttaagltatgagcgctcttccttggtgtcagt 4942
QY 4621 aatactcaagcactctcctccgagtcagaagatcaagaatgagtcctcaacaagaagaaa 4680
4943 aatactcaagcactctcctccgagtcagaagatcaagaatgagtcctcaacaagaagaaa 5002
QY 4681 caactaaagcttgcccaagagacagctctcgcagatcagatcttcacaacgcttggaagatt 4740
5003 caactaaagcttgcccaagagacagctctcgcagatcagatcttcacaacgcttggaagatt 5062
QY 4741 atgacagagactggaacacagaataatgltcaagggtgtgtgtcaatacaagggtgtgcat 4800
5063 atgacagagactggaacacagaataatgltcaagggtgtgtgtcaatacaagggtgtgcat 5122
QY 4801 gcaatcagcctcttcctcgaatgtatcaacaatgacacatcttcgcgggacacatgcaaaag 4860
5123 gcaatcagcctcttcctcgaatgtatcaacaatgacacatcttcgcgggacacatgcaaaag 5182
QY 4861 ggaagagaacctagacatctatggaatctgcttcaatcatccctgaaatctcaacaag 4920
5183 ggaagagaacctagacatctatggaatctgcttcaatcatccctgaaatctcaacaag 5242
QY 4921 cagcagctctcagaggtgtgctctgagtcgaacacatcagtcgatactcctgtgtccatctgt 4980
5243 cagcagctctcagaggtgtgctctgagtcgaacacatcagtcgatactcctgtgtccatctgt 5302
QY 4981 gtcatctttgcaatgtctcctcgtccagcagccttctgctatctcgtatccagagagcg 5040
5303 gtcatctttgcaatgtctcctcgtccagcagccttctgctatctcgtatccagagagagcg 5362
QY 5041 gtccagcaagaacacacactgcaatctcatcagtcgagtcgagcctgtcatctactgctc 5100
5363 gtccagcaagaacacacactgcaatctcatcagtcgagtcgagcctgtcatctactgctc 5422
QY 5101 tctaatttgtctggatgtgtaattacgtttgtcctcgtcaaacgtgtcatctatctc 5160
5423 tctaatttgtctggatgtgtaattacgtttgtcctcgtcaaacgtgtcatctatctc 5482
QY 5161 ttcatctgctccagcagaagtcctatgtgtccctccacaactctgcctgtgtagccctt 5220
5483 ttcatctgctccagcagaagtcctatgtgtccctccacaactctgcctgtgtagccctt 5542
QY 5221 ctactttgtctgtagtggtgtgtaatcaatcacactctcatgttaaccaagcctcttggtctc 5280
5543 ctactttgtctgtagtggtgtgtaatcaatcacactctcatgttaaccaagcctcttggtctc 5602
QY 5281 aagatcccaagacagcctatgtgtgtgtcaccagcgtgaaccccttcattatgcatat 5340
5603 aagatcccaagacagcctatgtgtgtgtcaccagcgtgaaccccttcattatgcatat 5662
QY 5341 ggcagcgtggccacaccttgctgtgagctgttcaaccgacaataagctgaataatcat 5400
5663 ggcagcgtggccacaccttgctgtgagctgttcaaccgacaataagctgaataatcat 5722
QY 5401 gatatccccaagctccgtgttctgtatcttccacaattttgctcgtggaagaggtctac 5460
5723 gatatccccaagctccgtgttctgtatcttccacaattttgctcgtggaagaggtctac 5782
QY 5461 gacatgtgtgaaacacacagcaatgtgctatgcccctggaagaggtttggggaatctcgtt 5520
5783 gacatgtgtgaaacacacagcaatgtgctatgcccctggaagaggtttggggaatctcgtt 5842
QY 5521 ggttaccattatctcttggaactgtgtggaacaaaccccttcgcacatgcccgtggaagg 5580
5843 ggttaccattatctcttggaactgtgtggaacaaaccccttcgcacatgcccgtggaagg 5902
QY 5581 gtcgtgttcttccatctactgttctgtatctcaagtaacagatctctcatcaaggccagact 5640
5903 gtcgtgttcttccatctactgttctgtatctcaagtaacagatctctcatcaaggccagact 5962
QY 5641 gtaaatgcaaaactatctccctctgaaatgaaatgaaatgtgagcggaagacag 5700
5963 gtaaatgcaaaactatctccctctgaaatgaaatgaaatgtgagcggaagacag 6022
QY 5701 agaattctgtatggtggaagccagaaatgacatcttagaaatcaagaagtgtgacgaagata 5760
6023 agaattctgtatggtggaagccagaaatgacatcttagaaatcaagaagtgtgacgaagata 6082
QY 5761 tataagaagaagccgaagcctgtctgtgacagatcttcgtgtggaatctccctctgtgag 5820
6083 tataagaagaagccgaagcctgtctgtgacagatcttcgtgtggaatctccctctgtgag 6142
QY 5821 tgccttgggctcctcgtggaatgaaatgaggtggaataatcaacatctcaagaatgtaaca 5880
6143 tgccttgggctcctcgtggaatgaaatgaggtggaataatcaacatctcaagaatgtaaca 6202
QY 5881 ggaatatacacatglttaaccagagagatgcttcccttaacaataatgatacttcaaac 5940
6203 ggaatatacacatglttaaccagagagatgcttcccttaacaataatgatacttcaaac 6262
QY 5941 atccatgaagtatcatagaaacatgaggtactgctccatgcttgaagccaatcaagaagctg 6000
6263 atccatgaagtatcatagaaacatgaggtactgctccatgcttgaagccaatcaagaagctg 6322
QY 6001 ttgactgggagagaacacgtggaatctcttgccttlttgaagagagatcccaagagaagaa 6060
6323 ttgactgggagagaacacgtggaatctcttgccttlttgaagagagatcccaagagaagaa 6382
QY 6061 gttcgcagaagttgtgtgagtcggcgaatctcggaactgagcctcgtggaatgataagaaaaa 6120
6383 gttcgcagaagttgtgtgagtcggcgaatctcggaactgagcctcgtggaatgataagaaaaa 6442
QY 6121 tatgctggttaactatggtgagggcaacaaacgaaactctctcaacacatgagcttgatc 6180
6443 tatgctggttaactatggtgagggcaacaaacgaaactctctcaacacatgagcttgatc 6502
QY 6181 ggcgggctcctcgtgtgtgttcttctgga tgaaccacacacagagcatgtgattcccaagcccg 6240
6503 ggcgggctcctcgtgtgtgttcttctgga tgaaccacacacagagcatgtgattcccaagcccg 6562
QY 6241 cggattctgtggaatgtgtgcccctaaagtgtgtcaagaagggagatcagatgtgtctaa 6300
6563 cggattctgtggaatgtgtgcccctaaagtgtgtcaagaagggagatcagatgtgtctaa 6622
QY 6301 tctcaatagtatggaagaatgtgaagcctcttgacataggaatggaatcaatgtgtcaatgga 6360
6623 tctcaatagtatggaagaatgtgaagcctcttgacataggaatggaatcaatgtgtcaatgga 6682
QY 6361 aggttcaggtgcttggcaggtgtccagacatcaaaaaataggttggagaaatgtgtataca 6420
6683 aggttcaggtgcttggcaggtgtgtccagacatcaaaaaataggttggagaaatgtgtataca 6742
QY 6421 atagttgtaagataagcaggtgtccaaacccgagactgtgaagcctgttcaagaaattcttgtga 6480

PS Claim 27, Page 144-150; 21pp; English.
 XX
 CC The present sequence encodes a human adenosine triphosphate (ATP)
 CC binding cassette protein (ABC) 1 polypeptide, and is isolated from
 CC a Tangier disease patient. ABC1 resides in cell membranes and utilises
 CC ATP hydrolysis to transport a wide variety of substrates across the
 CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
 CC mobilisation of intracellular cholesterol stores. ABC1 is defective in
 CC Tangier disease, a genetic disorder characterised by abnormal
 CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
 CC 9q22-qq31. The ABC1 genes and proteins are useful for developing
 CC pharmaceutical agents for the treatment of heart disease and other
 CC disorders associated with hypercholesterolemia and atherosclerosis. The
 CC genes are useful for developing screening assays to screen for compounds
 CC that regulate the expression of genes associated with cholesterol
 CC transport. The genes and proteins are also useful for are also useful
 CC as diagnostic indicators of cardiovascular disease and other disorders
 CC associated with hypercholesterolemia.
 XX
 SO Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

Query Match	100.0%;	Score 6802.4;	DB 22;	Length 10474;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 6803;	Conservative 0;	Indels 1;	Gaps 0;	

QY	1	atgcttggttgagctcaagctcagtgaggtgtgctgtctgtgtggaagaaccaccacttcagaagaaga	60
Db	323	atggcttggttgagcctcaagctcagtgaggtgtgctgtctgtgtggaagaaccaccacttcagaagaaga	382
QY	61	caaacatgctcaagctgtctactgtgaagtgtgctgtgagccctcattatcttcctgcagccgagtc	120
Db	383	caaacatgctcaagctgtctactgtgaagtgtgctgtgagccctcattatcttcctgcagccgagtc	442
QY	121	tcgttcgcgtcagctagctaccaccctatgaacaacatgaatgycatltttccaaataagcc	180
Db	443	tcgttcgcgtcagctagctaccaccctatgaacaacatgaatgycatltttccaaataagcc	502
QY	181	atgcccctgcaggaacacacttccttggttaaggagatctgttaatgtgcaacaacccc	240
Db	503	atgcccctgcaggaacacacttccttggttaaggagatctgttaatgtgcaacaacccc	562
QY	241	tgttcctgttaaccgagctcctggtggaggtctcccgagttgtgtgaaacttaacaatcc	300
Db	563	tgttcctgttaaccgagctcctggtggaggtctcccgagttgtgtgaaacttaacaatcc	622
QY	301	atgttggtcgcgcgtgttctcagatgtctcggaggtcttttatacgccaagaagacc	360
Db	623	atgttggtcgcgcgtgttctcagatgtctcggaggtcttttatacgccaagaagacc	682
QY	361	agcatgaagagacatgcgcacaagaatltctgagacaatctacagacatcagaagaatccactca	420
Db	683	agcatgaagagacatgcgcacaagaatltctgagacaatctacagacatcagaagaatccactca	742
QY	421	aacttgaagctccaagaattctcgtgtgacaaatgaaaacttcctcgtgtcctatataac	480
Db	743	aacttgaagctccaagaattctcgtgtgacaaatgaaaacttcctcgtgtcctatataac	802
QY	481	aacctctcctcccaagaatctacatgttgacaagaatgtctgggctcgtatctatccac	540
Db	803	aacctctcctcccaagaatctacatgttgacaagaatgtctgggctcgtatctatccac	862
QY	541	aaggtatatttgcagaagctaccagttacatttgacaagctcgtgcacatgcatgacaatatca	600
Db	863	aaggtatatttgcagaagctaccagttacatttgacaagctcgtgcacatgcatgacaatatca	922
QY	601	gaagagatgatattcaactctgtgtgaccagaagaattctgagcttgtgtgctaccacaagag	660
Db	923	gaagagatgatattcaactctgtgtgaccagaagaattctgagcttgtgtgctaccacaagag	982
QY	661	aaactgtgcgcagcagacgcagtaactcgttctccaacaatgacatcctggaagcaactctg	720
Db	983	aaactgtgcgcagcagacgcagtaactcgttctccaacaatgacatcctggaagcaactctg	1042

QY 721 agaacactaactctacatctccctcccgagcaagagctggtgaaagccacaaaaca 780
|||||
Db 1043 agaacactaactctacatctccctcccgagcaagagctggtgaaagccacaaaaca 1102
QY 781 ttgcgtacatagctctggagctctggcccgagagcttcaacatagaagagctgagttac 840
|||||
Db 1103 ttgcgtacatagctctggagctctggcccgagagcttcaacatagaagagctgagttac 1162
QY 841 atgcgacagagagtgatgttcttgaccaaagtgaacaagctccagctcccaacaaac 900
|||||
Db 1163 atgcgacagagagtgatgttcttgaccaaagtgaacaagctccagctcccaacaaac 1222
QY 901 taccagagctgtctcgtatcttcgcgagcaaccgagagagagggcgctgaaagataag 960
|||||
Db 1223 taccagagctgtctcgtatcttcgcgagcaaccgagagagagggcgctgaaagataag 1282
QY 961 tctctcaactggtatagagacaacaactacaagccctcttgagagcaatgagcaactgag 1020
|||||
Db 1283 tctctcaactggtatagagacaacaactacaagccctcttgagagcaatgagcaactgag 1342
QY 1021 gaagatgctgaaacctctctatacaactctcaactctctactgcaatgattgataag 1080
|||||
Db 1343 gaagatgctgaaacctctctatacaactctcaactctctactgcaatgattgataag 1402
QY 1081 aatttgagctagagctctctcccgcaatctctgaaagagctctgagcgctgctgct 1140
|||||
Db 1403 aatttgagctagagctctctcccgcaatctctgaaagagctctgagcgctgctgct 1462
QY 1141 ggggaagatccctgtatatacccttgacaactccagccacaagagcagtgcaatgagtgaaac 1200
|||||
Db 1463 ggggaagatccctgtatatacccttgacaactccagccacaagagcagtgcaatgagtgaaac 1522
QY 1201 aagaacctccagaaactgctgtgttccatgatacttgaaagagcagtgaggagaaactcaac 1260
|||||
Db 1523 aagaacctccagaaactgctgtgttccatgatacttgaaagagcagtgaggagaaactcaac 1582
QY 1261 cccaagatctgagacctctcatagagaaacagcaagaaatgagacctctccgagatgctgag 1320
|||||
Db 1583 cccaagatctgagacctctcatagagaaacagcaagaaatgagacctctccgagatgctgag 1642
QY 1321 gacagcagaggaacaatgacaacttttgagaaacagcagtgatgagtgcttaagattgagacac 1380
|||||
Db 1643 gacagcagaggaacaatgacaacttttgagaaacagcagtgatgagtgcttaagattgagacac 1702
QY 1381 caagacatcgtgctgtttttggccaagaccccgagagagatgccaagctgaatgttct 1440
|||||
Db 1703 caagacatcgtgctgtttttggccaagaccccgagagagatgccaagctgaatgttct 1762
QY 1441 gtttacacctgagagagaagcttccaacgagactaacacaggaatcccgagacatatctgc 1500
|||||
Db 1763 gtttacacctgagagagaagcttccaacgagactaacacaggaatcccgagacatatctgc 1822
QY 1501 ttcatgagatgtgttcaacctgaaacagctagaacccaatagcaacagaagtctggtcatc 1560
|||||
Db 1823 ttcatgagatgtgttcaacctgaaacagctagaacccaatagcaacagaagtctggtcatc 1882
QY 1561 aacaagtccatgagatgctgctgagatgagagaagtcttggtgctgtattgtttcatctgga 1620
|||||
Db 1883 aacaagtccatgagatgctgctgagatgagagaagtcttggtgctgtattgtttcatctgga 1942
QY 1621 attactccaagagcagatgtgctgctcccatcatgctcaagatacagaatcccaagagcat 1680
|||||
Db 1943 attactccaagagcagatgtgctgctcccatcatgctcaagatacagaatcccaagagcat 2002
QY 1681 gacaatgtgagagaggaacaataaatacaagatgagttactgagacctggttctctgagct 1740
|||||
Db 2003 gacaatgtgagagaggaacaataaatacaagatgagttactgagacctggttctctgagct 2062
QY 1741 gacctcttgaagacatgagtgatgctggtgaggggcttgctcacttgcaagatgtggtg 1800
|||||
Db 2063 gacctcttgaagacatgagtgatgctggtgaggggcttgctcacttgcaagatgtggtg 2122

QY 1801 gacgagcaatcatcagagtgctgacgggcaacgagagaagaactggtgtctatagca 1860
|||||
Db 2123 gacgagcaatcatcagagtgctgacgggcaacgagagaagaactggtgtctatagca 2182
QY 1861 cagatgccctatccctgttaccgttgatgacatcttctcggtgtatgacggtcaatg 1920
|||||
Db 2183 cagatgccctatccctgttaccgttgatgacatcttctcggtgtatgacggtcaatg 2242
QY 1921 cccctcttcatgagcgtggtgcttgatattactcagttgctgttgatcatcagaagcatctg 1980
|||||
Db 2243 cccctcttcatgagcgtggtgcttgatattactcagttgctgttgatcatcagaagcatctg 2302
QY 1981 tatgagaagagagcagcgtctgaaagagacatgctggaatcaltggtgctgtgacaacagata 2040
|||||
Db 2303 tatgagaagagagcagcgtctgaaagagacatgctggaatggtgctgtgacaacagata 2362
QY 2041 ctctggtttagctgttcaatagtaagctcaatccctcttctgtgaaagctggtgctgcta 2100
|||||
Db 2363 ctctggtttagctgttcaatagtaagctcaatccctcttctgtgaaagctggtgctgcta 2422
QY 2101 gttgtcatccctgaaagttgagaacctgtgctccacagtgatcccaagctgtgttctgct 2160
|||||
Db 2423 gttgtcatccctgaaagttgagaacctgtgctccacagtgatcccaagctgtgttctgct 2482
QY 2161 ttccgttcgtgttctgctgtgtgacaactcctgcaagtgtctcgtatgacaactctc 2220
|||||
Db 2483 ttccgttcgtgttctgctgtgtgacaactcctgcaagtgtctcgtatgacaactctc 2542
QY 2221 tccagagcaaacctggcagcagcgtgtggtgggcaatctatcttcaagctgttactctcc 2280
|||||
Db 2543 tccagagcaaacctggcagcagcgtgtggtgggcaatctatcttcaagctgttactctcc 2602
QY 2281 taagtcctgtgtgtgcaatggcagagcaacgttgagcttcaacactcaagatctctgtagc 2340
|||||
Db 2603 taagtcctgtgtgtgcaatggcagagcaacgttgagcttcaacactcaagatctctgtagc 2662
QY 2341 ctgctgtctcctgtggtcttgggtgtgctgtgagtaactttgccccttttgagagagag 2400
|||||
Db 2663 ctgctgtctcctgtggtcttgggtgtgctgtgagtaactttgccccttttgagagagag 2722
QY 2401 ggcattgagatgagatgaggaacaacctgtttgagagctcttgaggagaaatgagcttcaat 2460
|||||
Db 2723 ggcattgagatgagatgaggaacaacctgtttgagagctcttgaggagaaatgagcttcaat 2782
QY 2461 ctccacactctgatactcatgatagtctgtttgacaactctccctatagggtatgacacgtg 2520
|||||
Db 2783 ctccacactctgatactcatgatagtctgtttgacaactctccctatagggtatgacacgtg 2842
QY 2521 tacattgagatgctgtcttccagggcagtagcgaattcccaagccctgttatttccctgc 2580
|||||
Db 2843 tacattgagatgctgtcttccagggcagtagcgaattcccaagccctgttatttccctgc 2902
QY 2581 accaaggtcctactgtgttggcgagagaagtgaatgagagaagccacccgtgttccaacag 2640
|||||
Db 2903 accaaggtcctactgtgttggcgagagaagtgaatgagagaagccacccgtgttccaacag 2962
QY 2641 aagagaaatgtcaagaatctgcaatggagaggaacccacccacttgaagctggtgctgc 2700
|||||
Db 2963 aagagaaatgtcaagaatctgcaatggagaggaacccacccacttgaagctggtgctgc 3022
QY 2701 attcagaacctgttlaaagcttaccagagatggaatgaaagtgtgctgcatgacgtgca 2760
|||||
Db 3023 attcagaacctgttlaaagcttaccagagatggaatgaaagtgtgctgcatgacgtgca 3082
QY 2761 ctgaaattttatgagagggccaagatacactcctctcctggggccaacatgagagcgaggagcg 2820
|||||
Db 3083 ctgaaattttatgagagggccaagatacactcctcctcctggggccaacatgagagcgaggagcg 3142
QY 2821 accacatgttcaatcctgacaggtgtgttcccccagacctcgagcagccctatactctg 2880
|||||
Db 3143 accacatgttcaatcctgacaggtgtgttcccccagacctcgagcagccctatactctg 3202
QY 2881 ggaataagacatcgtctgtgagaatgagacacatccggcagaacctgtgggtgtgttccacag 2940

Db 3203 ggaagaaacattctgctctgagatgacacacccatcccgcaaaactcggggtctgctcccg 3262
QY 2941 cataacgtgctgtttgacatgctgactgtctgaaagaaacacatctgcttctatgcccgttg 3000
Db 3263 cataacgtgctgtttgacatgctgactgtctgaaagaaacacatctgcttctatgcccgttg 3322
QY 3001 aaagggtctctctgaaagacgctgaaagcggaatgagcagatgagcccttgatgttggc 3060
Db 3323 aaagggtctctctgaaagacgctgaaagcggaatgagcagatgagcccttgatgttggc 3382
QY 3061 ttgcatcaagcaagctgaaagcaaaacaaagcagctgcaagctgcaagctgcaagcaag 3120
Db 3383 ttgcatcaagcaagctgaaagcaaaacaaagcagctgcaagctgcaagctgcaagcaag 3442
QY 3121 ctatctgtgctgctgctgtgtctggtggtatctaagttgtcaatctctggaagaaacaca 3180
Db 3443 ctatctgtgctgctgctgtgtctggtggtatctaagttgtcaatctctggaagaaacaca 3502
QY 3181 gctgtgtggaaccccttactcccgcaagggaataatgagcctgctgtggaataacacaca 3240
Db 3503 gctgtgtggaaccccttactcccgcaagggaataatgagcctgctgtggaataacacaca 3562
QY 3241 ggcgcacacattatctctctacacacacacacacacacacacacacacacacacacac 3300
Db 3563 ggcgcacacattatctctctac 3622
QY 3301 attgcatcatctcccatgagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3360
Db 3623 attgcatcatctcccatgagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3682
QY 3361 cagctgaggaaacagctactac 3420
Db 3683 cagctgaggaaacagctactac 3742
QY 3421 tctctgagaaacagctactac 3480
Db 3743 tctctgagaaacagctactac 3802
QY 3481 agcagttctgagctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 3540
Db 3803 agcagttctgagctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 3862
QY 3541 tctgcatctccaactctac 3600
Db 3863 tctgcatctccaactctac 3922
QY 3601 gggcatgagctgacatattgctgcatattgctgcatattgctgcatattgctgcatattgct 3660
Db 3923 gggcatgagctgacatattgctgcatattgctgcatattgctgcatattgctgcatattgct 3982
QY 3661 ctctctcatgagattgagatgagcggctctcagaactgagcattctagttatgacatctca 3720
Db 3983 ctctctcatgagattgagatgagcggctctcagaactgagcattctagttatgacatctca 4042
QY 3721 ggaagacacctggaagaaatattctcagaagtgccgaagagagtgagggtgagatgctgag 3780
Db 4043 ggaagacacctggaagaaatattctcagaagtgccgaagagagtgagggtgagatgctgag 4102
QY 3781 acctcaagatgtaaccttgctgcaagcaagcaagcaagcagccttcgggggcaagcaagcag 3840
Db 4103 acctcaagatgtaaccttgctgcaagcaagcaagcaagcagccttcgggggcaagcaagcag 4162
QY 3841 tctcttgcgggttcaactgaaagatgctgctgcatccaatgattctgacatagaccaca 3900
Db 4163 tctcttgcgggttcaactgaaagatgctgctgcatccaatgattctgacatagaccaca 4222
QY 3901 gaatcagaagagacagactgtctcagtgagatgagatgagcaagaggttctacacagttgaa 3960
Db 4223 gaatcagaagagacagactgtctcagtgagatgagatgagcaagaggttctacacagttgaa 4282
QY 3961 ggcctggaacttacacagacagattgtgccccttctgagaaagagctgtaattggc 4020
Db 4283 ggcctggaacttacacagacagattgtgccccttctgagaaagagctgtaattggc 4342
QY 4021 agacggagtcggaagagattttgtgctcagatgttctgacagctgtgtgtctgcatc 4080
Db 4343 agacggagtcggaagagattttgtgctcagatgttctgacagctgtgtgtctgcatc 4402
QY 4081 ggcctgtgttcagcctgcatctgtgacaccccttgcaagatgacccacgctggaacttcag 4140
Db 4403 ggcctgtgttcagcctgcatctgtgacaccccttgcaagatgacccacgctggaacttcag 4462
QY 4141 ccttgagtgtaacacagcaatgacacatttgcagcaatgagctgctcctggaacacagga 4200
Db 4463 ccttgagtgtaacacagcaatgacacatttgcagcaatgagctgctcctggaacacagga 4522
QY 4201 accttggaactcttaaacgcccctacacaaagaccccttgctcggagccgctgatatgaa 4260
Db 4523 accttggaactcttaaacgcccctacacaaagaccccttgctcggagccgctgatatgaa 4582
QY 4261 ggaaccccaatcccaagacacgcccctgcaagcagggaggaagatgagcactgcccaca 4320
Db 4583 ggaaccccaatcccaagacacgcccctgcaagcagggaggaagatgagcactgcccaca 4482
QY 4321 gtcccccagacacatcagtgacacctctccagaaatgagacatgagacacacacacacac 4380
Db 4643 gtcccccagacacatcagtgacacctctccagaaatgagacatgagacacacacacacac 4702
QY 4381 cctgcatgacagctgtagcagcagcaaaatacagaagatgctgctgtgtgtgtgtgtgtgt 4440
Db 4703 cctgcatgacagctgtagcagcagcaaaatacagaagatgctgctgtgtgtgtgtgtgtgt 4762
QY 4441 gcaagggtggtgctcctccccaagaaacaaacacacacacacacacacacacacacacac 4500
Db 4763 gcaagggtggtgctcctccccaagaaacaaacacacacacacacacacacacacacacac 4822
QY 4501 acaggaagaaacacattctgagatctctgtgaaagcgtatgtgcagatcatagccaaagc 4560
Db 4823 acaggaagaaacacattctgagatctctgtgaaagcgtatgtgcagatcatagccaaagc 4882
QY 4561 ttaagaaacaaagacatctggtgaaatgagttcagatgagcagcttcccggtgtcagat 4620
Db 4883 ttaagaaacaaagacatctggtgaaatgagttcagatgagcagcttcccggtgtcagat 4942
QY 4621 aatactcaagcattctcctccagatcgaagaaatgaaatgaaatgaaatgaaatgaaatgaa 4680
Db 4943 aatactcaagcattctcctccagatcgaagaaatgaaatgaaatgaaatgaaatgaaatgaa 5002
QY 4681 caactaaagctggcgaaggaacagctgcatcagatctcagatctcagatctcagatctcag 4740
Db 5003 caactaaagctggcgaaggaacagctgcatcagatctcagatctcagatctcagatctcag 5062
QY 4741 atgacaggaactggaacacacagaataatgaaatgaaatgaaatgaaatgaaatgaaatg 4800
Db 5063 atgacaggaactggaacacacagaataatgaaatgaaatgaaatgaaatgaaatgaaatg 5122
QY 4801 gcaatcagcctcttccggaatgtaacataacatgcaattctccgggccaaccccgcaag 4860
Db 5123 gcaatcagcctcttccggaatgtaacataacatgcaattctccgggccaaccccgcaag 5182
QY 4861 ggaagaaacctagccaatttgaatatactgcttcaatcatcccttgaaatccacacag 4920
Db 5183 ggaagaaacctagccaatttgaatatactgcttcaatcatcccttgaaatccacacag 5242
QY 4921 cagcagctctcagaagtgctctgtagaacacatcaagtgtagatcctgtgtccatctgt 4980
Db 5243 cagcagctctcagaagtgctctgtagaacacatcaagtgtagatcctgtgtccatctgt 5302
QY 4981 gtacattctgcaatgtcctcgtcccaagcagcttgctgtaattccttgatccgaagagcg 5040
Db 5303 gtacattctgcaatgtcctcgtcccaagcagcttgctgtaattccttgatccgaagagcg 5362
QY 5041 gtacagcaagcaaaac 5100
Db 5363 gtacagcaagcaaaac 5422

QY 5101 tctaatcttgctgggataatgtaataagctgtccctgcacactgtcatatc 5160
 |||||
 Db 5423 tctaatcttgctgggataatgtaataagctgtccctgcacactgtcatatc 5482
 QY 5161 tctaatcttgctgggataatgtaataagctgtccctgcacactgtcatatc 5220
 |||||
 Db 5483 tctaatcttgctgggataatgtaataagctgtccctgcacactgtcatatc 5542
 QY 5221 ctactcttgctgggataatgtaataagctgtccctgcacactgtcatatc 5280
 |||||
 Db 5543 ctactcttgctgggataatgtaataagctgtccctgcacactgtcatatc 5602
 QY 5281 aagatcccaagcaagcactatgtgtctccacagcgttgaacccctcatatg 5340
 |||||
 Db 5603 aagatcccaagcaagcactatgtgtctccacagcgttgaacccctcatatg 5662
 QY 5341 ggcagcgttgccacactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5400
 |||||
 Db 5663 ggcagcgttgccacactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5722
 QY 5401 gatattccgaagctccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5460
 |||||
 Db 5723 gatattccgaagctccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5782
 QY 5461 gacatgt 5520
 |||||
 Db 5783 gacatgt 5842
 QY 5521 ggtccacactatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5580
 |||||
 Db 5843 ggtccacactatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5902
 QY 5581 ggt 5640
 |||||
 Db 5903 ggt 5962
 QY 5641 gtaataatgcaagcactatctgtgtgtgtgtgtgtgtgtgtgtgtgt 5700
 |||||
 Db 5963 gtaataatgcaagcactatctgtgtgtgtgtgtgtgtgtgtgtgtgt 6022
 QY 5701 agaatcttgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5760
 |||||
 Db 6023 agaatcttgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6082
 QY 5761 tatagaaggaagcagcagcagcagcagcagcagcagcagcagcagcag 5820
 |||||
 Db 6083 tatagaaggaagcagcagcagcagcagcagcagcagcagcagcagcag 6142
 QY 5821 tgccttggt 5880
 |||||
 Db 6143 tgccttggt 6202
 QY 5881 ggaagatccactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5940
 |||||
 Db 6203 ggaagatccactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6262
 QY 5941 atccatgaagatcatcagaacatgtgtgtgtgtgtgtgtgtgtgtgtgt 6000
 |||||
 Db 6263 atccatgaagatcatcagaacatgtgtgtgtgtgtgtgtgtgtgtgtgt 6322
 QY 6001 ttgactgtgagagaagcagcagcagcagcagcagcagcagcagcagcagcag 6060
 |||||
 Db 6323 ttgactgtgagagaagcagcagcagcagcagcagcagcagcagcagcagcag 6382
 QY 6061 gttgcaaggt 6120
 |||||
 Db 6383 gttgcaaggt 6442
 QY 6121 tatgt 6180
 |||||
 Db 6443 tatgt 6502

QY 6181 ggcgggctctctgt 6240
 |||||
 Db 6503 ggcgggctctctgt 6562
 QY 6241 cggctctgt 6300
 |||||
 Db 6563 cggctctgt 6622
 QY 6301 tctcatatgataaggaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6360
 |||||
 Db 6623 tctcatatgataaggaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6682
 QY 6361 aggttcaggt 6420
 |||||
 Db 6683 aggttcaggt 6742
 QY 6421 atagttgtatagatagcaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6480
 |||||
 Db 6743 atagttgtatagatagcaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6802
 QY 6481 ctgtcatctctgt 6540
 |||||
 Db 6803 ctgtcatctctgt 6862
 QY 6541 ccatctctcatctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6600
 |||||
 Db 6863 ccatctctcatctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6922
 QY 6601 ctccacatagaaagcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6660
 |||||
 Db 6923 ctccacatagaaagcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6982
 QY 6661 gccaaagaccaggaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6720
 |||||
 Db 6983 gccaaagaccaggaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7042
 QY 6721 gtagtgaagcgt 6780
 |||||
 Db 7043 gtagtgaagcgt 7102
 QY 6781 gtagtgaagcgt 6840
 |||||
 Db 7103 gtagtgaagcgt 7126

RESULT 6
 AAF24708
 ID AAF24708 standard; DNA; 10474 BP.
 XX
 AC AAF24708;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
 XX
 KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
 KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
 KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
 KW atherosclerosis; cholesterol transport; ss.
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT 323..7108
 FT CDS /*tag= a
 FT /product= "defective ABC1 polypeptide"
 PN W0200078971-A2.
 XX
 PD 28-DEC-2000.
 XX
 PF 16-JUN-2000; 2000MO-US16591.
 XX

QY	1561	aacacagtcacatgagactgctgtgatagagaggaagttctgtgagctgtgattgtgtcaactgga	1620
DB	1883	aacaagatccatgtagctgctgtgatagagaggaagtctctgagctgtgattgtgtcaactgga	1942
QY	1621	attaatccagagcagcatctgaagctgtcccatatctgtcaaggtacaaagatccgaatggaacatt	1680
DB	1943	attactccaagcagcagcatctgaagctgtcccatatctgtcaaggtacaaagatccgaatggaacatt	2002
QY	1681	gacaaatgtgagagaggaacaataaatacaaggaatgtggtactgtgagacctgtgtctccgaagct	1740
DB	2003	gacaaatgtgagagaggaacaataaatacaaggaatgtggtactgtgagacctgtgtctccgaagct	2062
QY	1741	gacctctctgaagagacatgtagctgtacgtctgtgaggggctctgcgtcaactgtgcagaaatgtgtgt	1800
DB	2063	gacctctctgaagagacatgtagctgtgtacgtctgtgaggggctctgcgtcaactgtgcagaaatgtgtgt	2122
QY	1801	gagcagaggaatcaatcaaggtgtgtgacagggcaacccgagaaagaaactgtgtgtctatatggcaa	1860
DB	2123	gagcagaggaatcaatcaaggtgtgtgacagggcaacccgagaaagaaactgtgtgtctatatggcaa	2182
QY	1861	cagatgtcccatccctcgtttacgtttgatactgttcacatctcttcgcgggtggaatgaagccggtaaatg	1920
DB	2183	cagatgtcccatccctcgtttacgtttgatactgttcacatctcttcgcgggtggaatgaagccggtaaatg	2242
QY	1921	ccctctctcaatgtagcagctgtgagctgtgaattctcaatgtagctgtgtgatacatcaagggatcgtgt	1980
DB	2243	ccctctctcaatgtagcagctgtgagctgtgaattctcaatgtagctgtgtgatacatcaagggatcgtgt	2302
QY	1981	tatgagaagagagacagcgtctgaagaagacatctgagatcatatgagcctgtgagacaacagcata	2040
DB	2303	tatgagaagagagacagcgtctgaagaagacatctgagatcatatgagcctgtgagacaacagcata	2362
QY	2041	ctctcgtgttgtagcgtgtgtcatatgaatgaacccatctctctctctgtgtgagagagctgtgcgtcta	2100
DB	2363	ctctcgtgttgtagcgtgtgtcatatgaatgaacccatctctctctctgtgtgagagagctgtgcgtcta	2422
QY	2101	gtgtgtcatccctgaaggtatgaagaaacaacccgtgcgtccctcaagtgatccccaagcgtgtgtttgttc	2160
DB	2423	gtgtgtcatccctgaaggtatgaagaaacaacccgtgcgtccctcaagtgatccccaagcgtgtgtttgttc	2482
QY	2161	ttctcgttcogtgtgttctgtctgtgtgtgacaatccctgacgtgtctctccctgtatgaacaacattcttc	2220
DB	2483	ttctcgttcogtgtgttctgtctgtgtgtgacaatccctgacgtgtgtctctccctgtatgaacaacattcttc	2542
QY	2221	tcacagagccaacccgtgagagagacccctctgtggggacatcatcttaactgaagctgtacctgtccc	2280
DB	2543	tcacagagccaacccgtgagagagacccctctgtggggacatcatcttaactgaagctgtacctgtccc	2602
QY	2281	tacgtccctgtgtgtgtgacatgtgcagagactacgtgtgagcttccacactcaaaagatcttcgtctagc	2340
DB	2603	tacgtccctgtgtgtgtgacatgtgtgcagagactacgtgtgagcttccacactcaaaagatcttcgtctagc	2662
QY	2341	ctgtcgtctcctgtgtgaccttttggtgtgtgtgctgtgtgaattgtgaccttttttgaagagagag	2400
DB	2663	ctgtcgtctcctgtgtgaccttttggtgtgtgtgtgctgtgtgaattgtgaccttttttgaagagagag	2722
QY	2401	ggcattgtgaagcgtgtgagagcaacccgttttgagagagcgtgtgtgaggaagatgtgcttcaat	2460
DB	2723	ggcattgtgaagcgtgtgagagcaacccgttttgagagagcgtgtgtgaggaagatgtgcttcaat	2782
QY	2461	ctcacaccactctgacatccacagatgtgtgtgaacaaccttccctctataggggtgtatgtgacctgtg	2520
DB	2783	ctcacaccactctgacatccacagatgtgtgtgtgaacaaccttccctctataggggtgtatgtgacctgtg	2842
QY	2521	tacattgtgagcgtgtcttctccaggtccagttaacggaaattcccaagccctgtgtatttctctgtc	2580
DB	2843	tacattgtgagcgtgtcttctccaggtccagttaacggaaattcccaagccctgtgtatttctctgtc	2902
QY	2581	accacagctctactcgtttgtgtgagaggaaggtgtgtgtgaagaagccaacctgtgtttccaacag	2640
DB	2903	accacagctctactcgtttgtgtgagaggaaggtgtgtgtgaagaagccaacctgtgtttccaacag	2962

QY	2641	aagsgaatgtcagaatctgcatactgagaggaaccaccacttgaagctgggctgctcc	2700
Db	2963	aaggaatgtccagaatctgcatactgagaggaaccaccacttgaagctgggctgctcc	3022
QY	2701	attcagaacctggtaaaagctctacccgagatggagagagtgagctgctgcagctgcagca	2760
Db	3023	attcagaacctggtaaaagctctacccgagatggagagagtgagagtgagctgctgcagctgcagca	3082
QY	2761	ctgaaattttttctgagggcccgagatccactctctccctgggccaatgagcggggaagacg	2820
Db	3083	ctgaaattttttctgagggcccgagatccactctctccctgggccaatgagcggggaagacg	3142
QY	2821	accaccatgtlcaatccctgaccgggtgtgttcccccgacctcgggacacgcctacatctcg	2880
Db	3143	accaccatgtlcaatccctgaccgggtgtgttcccccgacctcgggacacgcctacatctcg	3202
QY	2881	ggaaaaagacatctgcctctgagatgagacacatcccgacgaacctgggggtctgtccccaag	2940
Db	3203	ggaaaaagacatctgcctctgagatgagacacatcccgacgaacctgggggtctgtccccaag	3262
QY	2941	cataacgagctgtttctgacacgctgcagctgcctcgaagaacacatctgttctatgcccccttg	3000
Db	3263	cataacgagctgtttctgacacgctgcagctgcctcgaagaacacatctgttctatgcccccttg	3322
QY	3001	aaaaggtctctctgagaagcagctgtgaagcggagatgagacagatgagccctggaatgttgtt	3060
Db	3323	aaaaggtctctctgagaagcagctgtgaagcggagatgagacagatgagccctggaatgttgtt	3382
QY	3061	ttgcacatcaagcaagctgtgaaaagcaaaacagccagctgttcaagtgagatgcaagaagaag	3120
Db	3383	ttgcacatcaagcaagctgtgaaaagcaaaacagccagctgttcaagtgagatgcaagaagaag	3442
QY	3121	ctatctgtggccttggccttctgttcgggggatactcaaggtgttcattctgtgagaccacca	3180
Db	3443	ctatctgtggccttggccttctgttcgggggatactcaaggtgttcattctgtgagaccacca	3502
QY	3181	gcttggctgagaccttactccctccgacaggagatactggagctgtgcctgtaaaataccgcaaa	3240
Db	3503	gcttggctgagaccttactccctccgacaggagatactggagctgtgcctgtaaaataccgcaaa	3562
QY	3241	ggccgacacattatctctctctacacacaaatgtagatgaagcggaaatctctctggggagag	3300
Db	3563	ggccgacacattatctctctctacacacaaatgtagatgaagcggaaatctctctggggagag	3622
QY	3301	atttgcacatctcccatctggagaaagctgtgtgtgtgtgctctccctgttctctaaagac	3360
Db	3623	atttgcacatctcccatctggagaaagctgtgtgtgtgtgctctccctgttctctaaagac	3682
QY	3361	cagctctgggaaacagctactactctgacacctgtgtlcaagaagaatgtagaattcctccctcagt	3420
Db	3683	cagctctgggaaacagctactactctgacacctgtgtlcaagaagaatgtagaattcctccctcagt	3742
QY	3421	tccctcgagaacagtagtagacactgtgtcatctaccctgaaaaaaggagacagtggttctcag	3480
Db	3743	tccctcgagaacagtagtagacactgtgtcatctaccctgaaaaaaggagacagtggttctcag	3802
QY	3481	agcaagcttctgagctgtgcctctggagagacacatgagagtgagacacgtcgaacatcgatgtc	3540
Db	3803	agcaagcttctgagctgtgcctctggagagacacatgagagtgagacacgtcgaacatcgatgtc	3862
QY	3541	tctgtcatctccaaacctatcaagaagacatgtgtctgaaagcccggtctgtgtgaagaacata	3600
Db	3863	tctgtcatctccaaacctatcaagaagacatgtgtctgaaagcccggtctgtgtgaagaacata	3922
QY	3601	gggcatctgagctgacctatgtctgtgcataatgaagcgtctaaaggagggagcccttgttgaa	3660
Db	3923	gggcatctgagctgacctatgtctgtgcataatgaagcgtctaaaggagggagcccttgttgaa	3982
QY	3661	ctctttcaagaaatgtgagacaggctctccagacctgtggacatttcaagtatgtacatcca	3720
Db	3983	ctctttcaagaaatgtgagacaggctctccagacctgtggacatttcaagtatgtacatcca	4042
QY	3721	gaagcagacctggaagaatacttccctaaagctggccgaagaagatgtgggtgtgagtctgag	3780

Db 4043 gagagcagcccttgaaagaataattccctcaaggtgagccgaagagtgagggtgagtcgtcag 4102
QY 3781 acctcaatgatgacctgacagcaagaacgaagcgagcccttcggggaacaagcgaagc 3840
Db 4103 acctcagatgtagacctgacagcaagaacgaagcgagcccttcggggaacaagcgaagc 4162
QY 3841 tgtcttcgcccgttcacatgaagatgtagtgcgtgcattccaaatgattctgacatagaacca 3900
Db 4163 tgccttcgcccgttcacatgaagatgtagtgcgtgcattccaaatgattctgacatagaacca 4222
QY 3901 gaattccagagagacagactgctcagtgagatgtagtggaaagcgccctacacaggtgaa 3960
Db 4223 gaattccagagagacagactgctcagtgagatgtagtggaaagcgccctacacaggtgaa 4282
QY 3961 ggcctggaacttaacagacacagttgtgagccctttgtggaagagactgtaattgccc 4020
Db 4283 ggcctggaacttaacagacacagttgtgagccctttgtggaagagactgtaattgccc 4342
QY 4021 agacggagtgaggaaagatttttgcctcagattgtcttcagagctgtgttctgcatt 4080
Db 4343 agacggagtgaggaaagatttttgcctcagattgtcttcagagctgtgttctgcatt 4402
QY 4081 ggcctgtgttcagccttgatcgtgtgacaccccttgcgaagtaccccgactggaactcag 4140
Db 4403 ggcctgtgttcagccttgatcgtgtgacaccccttgcgaagtaccccgactggaactcag 4462
QY 4141 cccttgatgtacaaacgaacgaatgacattgtgcaagcatgtagtccctgaggaacgga 4200
Db 4463 cccttgatgtacaaacgaacgaatgacattgtgcaagcatgtagtccctgaggaacgga 4522
QY 4201 acccttgaaactcttaaacgcgcctcaacaaagacccctggtctcggaagccgcgtatgga 4260
Db 4523 acccttgaaactcttaaacgcgcctcaacaaagacccctggtctcggaagccgcgtatgga 4582
QY 4261 ggaacccaatcccaagacacgccttgacagcgagggaggaagatgagcaactgccc 4320
Db 4583 ggaacccaatcccaagacacgccttgacagcgagggaggaagatgagcaactgccc 4642
QY 4321 gtccccaagacacatctgagaccccttcgaagatggaactggaacatgagaacccctca 4380
Db 4643 gtccccaagacacatctgagaccccttcgaagatggaactggaacatgagaacccctca 4702
QY 4381 cctgtacgtcagtgtagcagcgacaacatcaagaagatgctgcctggtgtgtccccaagg 4440
Db 4703 cctgtacgtcagtgtagcagcgacaacatcaagaagatgctgcctggtgtgtccccaagg 4762
QY 4441 gcaaggggggtgcctcctccacaagaacaaacaacatgacatataccttcagagactg 4500
Db 4763 gcaaggggggtgcctcctccacaagaacaaacaacatgacatataccttcagagactg 4822
QY 4501 acaggaagaacatctcgatattatctgtgtgaagacgtatgtgcagatatacagcaaaagc 4560
Db 4823 acaggaagaacatctcgatattatctgtgtgaagacgtatgtgcagatatacagcaaaagc 4882
QY 4561 ttaagaagaacatctggtgtgaatgagtttagatgtagcggcttccctgggtgtcagt 4620
Db 4883 ttaagaagaacatctggtgtgaatgagtttagatgtagcggcttccctgggtgtcagt 4942
QY 4621 aatactcaagcactcctcccgagtcagaagatgtaatgtagcatataaacaatgaaagaa 4680
Db 4943 aatactcaagcactcctcccgagtcagaagatgtaatgtagcatataaacaatgaaagaa 5002
QY 4681 caactaaagctggaagaagacagttctgcaatcgaattctcaacagcttggaagatt 4740
Db 5003 caactaaagctggaagaagacagttctgcaatcgaattctcaacagcttggaagatt 5062
QY 4741 atgacaagacgtggaacacagaataatgtcaagtggtgtccaataacaagggtgcgat 4800
Db 5063 atgacaagacgtggaacacagaataatgtcaagtggtgtccaataacaagggtgcgat 5122
QY 4801 gcaacagactcttctcctaagtcatcaacatgcattctccgggccaactcgaag 4860
Db 5123 gcaacagactcttctcctaagtcatcaacatgcattctccgggccaactcgaag 5182
QY 4861 ggaagaaacccctagacatataggaattactgtcttcaatcatctccctgaatcacaag 4920
Db 5183 ggaagaaacccctagacatataggaattactgtcttcaatcatctccctgaatcacaag 5242
QY 4921 cagcagctcctcagagtggtcctcgtatgacacatcagtgatgagtcctgtgtccatcgt 4980
Db 5243 cagcagctcctcagagtggtcctcgtatgacacatcagtgatgagtcctgtgtccatcgt 5302
QY 4981 gtcatcttggaatgtccctgcctccagcagacttgcgtatctcctgacacagagcg 5040
Db 5303 gtcatcttggaatgtccctgcctccagcagacttgcgtatctcctgacacagagcg 5362
QY 5041 gtcaacaaagcaaaacacctcagttcacgttgagtggaagcctgtcactactgctc 5100
Db 5363 gtcaacaaagcaaaacacctcagttcacgttgagtggaagcctgtcactactgctc 5422
QY 5101 tctaatttgcctggatagtgcaaatcagtggtccctgcgaactggtcaatc 5160
Db 5423 tctaatttgcctggatagtgcaaatcagtggtccctgcgaactggtcaatc 5482
QY 5161 ttcaatctcctcagcagaagttccatggtgtccctcacaactgcctgtgtagccct 5220
Db 5483 ttcaatctcctcagcagaagttccatggtgtccctcacaactgcctgtgtagccct 5542
QY 5221 ctacttctgtatgtagtggtgcaatcaacacttcaatgtaaccagactccttgtgtc 5280
Db 5543 ctacttctgtatgtagtggtgcaatcaacacttcaatgtaaccagactccttgtgtc 5602
QY 5281 aagatcccaagcagaactcagtggtgtcacaagcggtgaaccccttcattgacat 5340
Db 5603 aagatcccaagcagaactcagtggtgtcacaagcggtgaaccccttcattgacat 5662
QY 5341 ggcagcgtgagcaactcgtgtgtgagcgtgtcaacgaacataagctgaaataatcaat 5400
Db 5663 ggcagcgtgagcaactcgtgtgtgagcgtgtgtcaacgaacataagctgaaataatcaat 5722
QY 5401 gatatcctggaatcgtgtgttccttgatctccacatttgccttggaagaggtc 5460
Db 5723 gatatcctggaatcgtgtgttccttgatctccacatttgccttggaagaggtc 5782
QY 5461 gacatgtgaaacaaacgaagcagatgagtcgagtccttggaaggttttggaagatcgtc 5520
Db 5783 gacatgtgaaacaaacgaagcagatgagtcgagtccttggaaggttttggaagatcgtc 5642
QY 5521 ggtcaccaatctcttgagacttggtggaacgaacactcttcgcacatgagcgtggaagg 5580
Db 5843 ggtcaccaatctcttgagacttggtggaacgaacactcttcgcacatgagcgtggaagg 5902
QY 5581 gtggtgttcttcctcattactgttttgatccagtagacagatttccatccagggcccaact 5640
Db 5903 gtggtgttcttcctcattactgttttgatccagtagacagatttccatccagggcccaact 5962
QY 5641 gtaatgcaagcattatccctcgaatgaaatgaaatgaaatgtgagcggaagaaacag 5700
Db 5963 gtaatgcaagcattatccctcgaatgaaatgaaatgaaatgtgagcggaagaaacag 6022
QY 5701 agaatcttctatgttgagagcagaatgacatcttggaatcaaggaatgtagcagaata 5760
Db 6023 agaatcttctatgttgagagcagaatgacatcttggaatcaaggaatgtagcagaata 6082
QY 5761 tatagaaggaagcgaagcctgtgttgacaggaattggtgaggaattcctcctgtgag 5820
Db 6083 tatagaaggaagcgaagcctgtgttgacaggaattggtgaggaattcctcctgtgag 6142
QY 5821 tgccttgagcctcctggaagttaatgaggtggaatcaacttcaagaatgtaataa 5880
Db 6143 tgccttgagcctcctggaagttaatgaggtggaatcaacttcaagaatgtaataa 6202
QY 5881 ggaagataccactgttaccagagagatgcttcccttaacaaataatgatactataaac 5940
Db 6203 ggaagataccactgttaccagagagatgcttcccttaacaaataatgatactataaac 6262

QY	421	aacttgaagctcaagattctctgtgtggaacatgaacacctctctggttccatatac	480
Db	495	aacttgaagctcaagattctctgtgtggaacatgaacacctctctggttccatatac	554
QY	481	aacctctctcccaagcttactgtggaacatgctgaagctgtatgtatctccac	540
Db	555	aacctctctcccaagcttactgtggaacatgctgaagctgtatgtatctccac	614
QY	541	aaggtatlttttgcaaggtacacagttacatttgacagctctgtacatgatacaatca	600
Db	615	aaggtatlttttgcaaggtacacagttacatttgacagctctgtacatgatacaatca	674
QY	601	gaagaaatattcaacttgtgtgacccaagaagttctgaagcttctgtgacctaccacaagag	660
Db	675	gaagaaatattcaacttgtgtgacccaagaagttctgaagcttctgtgacctaccacaagag	734
QY	661	aaactgtgcagcaagagagtaactcttccaaatagatcccttgaaagccaactcgt	720
Db	735	aaactgtgcagcaagagagtaactcttccaaatagatcccttgaaagccaactcgt	794
QY	721	agaacactaaactctacatccctcccgagcaagagagctgtgtgaagccaacaaca	780
Db	795	agaacactaaactctacatccctcccgagcaagagagctgtgtgaagccaacaaca	854
QY	781	ttgctcacaagctgtgtggaactctgtgccaagagagctgtgacatgaaagctgagag	840
Db	855	ttgctcacaagctgtgtggaactctgtgccaagagagctgtgacatgaaagctgagag	914
QY	841	atgcagcaagagagtgatgttcttgaccaatgtgaaacagctccagctccccaacatc	900
Db	915	atgcagcaagagagtgatgttcttgaccaatgtgaaacagctccagctccccaacatc	974
QY	901	taccagagctgtgtctcgtatgttctgccaagctcccgagagagagagctgtgaatcaag	960
Db	975	taccagagctgtgtctcgtatgttctgccaagctcccgagagagagagctgtgaatcaag	1034
QY	961	tctctcaactgttatgagagcaacaactacaagaagccctctctgtgagagcaatgagcctag	1020
Db	1035	tctctcaactgttatgagagcaacaactacaagaagccctctctgtgagagcaatgagcctag	1094
QY	1021	gaagatgtcgaacacctctctatgacaacctacactcccttactgtcaatgatttgaag	1080
Db	1095	gaagatgtcgaacacctctctatgacaacctacactcccttactgtcaatgatttgaag	1154
QY	1081	aatttgagagctagctccctcttccgcaattatcttgaaagctctgaagccgctgctgt	1140
Db	1155	aatttgagagctagctccctcttccgcaattatcttgaaagctctgaagccgctgctgt	1214
QY	1141	gggaagatctcgttatatacacttgacaactccagccaagagctgcatgagctgagac	1200
Db	1215	gggaagatctcgttatatacacttgacaactccagccaagagctgcatgagctgagac	1274
QY	1201	aagacctccaggaactgtgcgtgttccatgactcgtgaagcagtgtaggaagcaactcagc	1260
Db	1275	aagacctccaggaactgtgcgtgttccatgactcgtgaagcagtgtaggaagcaactcagc	1334
QY	1261	cccaagatctggaactctatgaggaacagccaagaatgagcctgtgccagatgactgtg	1320
Db	1335	cccaagatctggaactctatgaggaacagccaagaatgagcctgtgccagatgactgtg	1394
QY	1321	gacagcaagggacaatgacacttcttggaagaagcagtgtagcttagatgtgacagcc	1380
Db	1395	gacagcaagggacaatgacacttcttggaagaagcagtgtagcttagatgtgacagcc	1454
QY	1381	caagacatctgtgcgttcttgccaagaacccaagagagtgctccagtcagtaaatgttct	1440
Db	1455	caagacatctgtgcgttcttgccaagaacccaagagagtgctccagtcagtaaatgttct	1514
QY	1441	gtgtgaacacctggaagaaagcttccaagagataccaagcaatccggaacatatctgc	1500
Db	1515	gtgtgaacacctggaagaaagcttccaagagataccaagcaatccggaacatatctgc	1574
QY	1501	ttcatgtgagtggtgcaacctgaacaagctagaaccatagcaacagagctgtgctcatc	1560
Db	1575	ttcatgtgagtggtgcaacctgaacaagctagaaccatagcaacagagctgtgctcatc	1634
QY	1561	aacaaagttcattgagagctgtgtgataagagaagaaagttctgtgctgtatgttcaactgga	1620
Db	1635	aacaaagttcattgagagctgtgtgataagagaagaaagttctgtgctgtatgttcaactgga	1694
QY	1621	attactcaggaacagatgagctgtcccatatgataagatacaagatccgaatgagatc	1680
Db	1695	attactcaggaacagatgagctgtcccatatgataagatacaagatccgaatgagatc	1754
QY	1681	gacaatgtgagagagacaataataacaggaatgagtaactgtggaacccctgttcccgact	1740
Db	1755	gacaatgtgagagagacaataataacaggaatgagtaactgtggaacccctgttcccgact	1814
QY	1741	gacctcttgagagacatgagctgtacgttctgagagagctgtgcttacttgacagatgtgtg	1800
Db	1815	gacctcttgagagacatgagctgtacgttctgagagagctgtgcttacttgacagatgtgtg	1874
QY	1801	gagcaggaacatcatalcagagtgctgacgggacacccgagaagaactgtgtctatagcaa	1860
Db	1875	gagcaggaacatcatalcagagtgctgacgggacacccgagaagaactgtgtctatagcaa	1934
QY	1861	caagatccctatccctgttactacgttgatgacatcttctgcgggtgataagccggtcaatg	1920
Db	1935	caagatccctatccctgttactacgttgatgacatcttctgcgggtgataagccggtcaatg	1994
QY	1921	ccctcttcaatgagcgtgcgtgactgattactcagtgagctgtgatacaagagcagctgtg	1980
Db	1995	ccctcttcaatgagcgtgcgtgactgattactcagtgagctgtgatacaagagcagctgtg	2054
QY	1981	tatgagaagagagcagcgtgtgaagagacatgacgagatcatalgagcctgtgacaacaagcata	2040
Db	2055	tatgagaagagagcagcgtgtgaagagacatgacgagatcatalgagcctgtgacaacaagcata	2114
QY	2041	ctctggtttagcgtgtgtcattagtagctatctcctctcttctgtgagcgtgtgcctgcta	2100
Db	2115	ctctggtttagcgtgtgtcattagtagctatctcctctcttctgtgagcgtgtgcctgcta	2174
QY	2101	gtgtgatactctgagatgaagaaacctgtgcccataagtgatcccgagctgtgtgtgtc	2160
Db	2175	gtgtgatactctgagatgaagaaacctgtgcccataagtgatcccgagctgtgtgtgtc	2234
QY	2161	ttctgtccgtgtgttctgtgtgtgtgacatccctgtgcaatgtctctgtattgacacatcttc	2220
Db	2235	ttctgtccgtgtgttctgtgtgtgtgacatccctgtgcaatgtctctgtattgacacatcttc	2294
QY	2221	tccagagccaactgtgcaagcagcctgtgtgagagcatcatctaatctcagctgtgacagcc	2280
Db	2295	tccagagccaactgtgcaagcagcctgtgtgagagcatcatctaatctcagctgtgacagcc	2354
QY	2281	taagctcgtgtgtgtgcaatgagcaagctacgtgtgagcttccacactcaagaactctcgtagc	2340
Db	2355	taagctcgtgtgtgtgcaatgagcaagctacgtgtgagcttccacactcaagaactctcgtagc	2414
QY	2341	ctgctgtccctgtgcttctgtgtgtgtgtgctgtgaaatcttgccttttgaagaagag	2400
Db	2415	ctgctgtccctgtgcttctgtgtgtgtgtgctgtgaaatcttgccttttgaagaagag	2474
QY	2401	ggcattggagtgagtgaggaacaacctgttttgagagctcctgtgaggaagaatgagctcat	2460
Db	2475	ggcattggagtgagtgaggaacaacctgttttgagagctcctgtgtgaggaagaatgagctcat	2534
QY	2461	ctcaccaacttgatccatctgatactgctgttgaacacttccctataggggtgataagccgg	2520
Db	2535	ctcaccaacttgatccatctgatactgctgttgaacacttccctataggggtgataagccgg	2594
QY	2521	tacattgagctgtcttccaagcagtaaggaatcccaagccctgtgtatttctctgc	2580
Db	2595	tacattgagctgtcttccaagcagtaaggaatcccaagccctgtgtatttctctgc	2654
QY	2581	accaagttctactgtgttgagagaaagtgtatgagaaagcaccctgtgtccaacag	2640

Db	2655	accagatcctactggtgttggcgagggaaaagtgaatgagaagaagccacccttggttccaacag	2714
Qy	2641	aagagaatctcagaatctcgtcatctggagaggaagaaacccaccacttgaagctggcggtcc	2700
Db	2715	aagagaatctcagaatctcgtcatctggagaggaagaaacccaccacttgaagctggcggtcc	2774
Qy	2701	attcagaaccttggtaaagtctcacccgaaatgggataaggctgctcttgatggccctggca	2760
Db	2775	attcagaaccttggtaaagtctcacccgaaatgggataaggctgctcttgatggccctggca	2834
Qy	2761	ctgaattttatgagggccagaaatccctctctctctctggccacaatggagcgggagagcg	2820
Db	2835	ctgaattttatgagggccagaaatccctctctctctctggccacaatggagcgggagagcg	2894
Qy	2821	accaccaatgcaaatctctgacccgggtgttctcccccagacctccggagaccgcctataacctg	2880
Db	2895	accaccaatgcaaatctctgacccgggtgttctcccccagacctccggagaccgcctataacctg	2954
Qy	2881	ggaanaaacaatctgcgctctgagatggagacaatcccgagaaacctgggggtctgtcccaag	2940
Db	2955	ggaanaaacaatctgcgctctgagatggagacaatcccgagaaacctgggggtctgtcccaag	3014
Qy	2941	cataaagctgctgtttgacaatgctgacctgtcgaaagaacacatctggttctatgtcccgcttg	3000
Db	3015	cataaagctgctgtttgacaatgctgacctgtcgaaagaacacacatggttctatgtcccgcttg	3074
Qy	3001	aaagagctctctctgagaagcagcgtgaaagggcgagatgagacagatggccctggatgtgttg	3060
Db	3075	aaagagctctctctgagaagcagcgtgaaagggcgagatgagacagatggccctggatgtgttg	3134
Qy	3061	ttgcatacaagcaagctgtgaaaagcaaaacaacagcagctgtcaaggttgatgtacgagagaag	3120
Db	3135	ttgcatacaagcaagctgtgaaaagcaaaacaacagcagctgtcaaggttgatgtacgagagaag	3194
Qy	3121	ctatctgtggcccttgagccttgtgcggggagatctaaggtgttgcattctcggatgtgaaccaca	3180
Db	3195	ctatctgtggcccttgagccttgtgcggggagatctaaggtgttgcattctcggatgtgaaccaca	3254
Qy	3181	gctgtgtgtggaaccccttaacctcccgcaaggaggaataatggagctgctctgaaataccgacaa	3240
Db	3255	gctgtgtgtggaaccccttaacctcccgcaaggaggaataatggagctgctctgaaataccgacaa	3314
Qy	3241	ggccgacaccattatctctctctaaacacacatggagatggagacggaatcctctgggagacag	3300
Db	3315	ggccgacaccattatctctctctaaacacacatggagatggagacggaatcctctgggagacag	3374
Qy	3301	attgacacatctctccaatgggaagcgtgtgctgtgtgggctctctccctgttctcgaagaac	3360
Db	3375	attgacacatctctccaatgggaagcgtgtgctgtgtgggctctctccctgttctcgaagaac	3434
Qy	3361	cagctcgggaaacagcctactaacctcgacctgtgtctaaagaaagatgtggaatctctccctagt	3420
Db	3435	cagctcgggaaacagcctactaacctcgacctgtgtctaaagaaagatgtggaatctctccctagt	3494
Qy	3421	tccctgcagaacacatgataagacatgtcatcacttaaaaaagagagacagtgcttctcag	3480
Db	3495	tccctgcagaacacatgataagacatgtcatcacttaaaaaagagagacagtgcttctcag	3554
Qy	3481	agcagatctctgatgtcgtgccttggtggcagcgacatgagagtgcacagcgtcacatcgatgctc	3540
Db	3555	agcagatctctgatgtcgtgccttggtggcagcgacatgagagtgcacagcgtcacatcgatgctc	3614
Qy	3541	tctgtcatctccaactctcatatagaagaacatgttctcgaagcccggtctgtgtgaagaata	3600
Db	3615	tctgtcatctccaactctcatatagaagaacatgttctcgaagcccggtctgtgtgaagaata	3674
Qy	3601	gggcataagctgaacctatgctgtctgcacataagagctgtctaagagaggaagcctttgtgaa	3660
Db	3675	gggcataagctgaacctatgctgtctgcacataagagctgtctaagagaggaagcctttgtgaa	3734
Qy	3661	ctcttctcatagatgtgatgagaccggtctcagacctgggacatttctagtatgacatctca	3720
Db	3735	ctcttctcatagatgtgatgagaccggtctcagacctgggacatttctagtatgacatctca	3794

QY	3721	gagcgcgcgccttgaaagaaatctctccaaagctgagccgaagaagatggggttgatgtctgag	3780
Db	3795	gagacgcgcctctgaaagaataatctctcaaggttgagccgaagaagatggggttgatgtctgag	3854
QY	3781	accctcagaatgtaacctctgcccacagacgaagaacagcgcgagctctggggagacaagcagagc	3840
Db	3855	accctcagaatgtaacctctgcccacagacgaagaacagcgcgagctctggggagacaagcagagc	3914
QY	3841	tgcttcgcgccttgcaatcgaaagatgctgctgatccaaatgatctcttgacataagccca	3900
Db	3915	tgcttcgcgccttgcaatcgaaagatgctgctgatccaaatgatctcttgacataagccca	3974
QY	3901	gaatccagagagacacagactctgctccagctggagatgagatggacaagatgctccacagcggaaa	3960
Db	3975	gaatccagagagagacagactctgctccagctggagatgagatggacaagatgctccacagcggaaa	4034
QY	3961	ggctcggaaacttaacacagacaacagatctgtgagccctctgtggaagagactgctaattgcc	4020
Db	4035	ggctcggaaacttaacacagacaacagatctgtgagccctctgtggaagagactgctaattgcc	4094
QY	4021	agagcggagctcggaaagagatcttctgtccagatctgtcttcggacagctgtgtctgcatt	4080
Db	4095	agagcggagctcggaaagagatcttctgtccagatctgtcttcggacagctgtgtctgcatt	4154
QY	4081	ggccctgtgctcaacgcctgatacgcgcacacccctcttgacaagatcccccagcctggaaattcag	4140
Db	4155	ggccctgtgctcaacgcctgatacgcgcacacccctcttgacaagatcccccagcctggaaattcag	4214
QY	4141	cccttgatgtatcaacgaacgaacgatacattgtgcagcaatgtatgtcctctggagagacgggga	4200
Db	4215	cccttgatgtatcaacgaacgaacgatacattgtgcagcaatgtatgtcctctggagagacgggga	4274
QY	4201	accctcggaacacttaaacgcgcctccacacaagacccctgcttcctggagaccgcgtgtatgaa	4260
Db	4275	accctcggaacacttaaacgcgcctccacacaagacccctgcttcctggagaccgcgtgtatgaa	4334
QY	4261	ggaaaaacccaatcccaagacagccctctgcagcgacagggggagagatggaaacacatgcgccca	4320
Db	4335	ggaaaaacccaatcccaagacagccctctgcagcgacagggggagagatggaaacacatgcgccca	4394
QY	4321	gttcccccagacacatcaatggagacctcttcacaaatctggaacatggacatgcagaaccccttca	4380
Db	4395	gttcccccagacacatcaatggagacctcttcacaaatgggaacatggacatgcagaaccccttca	4454
QY	4381	ccctgatacgcagctgtagcagcgacgaacaaatcaagaagaatgctccctgtgtgtccccaggg	4440
Db	4455	ccctgatacgcagctgtagcagcgacgaacaaatcaagaagaatgctccctgtgtgtccccaggg	4514
QY	4441	gcacggggggctgcccctcccaagaagaacaaacacatgcacgatataccttccagagactg	4500
Db	4515	gcacggggggctgcccctcccaagaagaacaaacacatgcacgatataccttccagagactg	4574
QY	4501	acaggaagaagaacatcttgatctatctctgtgaagaacgtatgtgcagatcatagcccaaac	4560
Db	4575	acaggaagaagaacatcttgatctatctctgtgaagaacgtatgtgcagatcatagcccaaac	4634
QY	4561	ttaaagaacaagaatctgggtgtaatgtgaatgttaagtatgagcgctcttccctgggtgtcagt	4620
Db	4635	ttaaagaacaagaatctgggtgtaatgtgaatgttaagtatgagcgctcttccctgggtgtcagt	4694
QY	4621	aaatattcaagacacttccctccagctcgaagaagtttaatgtatgcatacaaaatgtagaaga	4680
Db	4695	aaatattcaagacacttccctccagctcgaagaagtttaatgtatgcatacaaaatgtagaaga	4754
QY	4681	caacttaaacctggccaagagacagttctgcagatcogattcttcaacagctctggagaagattt	4740
Db	4755	caacttaaacctggccaagagacagttctgcagatcogattcttcaacagctctggagaagattt	4814
QY	4741	atgacacgagcttgacaacagaataatgttcaagtttggtgttcaataacaaggtccggat	4800
Db	4815	atgacacgagcttgacaacagaataatgttcaagtttggtgttcaataacaaggtccggat	4874

```
QY 4801 gcaatcagctcttcctgaatgctcatcaaatgcatcttcctccggccaaactgcagaag 4860
    |||
Db 4875 gcaatcagctcttcctgaatgctcatcaaatgcatcttcctccggccaaactgcagaag 4934
QY 4861 ggaagagaaccttagcattatgaatctactgcttcaatcattcccttgatccatcaag 4920
    |||
Db 4935 ggaagagaaccttagcattatgaatctactgcttcaatcattcccttgatccatcaag 4994
QY 4921 cagcaactctcagaagtgctctgtatgacacatcagtgatgctctgtgtccatctgt 4980
    |||
Db 4995 cagcaactctcagaagtgctctgtatgacacatcagtgatgctctgtgtccatctgt 5054
QY 4981 gtaactcttgcaatgctctgtccagcagcagcttgctgtatcttccttgatccagagcg 5040
    |||
Db 5055 gtaactcttgcaatgctctgtccagcagcagcttgctgtatcttccttgatccagagcg 5114
QY 5041 gtaagcaagcaaaaacactgcatctcagtgaggtgaagcctgtcatctactgctc 5100
    |||
Db 5115 gtaagcaagcaaaaacactgcatctcagtgaggtgaagcctgtcatctactgctc 5174
QY 5101 tctaatctgtctgagatattgcaattacgttgcctccgcaacactgctatctatc 5160
    |||
Db 5175 tctaatctgtctgagatattgcaattacgttgcctccgcaacactgctatctatc 5234
QY 5161 ttcactctctccagcaagaagctcctatgtgtctccacacatctgcctgtgtaagcct 5220
    |||
Db 5235 ttcactctctccagcaagaagctcctatgtgtctccacacatctgcctgtgtaagcct 5294
QY 5221 ctactctgtctatgaggtgctcaacactccatcagtaacacgctccttctgtctc 5280
    |||
Db 5295 ctactctgtctatgaggtgctcaacactccatcagtaacacgctccttctgtctc 5354
QY 5281 aagatcccaagcacagcactatgtgtgtcctcagcagctgaaacctctcatctgacatt 5340
    |||
Db 5355 aagatcccaagcacagcactatgtgtgtcctcagcagctgaaacctctcatctgacatt 5414
QY 5341 ggcacagcgggccacacttctgtctgagagctgttcacgcagcaataagctgaataatac 5400
    |||
Db 5415 ggcacagcgggccacacttctgtctgagagctgttcacgcagcaataagctgaataatac 5474
QY 5401 gatatacctgaagctcgtgtctgtctgtctccacatttctgccttgagcgagggctcacc 5460
    |||
Db 5475 gatatacctgaagctcgtgtctgtctgtctccacatttctgccttgagcgagggctcacc 5534
QY 5461 gacatggtggaataaacagagcgaatgtgtgtgtcccttgaaaggttgaggagaatcgctt 5520
    |||
Db 5535 gacatggtggaataaacagagcgaatgtgtgtgtcccttgaaaggttgaggagaatcgctt 5594
QY 5521 ggttcacacattactctgagacttggtgagcaaacctctcgcacagcgctgtgaaagg 5580
    |||
Db 5595 ggttcacacattactctgagacttggtgagcaaacctctcgcacagcgctgtgaaagg 5654
QY 5581 gtgtgtgtctctccatctactgtctgtctgtccagatcagatctctcatcagggccagacct 5640
    |||
Db 5655 gtgtgtgtctctccatctactgtctgtctgtccagatcagatctctcatcagggccagacct 5714
QY 5641 gtaaatgcaaaagctatcctcctgaatgataaataaataatgtaagcgagcggaagacag 5700
    |||
Db 5715 gtaaatgcaaaagctatcctcctgaatgataaataaataatgtaagcgagcggaagacag 5774
QY 5701 agaatctctgtagtgagagcgcaaatgacatctctagaatcaagaggttgacgaataata 5760
    |||
Db 5775 agaatctctgtagtgagagcgcaaatgacatctctagaatcaagaggttgacgaataata 5834
QY 5761 tatagaaggaagcggaagcctgctgtgtgacagagattgctgtggcatctcctcctgtgag 5820
    |||
Db 5835 tatagaaggaagcggaagcctgctgtgtgacagagattgctgtggcatctcctcctgtgag 5894
QY 5821 tgccttgagcctcctgagagtttaatgtgagcgtaaaatcatcaacttccaagatgtaaca 5880
    |||
Db 5895 tgccttgagcctcctgagagtttaatgtgagcgtaaaatcatcaacttccaagatgtaaca 5954
QY 5881 ggaagataccactgttaccagagagagatgcttcccttaacaaaaataglatctatacaac 5940
    |||

Db 5955 ggaagataccactgttaccagagagagatgcttcccttaacaaaaataglatctatacaac 6014
QY 5941 atccatgaagtaactatcaagaatgagtgctactgctccctcaagtttgatccatcaagagctg 6000
    |||
Db 6015 atccatgaagtaactatcaagaatgagtgctactgctccctcaagtttgatccatcaagagctg 6074
QY 6001 ttgactggagaagaacaagtgagatctcttgcccttttgagaagaggtcccaagaagaagaa 6060
    |||
Db 6075 ttgactggagaagaacaagtgagatctcttgcccttttgagaagaggtcccaagaagaagaa 6134
QY 6061 gttggcaaggttggttgagtgagcggaatccggaactggcgctcgtgaagatgagagaataa 6120
    |||
Db 6135 gttggcaaggttggttgagtgagcggaatccggaactggcgctcgtgaagatgagagaataa 6194
QY 6121 tatgtgtgaactatagtgagggcaacaacagcaagctctctcaagcagatgcttgatc 6180
    |||
Db 6195 tatgtgtgaactatagtgagggcaacaacagcaagctctctcaagcagatgcttgatc 6254
QY 6181 ggcgggctcctgtgtgttcttgatgaaacccacacagcagcatgatacccaagcccg 6240
    |||
Db 6255 ggcgggctcctgtgtgttcttgatgaaacccacacagcagcatgatacccaagcccg 6314
QY 6241 cggctcttgaggaattgtgtgtcccttaaggtgtgaagagggagatcagtagtcttaca 6300
    |||
Db 6315 cggctcttgaggaattgtgtgtcccttaaggtgtgaagagggagatcagtagtcttaca 6374
QY 6301 tctcaatgatatgagaagaatgtgaagctctcttgacatagatgagtgacatcagtgatga 6360
    |||
Db 6375 tctcaatgatatgagaagaatgtgaagctctcttgacatagatgagtgacatcagtgatga 6434
QY 6361 aggttcaggtgctcttgagcaatgtccagcatctataaaataaggttggagatggttataca 6420
    |||
Db 6435 aggttcaggtgctcttgagcaatgtccagcatctataaaataaggttggagatggttataca 6494
QY 6421 atagttgtaagaatagcaaggtccaaacccgacctgaagcctgtccagatctcttga 6480
    |||
Db 6495 atagttgtaagaatagcaaggtccaaacccgacctgaagcctgtccagatctcttga 6554
QY 6481 ctgcatcttcccttggaagtgtctcttaaaagagaacacccggaacatgctatacaacagctt 6540
    |||
Db 6555 ctgcatcttcccttggaagtgtctcttaaaagagaacacccggaacatgctatacaacagctt 6614
QY 6541 ccatctctcatctctctcctgagcagagatcatcagatctctcccaaggcaaaaagcga 6600
    |||
Db 6615 ccatctctcatctctctcctgagcagagatcatcagatctctcccaaggcaaaaagcga 6674
QY 6601 ctccacatagaagaactactctgttcttcagacaacaacttgaccaagtatttgaaactt 6660
    |||
Db 6675 ctccacatagaagaactactctgttcttcagacaacaacttgaccaagtatttgaaactt 6734
QY 6661 gccaaaggaacaaagtatgatgacacacttaaaagcctctctctcaacaaaacagaca 6720
    |||
Db 6735 gccaaaggaacaaagtatgatgacacacttaaaagcctctctctcaacaaaacagaca 6794
QY 6721 gtagtgagcgttgagttctcatcatcttctctacaggaatgaagaagtgat 6780
    |||
Db 6795 gtagtgagcgttgagttctcatcatcttctctacaggaatgaagaagtgat 6854
QY 6781 gtagtgagaatctctgttaccag 6804
    |||
Db 6855 gtagtgagaatctctgttaccag 6878
    |||

RESULT 8
AAF83826
ID AAF83826 standard; DNA; 7860 BP.
XX
AC AAF83826;
XX
AT 06-AUG-2001 (first entry)
XX
DE Human ABC1 nucleotide sequence.
```


QY 1321 gacagcaggagacaatgacacatttgggaacagcaattgagtgcttaattggagacc 1380
|||||
Db 1395 gacagcaggagacaatgacacatttgggaacagcaattgagtgcttaattggagacc 1454
QY 1381 caagacatctgtgcttcttggccaagcaccagagagatgctcagtcagtaattgtct 1440
|||||
Db 1455 caagacatctgtgcttcttggccaagcaccagagagatgctcagtcagtaattgtct 1514
QY 1441 ggtgtaacctgagagaagaacttccaacagactaaccaagcaatcccgacaatccgc 1500
|||||
Db 1515 ggtgtaacctgagagaagaacttccaacagactaaccaagcaatcccgacaatccgc 1574
QY 1501 ttcatgagtggtgtcaacctgacaagctagaaacctatgacaacaagatctggtctatc 1560
|||||
Db 1575 ttcatgagtggtgtcaacctgacaagctagaaacctatgacaacaagatctggtctatc 1634
QY 1561 aacaagtcagtgagtgctgtgtgagagaaagttcctggtgtgtatgtgtctgga 1620
|||||
Db 1635 aacaagtcagtgagtgctgtgtgagagaaagttcctggtgtgtatgtgtctgga 1694
QY 1621 attactccagcagcaatgagctgccccatcaatgcaagtaacagatccgaatgacat 1680
|||||
Db 1695 attactccagcagcaatgagctgccccatcaatgcaagtaacagatccgaatgacat 1754
QY 1681 gacaaatgtgagagagacaataaatacaagagatggtaactgggacctgtgtcctgagct 1740
|||||
Db 1755 gacaaatgtgagagagacaataaatacaagagatggtaactgggacctgtgtcctgagct 1814
QY 1741 gaccccttgagagacaatgagctgccccatcaatgcaagtaacagatccgaatgacat 1800
|||||
Db 1815 gaccccttgagagacaatgagctgccccatcaatgcaagtaacagatccgaatgacat 1874
QY 1801 gacagcaggacaatcaacagagtgctgacagcaggaagaagaactggtctatattgca 1860
|||||
Db 1875 gacagcaggacaatcaacagagtgctgacagcaggaagaagaactggtctatattgca 1934
QY 1861 cagatgacctatccctgttgaacttgaatgacatcttctcgcggtgtgataagccgttcaatg 1920
|||||
Db 1935 cagatgacctatccctgttgaacttgaatgacatcttctcgcggtgtgataagccgttcaatg 1994
QY 1921 cccctcttcaatgacgtgctgacgtgatacttcaactgagtggtgataatcaagggacgtcg 1980
|||||
Db 1995 cccctcttcaatgacgtgctgacgtgatacttcaactgagtggtgataatcaagggacgtcg 2054
QY 1981 tatgagagagagcagcagctgaaagaagacaatgagatcatatgagccctggagacaagcata 2040
|||||
Db 2055 tatgagagagagcagcagctgaaagaagacaatgagatcatatgagccctggagacaagcata 2114
QY 2041 ctctggttgaactggtatcatatgagacttcaacttctctctgtgagagcgtgagctgcta 2100
|||||
Db 2115 ctctggttgaactggtatcatatgagacttcaacttctctctgtgagagcgtgagctgcta 2174
QY 2101 gttgtatccttgaagttaggaacaacctgtgacctacagtgatccagcgtgtgtctg 2160
|||||
Db 2175 gttgtatccttgaagttaggaacaacctgtgacctacagtgatccagcgtgtgtctg 2234
QY 2161 ttccctgctcgt 2220
|||||
Db 2235 ttccctgctcgt 2294
QY 2221 tccagagcaaaccttgagcagcagctgtgggggacatcatcttaactcaacgctgtacatccg 2280
|||||
Db 2295 tccagagcaaaccttgagcagcagctgtgggggacatcatcttaactcaacgctgtacatccg 2354
QY 2281 taactctgt 2340
|||||
Db 2355 taactctgt 2414
QY 2341 ctgctgtctcctgtgctgt 2400
|||||
Db 2415 ctgctgtctcctgtgctgt 2474
QY 2401 ggcattgagtgagtgagagacaactgtttgagagtgctgtgagagagatgagcttcaat 2460
|||||
Db 2475 ggcattgagtgagtgagagacaactgtttgagagtgctgtgagagagatgagcttcaat 2534
QY 2461 ctccacactctgactccatgatagtctgttgacaaccttctctatgttggtgagctgtg 2520
|||||
Db 2535 ctccacactctgactccatgatagtctgttgacaaccttctctatgttggtgagctgtg 2594
QY 2521 taactgagtgctgtcttccagcagtaagaaattccagagccctgtglatcttctctg 2580
|||||
Db 2595 taactgagtgctgtcttccagcagtaagaaattccagagccctgtglatcttctctg 2654
QY 2581 accaagctcactgt 2640
|||||
Db 2655 accaagctcactgt 2714
QY 2641 aagagatgttcaagaatctgcatgtgagagagaaaccccaacttgaagctgagctgtcc 2700
|||||
Db 2715 aagagatgttcaagaatctgcatgtgagagagaaaccccaacttgaagctgagctgtcc 2774
QY 2701 attagaacctgt 2760
|||||
Db 2775 attagaacctgt 2834
QY 2761 ctgaaatttlatgagggccagatcaactctctctgagccacaatgagggagagagag 2820
|||||
Db 2835 ctgaaatttlatgagggccagatcaactctctctgagccacaatgagggagagagag 2894
QY 2821 acccaatgttcaatctcgtacccgggtgtgttcccccgaactctgggacacgctacatctg 2880
|||||
Db 2895 acccaatgttcaatctcgtacccgggtgtgttcccccgaactctgggacacgctacatctg 2954
QY 2881 ggaanaagacatctcgtctgtgagagacacatccggcagaagaacttgggggtctgtccag 2940
|||||
Db 2955 ggaanaagacatctcgtctgtgagagacacatccggcagaagaacttgggggtctgtccag 3014
QY 2941 cataagtgctgtgttgacatgtgactgtcgaagaaacacatctgtgtctatgtccgctg 3000
|||||
Db 3015 cataagtgctgtgttgacatgtgactgtcgaagaaacacatctgtgtctatgtccgctg 3074
QY 3001 aaggggctctctgagagagcagctgagagagagatgagcagatgagccttgatgtgtgt 3060
|||||
Db 3075 aaggggctctctgagagagcagctgagagagagatgagcagatgagccttgatgtgtgt 3134
QY 3061 ttgcatcaagcagcagctgaaagaagcaaaacagcagctgtlcaagtgagaaatgagagaag 3120
|||||
Db 3135 ttgcatcaagcagcagctgaaagaagcaaaacagcagctgtlcaagtgagaaatgagagaag 3194
QY 3121 ctatctgtggt 3180
|||||
Db 3195 ctatctgtggt 3254
QY 3181 gctggtgtgagaccttcaatcccgaggggataatgagagctgctgtgaatatccgaca 3240
|||||
Db 3255 gctggtgtgagaccttcaatcccgaggggataatgagagctgctgtgaatatccgaca 3314
QY 3241 ggcgcgacaattatctctctacacaacacatgataagcagagctcctggggagag 3300
|||||
Db 3315 ggcgcgacaattatctctctacacaacacatgataagcagagctcctggggagag 3374
QY 3301 attgacatattcccatgtggaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3360
|||||
Db 3375 attgacatattcccatgtggaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3434
QY 3361 cagcttgagagagcgttactaacttgacactgtgtcaagaagaatgttgatccctccatg 3420
|||||
Db 3435 cagcttgagagagcgttactaacttgacactgtgtcaagaagaatgttgatccctccatg 3494
QY 3421 tccctgagagaagaatgagatgt 3480
|||||
Db 3495 tccctgagagaagaatgagatgt 3554
QY 3481 agcaattctgagtgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3540
|||||

Dh 3555 agcaattctgatctgagccttgagcagaccatgagagtgacagctgacacatgatgtc 3614
Qy 3541 tctgcatctccaacctcaatcaatgagacatgtgtctgaagcccgctggttgaaacata 3600
Dh 3615 tctgcatctccaacctcaatcaatgagacatgtgtctgaagcccgctggttgaaacata 3674
Qy 3601 gggcatgagctgacatgtgtctgacatatagaagctgtctaaaggagagacccctgtggaa 3660
Dh 3675 gggcatgagctgacatgtgtctgacatatagaagctgtctaaaggagagacccctgtggaa 3734
Qy 3661 ctcttcatgagatgtgataccggtctccagaacctgggacatttctaagtataggatctcca 3720
Dh 3735 ctcttcatgagatgtgataccggtctccagaacctgggacatttctaagtataggatctcca 3784
Qy 3721 gaagacacccctggaagaataattctccaaggtgcccgaagagagtggtgtgagtctgag 3780
Dh 3795 gagaagacccctggaagaataattctccaaggtgcccgaagagagtggtgtgagtctgag 3854
Qy 3781 acctcagatgtgatacttgcacagaacagacagcggtgaccttcgggggacaaagcagagc 3840
Dh 3855 acctcagatgtgatacttgcacagaacagacagcggtgaccttcgggggacaaagcagagc 3914
Qy 3841 tgtcttcgcccgttcaatgaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3900
Dh 3915 tgtcttcgcccgttcaatgaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3974
Qy 3901 gaatccagagagacagactgtgtcagtggtgagatgagtgagcaaaaggttctacacagtgaa 3960
Dh 3975 gaatccagagagacagactgtgtcagtggtgagatgagtgagcaaaaggttctacacagtgaa 4034
Qy 3961 ggtctggaacttcaacagcaacagttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4020
Dh 4035 ggtctggaacttcaacagcaacagttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4094
Qy 4021 agacgagatgtggaagagattttgtgtcagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4080
Dh 4095 agacgagatgtggaagagattttgtgtcagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4154
Qy 4081 ggccttgtgtcagctgtacgt 4140
Dh 4155 ggccttgtgtcagctgtacgt 4214
Qy 4141 ccctgagatgtacaacagcaacagttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4200
Dh 4215 ccctgagatgtacaacagcaacagttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4274
Qy 4201 acctgtgaaactttaaagccctccacaaagacccctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4260
Dh 4275 acctgtgaaactttaaagccctccacaaagacccctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4334
Qy 4261 ggaacccaatcccaagacagccctgacagcgagggagaggaagatgtgacacatgtgccca 4320
Dh 4335 ggaacccaatcccaagacagccctgacagcgagggagaggaagatgtgacacatgtgccca 4394
Qy 4321 gttcccccagacatcatgtgacatcttccagaatgtgaaactgtgaaactgtgaaactgtgaa 4380
Dh 4395 gttcccccagacatcatgtgacatcttccagaatgtgaaactgtgaaactgtgaaactgtgaa 4454
Qy 4381 cctgagatgcagtgtaagcagcgacaaaatcaagaagaatgtgtgtgtgtgtgtgtgtgtgtgt 4440
Dh 4455 cctgagatgcagtgtaagcagcgacaaaatcaagaagaatgtgtgtgtgtgtgtgtgtgtgtgt 4514
Qy 4441 gcaaggggggt 4500
Dh 4515 gcaaggggggt 4574
Qy 4501 acaggaagaacacattctgattatctgtgtgagaagatgtgtgacatcatagccaaagc 4560
Dh 4575 acaggaagaacacattctgattatctgtgtgagaagatgtgtgacatcatagccaaagc 4634
Qy 4561 ttaagaagaacacattctgattatctgtgtgagaagatgtgtgacatcatagccaaagc 4620
Dh 4635 ttaagaagaacacattctgattatctgtgtgagaagatgtgtgacatcatagccaaagc 4694

Qy 4621 aatactcaagacatctccctccagatgaagaagttaatgtatgtccatcaacaataagaagaa 4680
Dh 4695 aatactcaagacatctccctccagatgaagaagttaatgtatgtccatcaacaataagaagaa 4754
Qy 4681 cccctaaagcttgccaagaagacagttcttcaagatcatgtattctccaaacagcttggagaatt 4740
Dh 4755 caccataagcttggccaagaagacagttcttcaagatcatgtattctccaaacagcttggagaatt 4814
Qy 4741 atgacagacatgtgacacagaaataatgtcaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4800
Dh 4815 atgacagacatgtgacacagaaataatgtcaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4874
Qy 4801 gcaatcagctcttctctgataatgtatcaacaatgtccattcccgagccaaactgcaaaag 4860
Dh 4875 gcaatcagctcttctctgataatgtatcaacaatgtccattcccgagccaaactgcaaaag 4934
Qy 4861 ggaagaaacctagacatcatgaattacgtcttcaaatcaatcccttgatctcaacaag 4920
Dh 4935 ggaagaaacctagacatcatgaattacgtcttcaaatcaatcccttgatctcaacaag 4994
Qy 4921 cagcagctctcagagtggtctgtgataccacataagtgatgtctctgtgtgtgtgtgtgtgtgt 4980
Dh 4995 cagcagctctcagagtggtctgtgataccacataagtgatgtctctgtgtgtgtgtgtgtgtgtgt 5054
Qy 4981 gtaactcttgcaatgtctctctgtccagccagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5040
Dh 5055 gtaactcttgcaatgtctctctgtccagccagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5114
Qy 5041 gtcagcaagaacaaacacatctgacatcatcagtgagatgaagcctgtcatctgtctc 5100
Dh 5115 gtcagcaagaacaaacacatctgacatcatcagtgagatgaagcctgtcatctgtctc 5174
Qy 5101 tctaaatttgtctgggataatgtcaattacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5160
Dh 5175 tctaaatttgtctgggataatgtcaattacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5234
Qy 5161 ttcactgtctccagcagaagctctatgtgtctccacaaactgtgtgtgtgtgtgtgtgtgtgtgtgt 5220
Dh 5235 ttcactgtctccagcagaagctctatgtgtctccacaaactgtgtgtgtgtgtgtgtgtgtgtgtgt 5294
Qy 5221 ctacttctgtctatgt 5280
Dh 5295 ctacttctgtctatgt 5354
Qy 5281 aagatcccccagcaagcctatgt 5340
Dh 5355 aagatcccccagcaagcctatgt 5414
Qy 5341 ggcagcgtgtgacacatctgt 5400
Dh 5415 ggcagcgtgtgacacatctgt 5474
Qy 5401 gatattctcgaagtcctgt 5460
Dh 5475 gatattctcgaagtcctgt 5534
Qy 5461 gacatgtgtgaaaaacacagcaatgt 5520
Dh 5535 gacatgtgtgaaaaacacagcaatgt 5594
Qy 5521 ggtgtacacatcatcttgagctgt 5580
Dh 5595 ggtgtacacatcatcttgagctgt 5654
Qy 5581 ggt 5640
Dh 5655 ggt 5714
Qy 5641 gtaaatgtcaaaactatctctctgtgaatgtgaagaatgaagtgtgagcggtgaagaacag 5700
Dh 5715 gtaaatgtcaaaactatctctctgtgaatgtgaagaatgaagtgtgagcggtgaagaacag 5774

```

QY 5701 agaattcttgaatggtgagcccaagatgacatttagaatacaagagttgacgaagata 5760
DB 5775 agaattcttgaatggtgagcccaagatgacatttagaatacaagagttgacgaagata 5834
QY 5761 tatagaaggaagcggaagcctgtctgttgaagaatttcgttggcattccctgtgtgag 5820
DB 5835 tatagaaggaagcggaagcctgtctgttgaagaatttcgttggcattccctgtgtgag 5894
QY 5821 tgccttggcctccgggaattgaatgggctggaataatcatcaatttcaagaatgataca 5880
DB 5895 tgccttggcctccgggaattgaatgggctggaataatcatcaatttcaagaatgataca 5954
QY 5881 ggagataccactgttaccagaagagatgcttcccttaacaaataaglatcattacaac 5940
DB 5955 ggagataccactgttaccagaagagatgcttcccttaacaaataaglatcattacaac 6014
QY 5941 atccatgaatgatacgaacatgaggtgactgcccctgaatttgaatgacacagagctg 6000
DB 6015 atccatgaatgatacgaacatgaggtgactgcccctgaatttgaatgacacagagctg 6074
QY 6001 ttgaactggagagaacacgctggaatcttcttgcctttagagagagtcaccagaagaaga 6060
DB 6075 ttgaactggagagaacacgctggaatcttcttgcctttagagagagtcaccagaagaaga 6134
QY 6061 gttggcaaggttggtagtggtgagcttcggaacttggcctcgtgaagatggagaanaa 6120
DB 6135 gttggcaaggttggtagtggtgagcttcggaacttggcctcgtgaagatggagaanaa 6194
QY 6121 tatgctgtaactatagtgaggaacaaacgaagctctctacacacacatgcttgatc 6180
DB 6195 tatgctgtaactatagtgaggaacaaacgaagctctctacacacacatgcttgatc 6254
QY 6181 ggcgggctcctctgtgttcttctgtagaacacacacagagatgattcccaagccgg 6240
DB 6255 ggcgggctcctctgtgttcttctgtagaacacacacagagatgattcccaagccgg 6314
QY 6241 cggcttcttgggaattgtgcctcctgaagtgttgcagaagggagagatcagtagtcttaca 6300
DB 6315 cggcttcttgggaattgtgcctcctgaagtgttgcagaagggagagatcagtagtcttaca 6374
QY 6301 tctcatagatagtggaagaatgtagaagctcttgcactagatgacatcatctgttcaatga 6360
DB 6375 tctcatagatagtggaagaatgtagaagctcttgcactagatgacatcatctgttcaatga 6434
QY 6361 aggttcaagttgcttggcaggtgttccaagcatctaaataaggttggagatggtatataca 6420
DB 6435 aggttcaagttgcttggcaggtgttccaagcatctaaataaggttggagatggtatataca 6494
QY 6421 atagttgtacgaatagcaaggttccaacccggagcctggaagcctgttccagatcttcttga 6480
DB 6495 atagttgtacgaatagcaaggttccaacccggagcctggaagcctgttccagatcttcttga 6554
QY 6481 ctgtcaattctctggaagtgttctaaagaagaacacgggaacatgtctacaatcacagctt 6540
DB 6555 ctgtcaattctctggaagtgttctaaagaagaacacgggaacatgtctacaatcacagctt 6614
QY 6541 ccaatttcaattctcttctgcccagagatcttcagacatcccttcccaagaagaagaagcga 6600
DB 6615 ccaatttcaattctcttctgcccagagatcttcagacatcccttcccaagaagaagaagcga 6674
QY 6601 ctccacatagaagactactctgttctcagaacaacttgcacaaagtgttgaactt 6660
DB 6675 ctccacatagaagactactctgttctcagaacaacttgcacaaagtgttgaactt 6734
QY 6661 gccaaagaccaaagtgtatgagatgacacacttaaaagacttcaatatacaaaaacagaga 6720
DB 6735 gccaaagaccaaagtgtatgagatgacacacttaaaagacttcaatatacaaaaacagaga 6794
QY 6721 gtaatgacgcttgcagttctcacatctttctacagatgagaagtgaaagaagctat 6780
DB 6795 gtaatgacgcttgcagttctcacatctttctacagatgagaagtgaaagaagctat 6854
QY 6781 gtaatgacgcttgcagttctcacatctttctacagatgagaagtgaaagaagctat 6854

```

```

DB 6855 gtaatgacgcttgcagttctcacatctttctacagatgagaagtgaaagaagctat 6878
RESULT 9
AAD21326
ID AAD21326 standard; DNA: 7260 BP.
XX
XX AAD21326;
DE 28-JAN-2002 (first entry)
XX
XX Human ATP binding cassette transporter 1 (ABCI) gene.
XX
XX Human ATP binding cassette transporter 1; ABC1; coronary heart disease;
XX dermatological; atherosclerosis; cardiovascular; inflammatory disease;
XX immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 321..7106
FT /*tag= a
FT /*product= "Human ABC1 protein"
PN EPI136552-A1.
XX
XX 26-SEP-2001.
XX
XX 20-MAR-2000; 2000EP-0105820.
XX
XX 20-MAR-2000; 2000EP-0105820.
XX
XX (FARB ) BAYER AG.
XX
XX Schmitz G, Bodzioch M;
XX
XX WPI: 2001-640386/74.
XX
XX P-PSDB: AAE13022.
XX
XX New adenovine triphosphate binding cassette transporter-1 gene
XX polymorphisms, useful for diagnosing and treating lipid disorders,
XX cardiovascular diseases and inflammatory diseases
XX
XX Example 1; Fig 1; 48pp; English.
XX
XX The invention relates to four common polymorphisms in the gene encoding
XX ATP-binding cassette transporter-1 (ABCI). ABC1 is associated with
XX decreased ApoA-1 mediated efflux of cholesterol. The polymorphisms in
XX ABC1 directly affects cellular lipid homeostasis, which is a key factor
XX in the atherogenic processes. The ABC1 polymorphisms are useful for
XX diagnosing and treating lipid disorders, cardiovascular diseases
XX (coronary heart disease, atherosclerosis) and inflammatory diseases
XX (psoriasis, lupus erythematosus). The identification of ABC1 as a
XX transporter for interleukin-1beta (IL-1beta) identifies this gene as
XX a candidate for treatment of inflammatory diseases including rheumatoid
XX arthritis and septic shock. The present sequence is human ABC1 gene.
XX
XX Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other.
XX
Query Match 99.8%; Score 6788; DB 22; Length 7260;
Best local Similarity 99.9%; Pred. No. 0;
Matches 6794; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 atggtctgttggcctcagctgaggtgtgctgtgtggaagaacctcaattcagaagaaga 60
DB 321 atggtctgttggcctcagctgaggtgtgctgtgtggaagaacctcaattcagaagaaga 380
QY 61 caaactgtcagctgttaactggaagtggcctcattatattcttcatctgtc 120
DB 381 caaactgtcagctgttaactggaagtggcctcattatattcttcatctgtc 440

```

121 tctgttcgtgagctaacccactatgaacaacatgatccatttccaaataaagcc 180
|||||
441 tctgttcgtgagctaacccactatgaacaacatgatccatttccaaataaagcc 500
181 atgcccctgagagaacacttcttggtttcagggtatctctgtaattgcacaacccc 240
|||||
501 atgcccctgagagaacacttcttggtttcagggtatctctgtaattgcacaacccc 560
241 tgtttccgtttccggacccctggggaggctcccgagttgtttgnaaactttaacaatcc 300
561 tgtttccgtttccggacccctggggaggctcccgagttgtttgnaaactttaacaatcc 620
301 attgtgctcgcgcttcttcagatgctcggaggtcttctttatacagccagaagacacc 360
621 attgtgctcgcgcttcttcagatgctcggaggtcttctttatacagccagaagacacc 680
361 agcatgaagagacatgcgcaaaagttcttgagaacattacagcgacatacagaatccagctca 420
681 agcatgaagagacatgcgcaaaagttcttgagaacattacagcgacatacagaatccagctca 740
421 aacttgaagacttcaagattctcgtgtgacaatgaacactctctgggttccataccac 480
741 aacttgaagacttcaagattctcgtgtgacaatgaacactctctgggttccataccac 800
481 aacctctctcccaaaagtactatgtgacaagaatgctgagggctgatalcttccac 540
801 aacctctctcccaaaagtactatgtgacaagaatgctgagggctgatalcttccac 860
541 aaggatttttgcaggctcaccagattatattgaaagtctgttcagatggatcaaatca 600
861 aaggatttttgcaggctcaccagattatattgaaagtctgttcagatggatcaaatca 920
601 gaagagatgattcaacttctgtagcaagaagtttctgagcttctggtccataccaaaggag 660
921 gaagagatgattcaacttctgtagcaagaagtttctgagcttctggtccataccaaaggag 980
661 aaactgctcgcagcgagagagatcttcttccaaatggacatcttcaaacatcttcg 720
981 aaactgctcgcagcgagagagatcttcttccaaatggacatcttcaaacatcttcg 1040
721 agaacactaaactctacatctccctcccgagcaaggagctgctgtagaagccacaanaa 780
1041 agaacactaaactctacatctccctcccgagcaaggagctgctgtagaagccacaanaa 1100
781 ttgctgcataagttcttgagacttgcgcaaggagctggttcagcaatgaagaagctgtagac 840
1101 ttgctgcataagttcttgagacttgcgcaaggagctggttcagcaatgaagaagctgtagac 1160
841 atgcgagagagagtgatgtttcttgacaatgtgaaacagctcagctccccaacaaatc 900
1161 atgcgagagagagtgatgtttcttgacaatgtgaaacagctcagctccccaacaaatc 1220
901 taccagagctgtgctcgttattgtctgcgggcatcccgaggaggagggtcgtgaagatcaag 960
1221 taccagagctgtgctcgttattgtctgcgggcatcccgaggaggagggtcgtgaagatcaag 1280
961 tctctcaactggtatagaggaacaacatacaaaagcccttctggaggagatgagcctgag 1020
1281 tctctcaactggtatagaggaacaacatacaaaagcccttctggaggagatgagcctgag 1340
1021 gaagatgctgaacactctatgacaactctacaactccttactatgcatattgtatgag 1080
1341 gaagatgctgaacactctatgacaactctacaactccttactatgcatattgtatgag 1400
1081 aatttgaagctagctcctcttccgcatatctggaagaagctctgaagccgctgctgct 1140
1401 aatttgaagctagctcctcttccgcatatctggaagaagctctgaagccgctgctgct 1460
1141 gggaagatctctgtatataccttggaactccagccaagaagcaggttcatggtcaggtgaac 1200
1461 gggaagatctctgtatataccttggaactccagccaagaagcaggttcatggtcaggtgaac 1520

1201 aagacctccagagactggtgtttccatgatctgtgaaagcactgtaggaagactcagc 1260
1521 aagacctccagagactggtgtttccatgatctgtgaaagcactgtaggaagactcagc 1580
1261 cccaagatctgagaccttatgagagaacagccaagaatgagacttgcggatgctgtg 1320
1581 cccaagatctgagaccttatgagagaacagccaagaatgagacttgcggatgctgtg 1640
1321 gacagcaaggagaacatgacacacttctggaaacagcagttgtatggtatgttgaaagcc 1380
1641 gacagcaaggagaacatgacacacttctggaaacagcagttgtatggtatgttgaaagcc 1700
1381 caagacatcgtggtgttttcttgccaagaccagagatgtccagttccaataatgtcttc 1440
1701 caagacatcgtggtgttttcttgccaagaccagagatgtccagttccaataatgtcttc 1760
1441 ggtlacacttggagagaagacttccaagagacttaacaggaatccgagacatatctgc 1500
1761 ggtlacacttggagagaagacttccaagagacttaacaggaatccgagacatatctgc 1820
1501 ttcatggaagtgtgtcaacctgaaacgttaagaaccataagcaagaagctggtcctatc 1560
1821 ttcatggaagtgtgtcaacctgaaacgttaagaaccataagcaagaagctggtcctatc 1880
1561 aacaagttcatggaagctgtcgtgatgagagaagttctggtgtatgtgttcaactgga 1620
1881 aacaagttcatggaagctgtcgtgatgagagaagttctggtgtatgtgttcaactgga 1940
1621 atthactccaagagatctgagctgccccatcatgtcaagtcaagaatccgaatgtgaact 1680
1941 atthactccaagagatctgagctgccccatcatgtcaagtcaagaatccgaatgtgaact 2000
1681 gacaagtgtgaaagagaacaataaatacaagaatgggtactcggagccctggtcccgagct 1740
2001 gacaagtgtgaaagagaacaataaatacaagaatgggtactcggagccctggtcccgagct 2060
1741 gaccctcttgagagacatgctggtacgtctgagggggtctcgccacttgcagagatgtgtg 1800
2061 gaccctcttgagagacatgctggtacgtctgagggggtctcgccacttgcagagatgtgtg 2120
1801 gacgaaggacatcatcaggtgtgtcgcgggacccggaggaagaactggtgtatcatgcaa 1860
2121 gacgaaggacatcatcaggtgtgtcgcgggacccggaggaagaactggtgtatcatgcaa 2180
1861 cagatgccatccctggttactgtagacatcttctgcgggtgtagtgcggttcaatg 1920
2181 cagatgccatccctggttactgtagacatcttctgcgggtgtagtgcggttcaatg 2240
1921 cccctctcaatgacgtcgtgcttgatcttactcagtggtctgtagatcaagaagcagctg 1980
2241 cccctctcaatgacgtcgtgcttgatcttactcagtggtctgtagatcaagaagcagctg 2300
1981 tatgagaagagagcagagctggaagaagacatgagatcatgtgacctggaacaagacata 2040
2301 tatgagaagagagcagagctggaagaagacatgagatcatgtgacctggaacaagacata 2360
2041 ctctgtgttagcgtgttcatatgtagcctcatctctctctgtgagcgtcgtgctgcta 2100
2361 ctctgtgttagcgtgttcatatgtagcctcatctctctctgtgagcgtcgtgctgcta 2420
2101 gtgtgataccttgaagttaggaacactcgtgcgcttaagtgatcccgaggtgtgttttc 2160
2421 gtgtgataccttgaagttaggaacactcgtgcgcttaagtgatcccgaggtgtgttttc 2480
2161 ttccgtgcgtgtgtgtgtgtgtgtagacaatccctgtagtcttccctgattagcaactcttc 2220
2481 ttccgtgcgtgtgtgtgtgtgtgtagacaatccctgtagtcttccctgattagcaactcttc 2540
2221 tccagagccaactcgtgagcagcctgtgtggggacatctcacttaacagctgtgaactgcc 2280
2541 tccagagccaactcgtgagcagcctgtgtggggacatctcacttaacagctgtgaactgcc 2600
2281 taagtctgtgtgtgtgtgtgtgtgtagcagagtaagtggtgttcaactcaagaactcttcgtagc 2340

4501 acaggagaagaacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 4560
|||||
4821 acaggagaagaacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 4880
|||||
4561 ttaagaagaagaacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 4620
|||||
4881 ttaagaagaagaacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 4940
|||||
4621 aatactcaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 4680
|||||
4941 aatactcaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5000
|||||
4681 caactcaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 4740
|||||
5001 caactcaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5060
|||||
4741 atgacagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 4800
|||||
5061 atgacagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5120
|||||
4801 gcaatcaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 4860
|||||
5121 gcaatcaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5180
|||||
4861 ggaagagaacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 4920
|||||
5181 ggaagagaacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5240
|||||
4921 caagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 4980
|||||
5241 caagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5300
|||||
4981 gtacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5040
|||||
5301 gtacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5360
|||||
5041 gtagagaagaacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5100
|||||
5361 gtagagaagaacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5420
|||||
5101 tcaatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5160
|||||
5421 tcaatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5480
|||||
5161 tcaatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5220
|||||
5481 tcaatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5540
|||||
5221 ctacttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5280
|||||
5541 ctacttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5600
|||||
5281 aagatcccaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5340
|||||
5601 aagatcccaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5660
|||||
5341 ggcagcgtagcagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5400
|||||
5661 ggcagcgtagcagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5720
|||||
5401 gatacttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5460
|||||
5721 gatacttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5780
|||||
5461 gatacttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5520
|||||
5781 gatacttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5840
|||||
5521 gtagcagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5580
|||||
5841 gtagcagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5900
|||||

5581 gtggttcttcctactatctgttggaagacgtatgtgacagatcatagccaaagc 5640
|||||
5901 gtggttcttcctactatctgttggaagacgtatgtgacagatcatagccaaagc 5960
|||||
5641 gtaagtcaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5700
|||||
5961 gtaagtcaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6020
|||||
5701 aagaatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5760
|||||
6021 aagaatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6080
|||||
5761 taaagaagaagaacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5820
|||||
6081 taaagaagaagaacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6140
|||||
5821 tgccttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5880
|||||
6141 tgccttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6200
|||||
5881 ggaagagaacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 5940
|||||
6201 ggaagagaacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6260
|||||
5941 atccatgaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6000
|||||
6261 atccatgaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6320
|||||
6001 ttgacttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6060
|||||
6321 ttgacttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6380
|||||
6061 gtagcagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6120
|||||
6381 gtagcagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6440
|||||
6121 tatgttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6180
|||||
6441 tatgttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6500
|||||
6181 ggcagcgtagcagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6240
|||||
6501 ggcagcgtagcagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6560
|||||
6241 cggcttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6300
|||||
6561 cggcttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6620
|||||
6301 tctcatgaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6360
|||||
6621 tctcatgaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6680
|||||
6361 aagatcccaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6420
|||||
6681 aagatcccaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6740
|||||
6421 atagtttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6480
|||||
6741 atagtttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6800
|||||
6481 ctgcatccgtagcagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6540
|||||
6801 ctgcatccgtagcagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6860
|||||
6541 ccatcttcattatctgttggaagacgtatgtgacagatcatagccaaagc 6600
|||||
6861 ccatcttcattatctgttggaagacgtatgtgacagatcatagccaaagc 6920
|||||
6601 ctccacataagaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6660
|||||
6921 ctccacataagaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6980
|||||
6661 gccaaggaagaagacatttcgattatctgttggaagacgtatgtgacagatcatagccaaagc 6720
|||||

```

Db 6981 gccaaagaccacaaatgatgatgaccccttaaaagacctctcatcaccaaaacagaca 7040
Qy 6721 gtagtgagcgtgacgttctacatcttcttacaagatgagaagtgaaagaaatcat 6780
Db 7041 gtagtgagcgtgacgttctacatcttcttacaagatgagaagtgaaagaaatcat 7100
Qy 6781 gtagtgagcgttctacatcttcttacaagatgagaagtgaaagaaatcat 6804
Db 7101 gtagtgagcgttctacatcttcttacaagatgagaagtgaaagaaatcat 7124

RESULT 10
AAI70315
ID AAI70315 standard; cDNA: 7260 BP.
XX
AC AAI70315;
XX
DT 07-JAN-2002 (first entry)
XX
DE Human ATP binding cassette transporter 1 (ABCI) cDNA.
XX
KW ATP binding cassette transporter 1; ABC1; human; lipid disorder;
KW cholesterol; cardiovascular disease; inflammatory disease;
KW antiinflammatory; antipapemic; antipsoriatic; dermatological;
KW Tangier disease; coronary heart disease; diagnosis; gene therapy;
KW polymorphism; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 321..7106
FT FT /*tag= a
FT FT 501..7106
FT FT /*tag= b
FT FT /note= "alternative open reading frame of AAI70314"
FT FT replacement(976,A)
FT FT /*tag= c
FT FT replacement(1516,C)
FT FT /*tag= d
FT FT replacement(2969,G)
FT FT /*tag= e
FT FT replacement(3836,C)
FT FT /*tag= f
XX
PN EPI136554-A1.
XX
PD 26-SEP-2001.
XX
PE 24-MAR-2000; 2000EP-0106401.
XX
PR 24-MAR-2000; 2000EP-0106401.
XX
PA (FARB ) BAYER AG.
XX
PI Schmitz G, Bodzioch M;
XX
DR WPI: 2001-640389/74.
XX
P-PSDB: AAM50228.
XX
PT New adenosine triphosphate binding cassette transporter gene
PT polymorphisms, useful for diagnosing and treating lipid disorders,
PT cardiovascular diseases and inflammatory diseases
XX
PS Disclosure: Page 26-28; 41pp; English.
XX
CC The present sequence is that of cDNA encoding the human adenosine
CC triphosphate (ATP) binding cassette transporter 1 (ABCI) protein
CC (see AAM50227). The sequence includes an extended open reading
CC frame (ORF) to that provided by the sequence in AAI70314, using
CC an alternative ATG codon as initiation codon and thereby adding an
CC extra 40 N-terminal amino acids to the encoded ABC1 protein (see
CC AAM50228). The invention provides 4 common polymorphisms in the

```

```

CC ABC1 gene. These were identified by sequencing the ABC1 gene in
CC different Tangier kindreds. In the variant genes (numbering as in
CC AAI70314), G is changed to A at position 596, T is changed to C at
CC position 1136, A is changed to G at position 2589 or G is changed
CC to C at position 3456, or any combination of these. All of these
CC polymorphisms alter the amino acid sequence of ABC1 and therefore
CC may affect its function. The 2 most common polymorphisms (G556A
CC and A2589G) are both associated with a decreased in vitro ApoA-I
CC mediated efflux of cholesterol from mononuclear phagocytes, a
CC feature typical of Tangier disease. 3 Of the variants (G556A,
CC A2589G and G3456C) are significantly increased in a population of
CC men having low high density lipoprotein-cholesterol levels and
CC established coronary heart disease (CHD) relative to CHD-free
CC control subjects. The use of the provided ABC1 polymorphisms for
CC the diagnosis and treatment of lipid disorders, cardiovascular
CC diseases, and inflammatory diseases (e.g. psoriasis, lupus
CC erythematoses) is claimed. Modulation of ABC1 transcripts or
CC proteins by antisense or ribozyme technology or RNA decoys is also
CC claimed.
XX
SO Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;

Query Match 99.8%; Score 6788; DB 22; Length 7260;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6794; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 atggtctgttggtcctcagctgaggtgctgctgtggaagaacctcattcagaagaaga 60
Db 321 atggtctgttggtcctcagctgaggtgctgctgtggaagaacctcattcagaagaaga 380
Qy 61 caacatgctcagctgttaccggaagtgtgctgctcattcttctccgaccgcat 120
Db 381 caacatgctcagctgttaccggaagtgtgctgctcattcttctccgaccgcat 440
Qy 121 tctgttcgctgagctaccaccctatgaaacaatgatgcatcttccaataaagcc 180
Db 441 tctgttcgctgagctaccaccctatgaaacaatgatgcatcttccaataaagcc 500
Qy 181 atgcccctcgaagaaacattccttggttcaggaggttaccgtatgccaacacccc 240
Db 501 atgcccctcgaagaaacattccttggttcaggaggttaccgtatgccaacacccc 560
Qy 241 tgtttccgttaccgacctctggtggaaggtcccgaggtgtgtggaacttaacaatcc 300
Db 561 tgtttccgttaccgacctctggtggaaggtcccgaggtgtgtggaacttaacaatcc 620
Qy 301 atgtgtcgtcgtgttctcagatgctcggaggtcttcttatacagccaagaagaccc 360
Db 621 atgtgtcgtcgtgttctcagatgctcggaggtcttcttatacagccaagaagaccc 680
Qy 361 agcatgaagagacatgacgaagtctgagacacattacaagacagaacaatccaactca 420
Db 681 agcatgaagagacatgacgaagtctgagacacattacaagacagaacaatccaactca 740
Qy 421 aacttgaagcttaagaattcctcgtgtggaacatgaaacctctctgtggttactatac 480
Db 741 aacttgaagcttaagaattcctcgtgtggaacatgaaacctctctgtggttactatac 800
Qy 481 aacctctctcccaagaagtactgtggaacaagatctgagggctgatactctccac 540
Db 801 aacctctctcccaagaagtactgtggaacaagatctgagggctgatactctccac 860
Qy 541 aaggtattttggaagctaccagttacattgacaagctctgtcaatgatacaaatca 600
Db 861 aaggtattttggaagctaccagttacattgacaagctctgtcaatgatacaaatca 920
Qy 601 gaagagatgattaaactgttgacccaagaagttctggaacttgtgctaccagaaggg 660
Db 921 gaagagatgattaaactgttgacccaagaagttctggaacttgtgctaccagaaggg 980
Qy 661 aaactgctcacaagacagagactctgtccaatgatacctctgaagcaatctcg 720

```

Db 981 aaactgctgcagcagagcagtlacttcgtccaaatgacatccctgaaagccatctgt 1040
QY 721 agaacataaactacatctccctccctcccgagcaaggagctgtgagccacaaaaca 780
Db 1041 agaacataaactacatctccctccctcccgagcaaggagctgtgagccacaaaaca 1100
QY 781 ctgctgcatagtctctgggaactctggccagagactgttccaacatgagaagctgtgaftgac 840
Db 1101 ctgctgcatagtctctgggaactctggccagagactgttccaacatgagaagctgtgaftgac 1160
QY 841 atgcgcacagagagtgatgttcttcgaccaaagtgaacagctccctccacccaacatc 900
Db 1161 atgcgcacagagagtgatgttcttcgaccaaagtgaacagctccctccacccaacatc 1220
QY 901 taaccagctgtgtctcgttaattgtctgcgggcatcccgagggagggggtcgtgaataaag 960
Db 1221 taaccagctgtgtctcgttaattgtctgcgggcatcccgagggagggggtcgtgaataaag 1280
QY 961 tctctcaactgtgatgagagacaacaactacaagacccctcttgaggagcaatgagcactgag 1020
Db 1281 tctctcaactgtgatgagagacaacaactacaagacccctcttgaggagcaatgagcactgag 1340
QY 1021 gaagatgcctgaacacctctctacacactctacacactcttactgcaatgattgagag 1080
Db 1341 gaagatgcctgaacacctctctacacactctacacactcttactgcaatgattgagag 1400
QY 1081 aatttgagatctagctctctctcccgcaatctctggaagagctctgaaagcgtctcgtt 1140
Db 1401 aatttgagatctagctctctctcccgcaatctctggaagagctctgaaagcgtctcgtt 1460
QY 1141 gggaaagatcctgtatatacactcgaactccagccagcaagagcagtgatgctgaggtgagac 1200
Db 1461 gggaaagatcctgtatatacactcgaactccagccagcaagagcagtgatgctgaggtgagac 1520
QY 1201 aagacctccagagaactggtgtgtctccactgactctgaaagagctgtgggaaggaactcagc 1260
Db 1521 aagacctccagagaactggtgtgtctccactgactctgaaagagctgtgggaaggaactcagc 1580
QY 1261 cccaagaatctggaactctcatatgagagaacagccaagaaatgagactgtgtccggatgtcgttg 1320
Db 1581 cccaagaatctggaactctcatatgagagaacagccaagaaatgagactgtgtccggatgtcgttg 1640
QY 1321 gacagcgaggagacaatgagacacctcttgaggaaacagcagttgagctgactatctggacagcc 1380
Db 1641 gacagcgaggagacaatgagacacctcttgaggaaacagcagttgagctgactatctggacagcc 1700
QY 1381 caaagacatcgttggttcttctgccaagcaccagagagatgtccagtcacgtatggttct 1440
Db 1701 caaagacatcgttggttcttctgccaagcaccagagagatgtccagtcacgtatggttct 1760
QY 1441 gtgtacacactgagagagaagcttccaacgagactaaacagggcaatcccgagccatattctgc 1500
Db 1761 gtgtacacactgagagagaagcttccaacgagactaaacagggcaatcccgagccatattctgc 1820
QY 1501 ttctgtgagtggtgtcaacactggaacaaagctagaacccaatagcaacaagaatctgtgcccacac 1560
Db 1821 ttctgtgagtggtgtcaacactggaacaaagctagaacccaatagcaacaagaatctgtgcccacac 1880
QY 1561 aacaagtcacatgagagctgtctgagatgagaggaagcttctggctgtgattgtgtcactgtga 1620
Db 1881 aacaagtcacatgagagctgtctgagatgagaggaagcttctggctgtgattgtgtcactgtga 1940
QY 1621 attactcagagcaacatgtgagctgtgcccacatgataagataagaagatccgaatggagcatt 1680
Db 1941 attactcagagcaacatgtgagctgtgcccacatgataagataagaagatccgaatggagcatt 2000
QY 1681 gacaaatgtgagagagacaataaataaataaagatgtgtactgtgagacccctgtgtccctgagct 1740
Db 2001 gacaaatgtgagagagacaataaataaataaagatgtgtactgtgagacccctgtgtccctgagct 2060
QY 1741 gaccccttgagagacatgctgactgtggtgggggtcttgccctactctgacagagatgtggtg 1800
Db 2061 gaccccttgagagacatgctgactgtggtgggggtcttgccctactctgacagagatgtggtg 2120

QY 1801 gacagcgacaatcatcagaggtgtctacgggacccgagagaagaataatgtgtctatgtgcaa 1860
Db 2121 gacagcgacaatcatcagaggtgtctacgggacccgagagaagaataatgtgtctatgtgcaa 2180
QY 1861 cagatgcccataccctgttactgatagtacatcttctctgggtgtgataagccgtgtcaatg 1920
Db 2181 cagatgcccataccctgttactgatagtacatcttctctgggtgtgataagccgtgtcaatg 2240
QY 1921 cccctcttaacatgacgtggtggtggttactcaatgtggtgtgatacacaaggggcatcgtg 1980
Db 2241 cccctcttaacatgacgtggtggtggttactcaatgtggtgtgatacacaaggggcatcgtg 2300
QY 1981 tatgagaagagagcagcgtgtgaaagagacacatgctggaatcatatggtggtcgtgacaagcata 2040
Db 2301 tatgagaagagagcagcgtgtgaaagagacacatgctggaatcatatggtggtcgtgacaagcata 2360
QY 2041 ctctggtttagctgtgttcaatagtagctcattctctctctgtgagagcgtggtgcta 2100
Db 2361 ctctggtttagctgtgttcaatagtagctcattctctctctgtgagagcgtggtgcta 2420
QY 2101 gtgtgtatcctgtgaagttaggaacactgtgcccctacagtgatcccaagctgtgtgtgtc 2160
Db 2421 gtgtgtatcctgtgaagttaggaacactgtgcccctacagtgatcccaagctgtgtgtgtc 2480
QY 2161 ttctctgtcgtgtgtgtgtgtgtgtgataacatccctgacagtgcttctcgtatagacactcttc 2220
Db 2481 ttctctgtcgtgtgtgtgtgtgtgtgataacatccctgacagtgcttctcgtatagacactcttc 2540
QY 2221 tccagagccaacactgtgacagcagctgtgtggggacatcatctactcaagctgtactgtccc 2280
Db 2541 tccagagccaacactgtgacagcagctgtgtggggacatcatctactcaagctgtactgtccc 2600
QY 2281 taagtcctgt 2340
Db 2601 taagtcctgt 2660
QY 2341 ctgctgtcctctgt 2400
Db 2661 ctgctgtcctctgt 2720
QY 2401 ggcattgagatgcaatgtgaggaacacctgtgtgagagctcctgtgtgagagagatgtgctcaat 2460
Db 2721 ggcattgagatgcaatgtgaggaacacctgtgtgagagctcctgtgtgagagagatgtgctcaat 2780
QY 2461 ctccacacactcgaatctccacatgacgtcgttttgacacactctcctctataggggtgtgacctgg 2520
Db 2781 ctccacacactcgaatctccacatgacgtcgttttgacacactctcctctataggggtgtgacctgg 2840
QY 2521 tacattgagctgtcttctccagccagtaacggaatcccaagcctgtgtatcttctctgc 2580
Db 2841 tacattgagctgtcttctccagccagtaacggaatcccaagcctgtgtatcttctctgc 2900
QY 2581 accaagctcactgt 2640
Db 2901 accaagctcactgt 2960
QY 2641 aagaagatgtcagaaatctcatgtgagaggaacccaacacttgaaagctgtggcgtgtctc 2700
Db 2961 aagaagatgtcagaaatctcatgtgagaggaacccaacacttgaaagctgtggcgtgtctc 3020
QY 2701 attcagaacactgtgtaaaagcttaccagagatgagatggaaggtgtgctgtcgtatggtcctggca 2760
Db 3021 attcagaacactgtgtaaaagcttaccagagatgagatggaaggtgtgctgtcgtatggtcctggca 3080
QY 2761 ctggaatt 2820
Db 3081 ctggaatt 3140
QY 2821 accacacatgtaacatcctgtgacgggtgtgttcccccgacactcgggacacgcttacaatcctgt 2880
Db 3141 accacacatgtaacatcctgtgacgggtgtgttcccccgacactcgggacacgcttacaatcctgt 3200

[illegible][illegible]

Dh 5361 gtcaagcaagcaaaacacctgcacgttccatcagtgtagtgagctgctgtaacttgcgc 5420
Qy 5101 tctaatttgcctggagatagtgtaacttaagttgctccctgcacacacgtgcatcattacac 5160
Dh 5421 tctaatttgcctggagatagtgtaacttaagttgctccctgcacacacgtgcatcattacac 5480
Qy 5161 tctaatttgcctggagatagtgtaacttaagttgctccctgcacacacgtgcatcattacac 5220
Dh 5481 tctaatttgcctggagatagtgtaacttaagttgctccctgcacacacgtgcatcattacac 5540
Qy 5221 ctactttgtctgtagtgtagtgtaacttaagttgctccctgcacacacgtgcatcattacac 5280
Dh 5541 ctactttgtctgtagtgtagtgtaacttaagttgctccctgcacacacgtgcatcattacac 5600
Qy 5281 aagatccccac 5340
Dh 5601 aagatccccac 5660
Qy 5341 ggcagcgtgac 5400
Dh 5661 ggcagcgtgac 5720
Qy 5401 gataccctgagac 5460
Dh 5721 gataccctgagac 5780
Qy 5461 gacatggtgagac 5520
Dh 5781 gacatggtgagac 5840
Qy 5521 gtgac 5580
Dh 5841 gtgac 5900
Qy 5581 gtgac 5640
Dh 5901 gtgac 5960
Qy 5641 gtaaaatgcaaaagctatct 5700
Dh 5961 gtaaaatgcaaaagctatct 6020
Qy 5701 agaatctctgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtag 5760
Dh 6021 agaatctctgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtag 6080
Qy 5761 tataagaaggaagcgaagcgtgctgtagacaggaattgctgtaggacatctccctcctgtagag 5820
Dh 6081 tataagaaggaagcgaagcgtgctgtagacaggaattgctgtaggacatctccctcctgtagag 6140
Qy 5821 tgccttgtaggctcctgtaggagtagtgtaggagtagtgtaggagtagtgtaggagtagtgtagg 5880
Dh 6141 tgccttgtaggctcctgtaggagtagtgtaggagtagtgtaggagtagtgtaggagtagtgtagg 6200
Qy 5881 ggaataaccactgttaccag 5940
Dh 6201 ggaataaccactgttaccag 6260
Qy 5941 atccatgaagtagacagacag 6000
Dh 6261 atccatgaagtagacagacag 6320
Qy 6001 ttgacttggaag 6060
Dh 6321 ttgacttggaag 6380
Qy 6061 gttagcgaaggt 6120
Dh 6381 gttagcgaaggt 6440
Qy 6121 tatgtctgttaactatagt 6180
Dh 6441 tatgtctgttaactatagt 6500

Qy 6181 ggcgggacctctgt 6240
Dh 6501 ggcgggacctctgt 6560
Qy 6241 cggctctgt 6300
Dh 6561 cggctctgt 6620
Qy 6301 tctcatagtaggaagatgtgaagctcttctgcatgaagtagtgcatatagtgtagga 6360
Dh 6621 tctcatagtaggaagatgtgaagctcttctgcatgaagtagtgcatatagtgtagga 6680
Qy 6361 aggttcaggt 6420
Dh 6681 aggttcaggt 6740
Qy 6421 atagttgtacagatagcagaggtcccaaccgacacacacacacacacacacacacacacacacac 6480
Dh 6741 atagttgtacagatagcagaggtcccaaccgacacacacacacacacacacacacacacacacac 6800
Qy 6481 ctgtcatctctgtgaagtggtcttaaaagaagaacacacacacacacacacacacacacacacacac 6540
Dh 6801 ctgtcatctctgtgaagtggtcttaaaagaagaacacacacacacacacacacacacacacacacac 6860
Qy 6541 ccatctctgtatctctctctgt 6600
Dh 6861 ccatctctgtatctctctctgt 6920
Qy 6601 ctccacatagaagatctctgt 6660
Dh 6921 ctccacatagaagatctctgt 6980
Qy 6661 gccaaagaccaaagtgatgtagcacttaaaagcctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6720
Dh 6981 gccaaagaccaaagtgatgtagcacttaaaagcctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7040
Qy 6721 gtagtgacgtgtgacgt 6780
Dh 7041 gtagtgacgtgtgacgt 7100
Qy 6781 gtagtgacgtgtgacgt 6840
Dh 7101 gtagtgacgtgtgacgt 7124

RESULT 11
AAS06120
ID AAS06120 standard; cDNA; 9741 BP.
XX
AC AAS06120;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human ABC1 DNA sequence #1.
XX
KW Human: ABC1 gene; atherosclerosis; reverse transport; cholesterol;
KW Cardiovascular; neurological; Tangier disease; LCAT deficiency;
KW Lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 185..6967
FT /tag= a
FT /product= "Human ABC1 protein"
XX
PD WO200130848-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000MO-EP10886.
XX

PR 26-OCM-1999; 99EP-0402668.
 PR 01-MAR-2000; 2000US-0186260.
 XX
 PA (AVET) AVENTIS PHARMA SA.
 XX
 PI Deneffe P, Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L;
 PI Lemoine C, Duverger N, Jaye M, Searious GH, Kemaley A, Brewer HB;
 PI Dean M;
 XX WPI; 2001-316327/33.
 DR P-PSDB; AA002176.
 XX
 PT New human ABC1 nucleic acids and polypeptides for treating
 PT atherosclerosis, malaria and diabetes -
 XX
 PS Claim 1; Page 204-208; 368pp; English.
 XX
 CC The sequence represents the coding sequence #1 of human ABC1. The
 CC nucleic acid sequence, primers and probes derived from the ABC1 sequence,
 CC and polypeptides and vectors are useful for the prevention of
 CC atherosclerosis, in a subject affected by a dysfunction in the reverse
 CC transport of cholesterol. The polypeptide encoded by the ABC1 gene is
 CC useful for screening for an active ingredient for the prevention or
 CC treatment of a disease resulting from dysfunction in the reverse
 CC transport of cholesterol. The nucleic acids and polypeptides are also
 CC useful for treating and preventing cardiovascular and neurological
 CC pathologies, and other diseases e.g. Tangier disease, lecithin-
 CC cholesterol (LCAT) deficiency, malaria and diabetes.
 CC
 SQ Sequence 9741 BP; 2650 A; 2180 C; 2290 G; 2620 T; 1 other;

Query Match 99.7%; Score 6784.8; DB 22; Length 9741;
 Best Local Similarity 99.8%; Pred No. 0;
 Matches 6792; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 atggtctgttgccctagctgaggtgctgctgtgtggaagaacccacttcagaagaaga 60
 Db 185 atgctgtgttgccctagctgaggtgctgctgtgtggaagaacccacttcagaagaaga 244
 QY 61 caaactgtacgtgttactggaagtgctgtgctcttattctctctgtatc 120
 Db 245 caaactgtacgtgttactggaagtgctgtgctcttattctctctgtatc 304
 QY 121 tctgtctgtgctgactacccacttgaacaacatgacatgcatcttcaataaagcc 180
 Db 305 tctgtctgtgctgactacccacttgaacaacatgacatgcatcttcaataaagcc 364
 QY 181 atgacctctgcaggaacactctctgtgttcaaggagatcatctgtatgccaacaccc 240
 Db 365 atgacctctgcaggaacactctctgtgttcaaggagatcatctgtatgccaacaccc 424
 QY 241 tgttccgttaccgcgactctgtggaagctcccgaggtgttggaacattacaatacc 300
 Db 425 tgttccgttaccgcgactctgtggaagctcccgaggtgttggaacattacaatacc 484
 QY 301 atgtgtgtcgtcgtgttctcagatgctcgaggtcttcttitaacaagcagaagaacac 360
 Db 485 atgtgtgtcgtcgtgttctcagatgctcgaggtcttcttitaacaagcagaagaacac 544
 QY 361 agcatgaagagacatgcgcaaaagtcttggaacattacagcagatacaagaatccagctca 420
 Db 545 agcatgaagagacatgcgcaaaagtcttggaacattacagcagatacaagaatccagctca 604
 QY 421 aacttgaagacttcaagattctctgtgtgacaatgaacactctctgtgttctctatcac 480
 Db 605 aacttgaagacttcaagattctctgtgtgacaatgaacactctctgtgttctctatcac 664
 QY 481 aacctctctctccaaagtctactgtgacaagaatgctgagggctgcatctatctccac 540
 Db 665 aacctctctctccaaagtctactgtgacaagaatgctgagggctgcatctatctccac 724
 QY 541 aagtatatttgcaggtctacaggtacatttgacaagtctgtgaatgatcaaatca 600

Db 725 aagtatatttgcaggtctacaggtacatttgacaagtctgtgaatgatcaaatca 784
 QY 601 gaagagatgtatccaactgtgtgacccaagaagttcttgagcttctgtgctccaaagag 660
 Db 785 gaagagatgtatccaactgtgtgacccaagaagttcttgagcttctgtgctccaaagag 844
 QY 661 aactgtgtcgcagcagagagatctctgttccaaacatggaacatctcctaagccaactctg 720
 Db 845 aactgtgtcgcagcagagagatctctgttccaaacatggaacatctcctaagccaactctg 904
 QY 721 agaacaactaactatcatctccctcccgagcaagagagctgtgtgaagccacaanaaca 780
 Db 905 agaacaactaactatcatctccctcccgagcaagagagctgtgtgaagccacaanaaca 964
 QY 781 ttgtctgcatgtctgtgagctctgtgcccagagctgttccagatgagaagcttgtagac 840
 Db 965 ttgtctgcatgtctgtgagctctgtgcccagagctgttccagatgagaagcttgtagac 1024
 QY 841 atgcgacagaggtgagtttcttgaccaaagtgtgaacagctccacccccaatc 900
 Db 1025 atgcgacagaggtgagtttcttgaccaaagtgtgaacagctccacccccaatc 1084
 QY 901 taccaggtgtgtctcgtatgtctgtcgagatcccgagagaggggctgtgaagatcaag 960
 Db 1085 taccaggtgtgtctcgtatgtctgtcgagatcccgagagaggggctgtgaagatcaag 1144
 QY 961 tctctcaactgtatgagagacaacaactacaagaacccctcttgtaggcaatgtagctgag 1020
 Db 1145 tctctcaactgtatgagagacaacaactacaagaacccctcttgtaggcaatgtagctgag 1204
 QY 1021 gaagtgcttgaacactcttatgacaactctcaactcttaactgtgaatgtatgtagaag 1080
 Db 1265 gaagtgcttgaacactcttatgacaactctcaactcttaactgtgaatgtatgtagaag 1264
 QY 1141 gggaaagatcctgtatacactgtacactccagccaagaagctgcatgtgtagtgagac 1200
 Db 1325 gggaaagatcctgtatacactgtacactccagccaagaagctgcatgtgtagtgagac 1384
 QY 1201 aagacctccaggaactgagctgttccatgacttggaagagatgtgtggaggaactagc 1260
 Db 1385 aagacctccaggaactgagctgttccatgacttggaagagatgtgtggaggaactagc 1444
 QY 1261 cccaagatctgacacttcatgtgaacaacagccaagaatggaacttgcggatgtgttg 1320
 Db 1445 cccaagatctgacacttcatgtgaacaacagccaagaatggaacttgcggatgtgttg 1504
 QY 1321 gacagcaggggacaatgacactcttcttggaacaagatgtgtagcttagatgtgaagcc 1380
 Db 1505 gacagcaggggacaatgacactcttcttggaacaagatgtgtagcttagatgtgaagcc 1564
 QY 1381 caagacatctgtgagcttcttgccaagcaccccaagaagatgtccagttccaatgtgttc 1440
 Db 1565 caagacatctgtgagcttcttgccaagcaccccaagaagatgtccagttccaatgtgttc 1624
 QY 1441 ggtgacaccttggaagaagacttccaacgagacttaaccaggaactccggacatatctgc 1500
 Db 1625 ggtgacaccttggaagaagacttccaacgagacttaaccaggaactccggacatatctgc 1684
 QY 1501 ttcatgagtggttcaaacctgaacagctgaagccatgacccaagaagtctgtgcatc 1560
 Db 1685 ttcatgagtggttcaaacctgaacagctgaagccatgacccaagaagtctgtgcatc 1744
 QY 1561 aacaagtccaatgagctgtctggaatgagagagatcttgggctgtatctgttccaatgga 1620
 Db 1745 aacaagtccaatgagctgtctggaatgagagagatcttgggctgtatctgttccaatgga 1804
 QY 1621 attactccaagcagcatgtgagctgtcccatcatgtcaagtacaagaatccggaatggaact 1680

D	b	1805	attatctccaggcagcatctgtagctctccccaatcatgtcaagtacaaagatccgaatgagacatt	1864
O	y	1681	gacacatctgtagagagacaataataatacaagatggtactctgtagacccctgtgtccctgagct	1740
D	b	1665	gacacatgtagagagagacaataataatacaagatggtactctgtagacccctgtgtccctgagct	1924
O	y	1741	gaaccccttgaagagacatgcggttaagctctcgggggggcttcgcctactctgcagagatggtgt	1800
D	b	1925	gaaccccttgaagagacatgcggttaagctctcgggggggcttcgcctactctgcagagatggtgt	1984
O	y	1801	gagcagagcaatcatcagaggctgtctgcacggcagcccggaagaaactgtgtctatgca	1860
D	b	1985	gagcagagcaatcatcagaggctgtgtctgcacggcagcccggaagaaactgtgtctatgca	2044
O	y	1861	cagatgcctatccctgttaagctgatatgacalcttctctgagggtgatagagccggtcaatg	1920
D	b	2045	cagatgcctatccctgttaagctgatatgacalcttctctgagggtgatagagccggtcaatg	2104
O	y	1921	ccccccttcatagagctctggccctggagatttactaagtgagctgtgacatcaagaagagatcgt	1980
D	b	2105	ccccccttcatagagctctggccctggagatttactaagtgagctgtgacatcaagaagagatcgt	2164
O	y	1981	tatgataagagagagacagcgctgtgaaagagacacatgvcgagatcatgvggcctgagacaagcata	2040
D	b	2165	tatgataagagagagacagcgctgtgaaagagacacatgvcgagatcatgvggcctgagacaagcata	2224
O	y	2041	ctctcggttagagctgtgtcaatagtagccctatccctctctcttcttgagagagctgcgctctcta	2100
D	b	2225	ctctcggttagagctgtgtgtcaatagtagccctatccctctctcttcttgagagagctgcgctctcta	2284
O	y	2101	gttggtcatctctgaaagttaagaaacaacccgctgcgcccatacagtatccccaagcggtgtttgttc	2160
D	b	2285	gttggtcatctctgaaagttaagaaacaacccgctgcgcccatacagtatccccaagcggtgtttgttc	2344
O	y	2161	ttctctgtccggtgtttgtgtgtgtgataacaatccctgcagctgtccctctgataagacacctcttc	2220
D	b	2345	ttctctgtccggtgtttgtgtgtgtgataacaatccctgcagctgtccctctgataagacacctcttc	2404
O	y	2221	ttccagagccaacccgtagcagagacgctctgtgggggagatcatctacttlaacgctgtlaacctgcc	2280
D	b	2405	ttccagagccaacccgtagcagagacgctctgtgggggagatcatctacttlaacgctgtlaacctgcc	2464
O	y	2281	taagctcctgtgtgtgtgcatagtagcagagatcagctgcgtgagcttacaacctaaagatctctgtctagc	2340
D	b	2465	taagctcctgtgtgtgtgcatagtagcagagatcagctgcgtgagcttacaacctaaagatctctgtctagc	2524
O	y	2341	ctgcgctctccctgtgcgctcttcttgaggttggtgcgtgtgagatctatggcccttcttgagagagcag	2400
D	b	2525	ctgcgctctccctgtgcgctcttcttgaggttggtgcgtgtgagatctatggcccttcttgagagagcag	2584
O	y	2401	ggcatttgaagtgtgcagtgtggagacaacctgtttgagaagctcctgtgtgaggagaagatvgcttcaat	2460
D	b	2585	ggcatttgaagtgtgcagtgtggagacaacctgtttgagaagctcctgtgtgaggagaagatvgcttcaat	2644
O	y	2461	ctccaccacttgcattctccatagatgctgttttgagaacacctctctatgagggtgtgagtgcacgg	2520
D	b	2645	ctccaccacttgcattctccatagatgctgttttgagaacacctctctctatgagggtgtgagtgcacgg	2704
O	y	2521	tacatttgaagctgtgcttcttccagagccagtaagagatctcccaagccctgtgatttccctgtgc	2580
D	b	2705	tacatttgaagctgtgcttcttccagagccagtaagagatctcccaagccctgtgatttccctgtgc	2764
O	y	2581	accacaagctccctctgtgtttggggagagaaagtgatggaagaagagccaacctgtgttccaaacag	2640
D	b	2765	accacaagctccctctgtgtgtttggggagagaaagtgatggaagaagagccaacctgtgttccaaacag	2824
O	y	2641	aagagaatctgtagaagaatctgcatctgtagagagaaacccaacccacttgaagcttggtgcgtgtctc	2700
D	b	2825	aagagaatatacgaagaatctgtgatagtgagagaaacccaacccacttgaagcttggtgcgtgtctc	2884
O	y	2701	attcagaacacctgtgataaagcttaccagagatgaggaatgaaggtgtgcgtctgcatgagctctgtgca	2760
D	b	2885	attcagaacacctgtgataaagcttaccagagatgaggaatgaaggtgtgcgtctgcatgagctctgtgca	2944

QY	2761	ctgaatttttatbagaagccagatccacctctctctctcctggcccaaatbgaacgagggaagacg	2820
Db	2945	ctgaatttttatbagaagccagatccacctctctctcctggcccaaatbgaacgagggaagacg	3004
QY	2821	accacatctcaatctctgacccggtgtgtcccccgaacctgggacacggctcatctccg	2880
Db	3005	accacatctcaatctctgacccggtgtgtcccccgaacctgggacacggctcatctccg	3064
QY	2881	ggaaaacacatctgcctctgagatbgaacacatcccgccagaaacctgggggtctgtcccaag	2940
Db	3065	ggaaaacacatctgcctctgagatbgaacacatcccgccagaaacctgggggtctgtcccaag	3124
QY	2941	cataacgtgcctgtttgacatbgtcactgtctgaaagaacacatctgtttctatgtcccgcttg	3000
Db	3125	cataacgtgcctgtttgacatbgtcactgtctgaaagaacacatctgtttctatgtcccgcttg	3184
QY	3001	aaagagcctctctgagaagacacgtgaaagcgtggagatctggaagacagatctggccctgattgtgt	3060
Db	3185	aaagagcctctctgagaagacacgtgaaagcgtggagatctggaagacagatctggccctgattgtgt	3244
QY	3061	ttgccaatcaagcaagcgtgaaagaacaaacaaagccagctgtcaagttggaatgacagagaag	3120
Db	3245	ttgccaatcaagcaagcgtgaaagaacaaacaaagccagctgtcaagttggaatgacagagaag	3304
QY	3121	ctatctgtgagccttgagcctttgtccgggggaatctaaagttgtcaatctctgagatbgaacccaca	3180
Db	3305	ctatctgtgagccttgagcctttgtccgggggaatctaaagttgtcaatctctgagatbgaacccaca	3364
QY	3181	gctctgtctggaaccccttaacctcccgcaagggaatactggaagcctgtcctgaaataccggaaca	3240
Db	3365	gctctgtctggaaccccttaacctcccgcaagggaatactggaagcctgtcctgaaataccggaaca	3424
QY	3241	ggccgcacccattatctctctataccacacacatagatgaaagccgagacgtctccctggggagacag	3300
Db	3425	ggccgcacccattatctctctataccacacacacatagatgaaagccgagacgtctccctggggagacag	3484
QY	3301	attgtgcacatcatctcccatctgggaagcctgtgctgtgtgtgagcctccctccgtttctgaaagac	3360
Db	3485	attgtgcacatcatctcccatctgggaagcctgtgctgtgtgtgagcctccctccgtttctgaaagac	3544
QY	3361	caagctgggaaacagcgtactacactgacacctgtgtgaagaagaagatgtgaaatctctccctgaat	3420
Db	3545	caagctgggaaacagcgtactacactgacacctgtgtgaagaagaagatgtgaaatctctccctgaat	3604
QY	3421	tcctctcaagaacagtagtagaacctgtctcaactccttaaaagaagagacagatgttctccag	3480
Db	3605	tcctctcaagaacagtagtagaacctgtctcaactccttaaaagaagagacagatgttctccag	3664
QY	3481	agcaagttctgatatgctgtgcctgtggcagcgacatctgaaagtgtgaacgcctgtacatctgatgttc	3540
Db	3665	agcaagttctgatatgctgtgcctgtggcagcgacatctgaaagtgtgaacgcctgtacatctgatgttc	3724
QY	3541	tcctgcatatctccaacctatagaagaacatgtgtctcgaagcccggtctgtgtgaaagacata	3600
Db	3725	tcctgcatatctccaacctatagaagaacatgtgtctcgaagcccggtctgtgtgaaagacata	3784
QY	3601	gggcatagagcctgacactatgtctgtcccatatgaagcctgtctaaagagagagcctcttgttgaa	3660
Db	3785	gggcatagagcctgacactatgtctgtcccatatgaagcctgtctaaagagagagcctcttgttgaa	3844
QY	3661	ctctttcatagaaattgtagaacccggtctccagacctgtggacatttcagattatgacatccca	3720
Db	3845	ctctttcatagaaattgtagaacccggtctccagacctgtggacatttcagattatgacatccca	3904
QY	3721	gagacgacaccttgaaagaataatctccctaaagctgtgcccgaagaagatgtgggtgtgattgtgag	3780
Db	3905	gagacgacaccttgaaagaataatctccctaaagctgtgcccgaagaagatgtgggtgtgattgtgag	3964
QY	3781	acctcaagatgttacctgttcccgcaagaagcaagacagcgggctcttcgggggacaagaagacg	3840
Db	3965	acctcaagatgttacctgttcccgcaagaagcaagacagcgggctcttcgggggacaagaagacg	4024

QY 3841 tgcctccgcctcactgaagatgatgctgctgcatcccaatgattcttgacatagacca 3900
|||||
Db 4025 tgcctccgcctcactgaagatgatgctgcatcccaatgattcttgacatagacca 4084
QY 3901 gaatccagaagacagacttgctcagtgaggatgagcgaaggtctccacagtgtaa 3960
|||||
Db 4085 gaatccagaagacagacttgctcagtgaggatgagcgaaggtctccacagtgtaa 4144
QY 3961 ggcctggaactctacacagcgaacagtttgcccttcttgaggagactgtaattgcc 4020
|||||
Db 4145 ggcctggaactctacacagcgaacagtttgcccttcttgaggagactgtaattgcc 4204
QY 4021 agacgagctcggaagagatttttgcctcagatttctgcagctggtgttgctgatt 4080
|||||
Db 4205 agacgagctcggaagagatttttgcctcagatttctgcagctggtgttgctgatt 4264
QY 4081 ggccttgctcagcctgcatcgtgccaaccccttggccaagtaccacagcctggaactcag 4140
|||||
Db 4265 ggccttgctcagcctgcatcgtgccaaccccttggccaagtaccacagcctggaactcag 4324
QY 4141 cccctggaatgtaacagcgaacagtaacacttggtaagaatgtaagtccttgagacagga 4200
|||||
Db 4325 cccctggaatgtaacagcgaacagtaacacttggtaagaatgtaagtccttgagacagga 4384
QY 4201 accctggaactcttaacagcctcacaacaaagaccctggtctcggaacccctgtatggaa 4260
|||||
Db 4385 accctggaactcttaacagcctcacaacaaagaccctggtctcggaacccctgtatggaa 4444
QY 4261 ggaaccccaatcccaagacacgcccctgcagcgagggaggaagatggaacactgtccca 4320
|||||
Db 4445 ggaaccccaatcccaagacacgcccctgcagcgagggaggaagatggaacactgtccca 4504
QY 4321 gtcccccagacacatcagacccctcctccagaatgggaacccggaactggaacccctta 4380
|||||
Db 4505 gtcccccagacacatcagacccctcctccagaatgggaacccggaacccctta 4564
QY 4381 cctgcatgacagatgtagcagcgacgaacaaatcaagaagatgctgcctatggtcccccaggg 4440
|||||
Db 4565 cctgcatgacagatgtagcagcgacgaacaaatcaagaagatgctgcctatggtcccccaggg 4624
QY 4441 ggaagggggctgctcctccacaagaagaacaaacacacgacgatactcctcagaacctg 4500
|||||
Db 4625 ggaagggggctgctcctccacaagaagaacaaacacacgacgatactcctcagaacctg 4684
QY 4501 acaggaagaacacatcctcgatattctggtgaagacgtatgtagacatcagaacaaagc 4560
|||||
Db 4685 acaggaagaacacatcctcgatattctggtgaagacgtatgtagacatcagaacaaagc 4744
QY 4561 ttaagaacaaagatcctgggtgaatgagtttagttagtcgagcttccctgggtgtagt 4620
|||||
Db 4745 ttaagaacaaagatcctgggtgaatgagtttagttagtcgagcttccctgggtgtagt 4804
QY 4621 aatactcaagcactcctcccgatcaagaagttaatgtagcatcaaaaatggaagaa 4680
|||||
Db 4805 aatactcaagcactcctcccgatcaagaagttaatgtagcatcaaaaatggaagaa 4864
QY 4681 caactaagaactggccaaggaacgttctgcagatcgatttccaagacttgggaagatt 4740
|||||
Db 4865 caactaagaactggccaaggaacgttctgcagatcgatttccaagacttgggaagatt 4924
QY 4741 atgacagagctggacacccgaagaataatgctgaggtggttaataaagaagcctgcat 4800
|||||
Db 4925 atgacagagctggacacccgaagaataatgctgaggtggttaataaagaagcctgcat 4984
QY 4801 gcaatcagctcttccctgaatgctatcaacaatgcatcttcccgccgaactcgtgaagaa 4860
|||||
Db 4985 gcaatcagctcttccctgaatgctatcaacaatgcatcttcccgccgaactcgtgaagaa 5044
QY 4861 ggaaggaacccctagcattatggaattactgttccaatccctcgtgaatccaag 4920
|||||
Db 5045 ggaaggaacccctagcattatggaattactgttccaatccctcgtgaatccaag 5104
QY 4921 cagcagctctcagagtggtctgtagccacatcagtgatgctctgttccaatcgt 4980
|||||

Db 5105 cagcagctctcagagtggtctcgtatgacacacatcagtgatgctctgttccaatcgt 5164
QY 4981 gtaactcttgcaatgctcctccgcagcgaacttctgctgattcttcgaatcagaagcgg 5040
|||||
Db 5165 gtaactcttgcaatgctcctccgcagcgaacttctgctgattcttcgaatcagaagcgg 5224
QY 5041 gtaagaagaacgaacacccctgacttcaatcagtggaagtggaacccgtcatcagctc 5100
|||||
Db 5225 gtaagaagaacgaacacacccctgacttcaatcagtggaagtggaacccgtcatcagctc 5284
QY 5101 tctaatttgcctggtgaatgtaacatgaatgctgctccctgcacaactggtcatatc 5160
|||||
Db 5285 tctaatttgcctggtgaatgtaacatgaatgctgctccctgcacaactggtcatatc 5344
QY 5161 ttaactgctcccaagaagaatcctatgctgctcccaacactgcccgtgctgagccct 5220
|||||
Db 5345 ttaactgctcccaagaagaatcctatgctgctcccaacactgcccgtgctgagccct 5404
QY 5221 ctaacttggctgtaagtggtgtaacatcacaactcactgtaacccagcctccttggcttc 5280
|||||
Db 5405 ctaacttggctgtaagtggtgtaacatcacaactcactgtaacccagcctccttggcttc 5464
QY 5281 aagatccccaagacagcctatggtggtgctcaacagcgtgaaactcttcattggcaaat 5340
|||||
Db 5465 aagatccccaagacagcctatggtggtgctcaacagcgtgaaactcttcattggcaaat 5524
QY 5341 ggaacgctggaacaccccttgcctgtagctgttccacccaataagcgtgaataatataat 5400
|||||
Db 5525 ggaacgctggaacaccccttgcctgtagctgttccacccaataagcgtgaataatataat 5584
QY 5401 gatacctggaagtcggttcttgatctcccaacttggctggaagagggctc 5460
|||||
Db 5585 gatacctggaagtcggttcttgatctcccaacttggctggaagagggctc 5644
QY 5461 gacatggtgaacaaacagcgaatgctgtagtcccttggaagaagtttggggagaaactgtt 5520
|||||
Db 5645 gacatggtgaacaaacagcgaatgctgtagtcccttggaagaagtttggggagaaactgtt 5704
QY 5521 gttcaacatatacttgggaacttggtggaagaaactcttcgcaagcgtggaaggg 5580
|||||
Db 5705 gttcaacatatacttgggaacttggtggaagaaactcttcgcaagcgtggaaggg 5764
QY 5581 gttggttcttccctcattactggtctgataccagaatgatttcttcaacagccagacct 5640
|||||
Db 5765 gttggttcttccctcattactggtctgataccagaatgatttcttcaacagccagacct 5824
QY 5641 gtaaatggaagctatacctcctcgtgaatgaatgaatgaatgtagcggggaagacag 5700
|||||
Db 5825 gtaaatggaagctatacctcctcgtgaatgaatgaatgaatgtagcggggaagacag 5884
QY 5701 agaatcttggatggtggaagcgaagaatgataccttagaatacagaagatgtgacgaagata 5760
|||||
Db 5885 agaatcttggatggtggaagcgaagaatgataccttagaatacagaagatgtgacgaagata 5944
QY 5761 tataagaagaagcgaagcctgctgctgacagaagatttgcctgggacattcctccctgtgag 5820
|||||
Db 5945 tataagaagaagcgaagcctgctgctgacagaagatttgcctgggacattcctccctgtgag 6004
QY 5821 tgccttgggctcctgggaagttaatgaggctggaataatcaatcaacttccaagtgttaaca 5880
|||||
Db 6005 tgccttgggctcctgggaagttaatgaggctggaataatcaatcaacttccaagtgttaaca 6064
QY 5881 ggaatataccactgttaccagaagagatgcttctccttaacaaatagtgtatataaac 5940
|||||
Db 6065 ggaatataccactgttaccagaagagatgcttctccttaacaaatagtgtatataaac 6124
QY 5941 atccatgaagtatacagaaacatggaatgctgctcctcagtttgaatgcatcaacagctg 6000
|||||
Db 6125 atccatgaagtatacagaaacatggaatgctgctcctcagtttgaatgcatcaacagctg 6184
QY 6001 ttgactggggaagaacacggtggaagttccttggccctttagagagagtcaccaagaagaa 6060
|||||

```

Db 6185 ttgactggagagaaacagtgagltcttcccttttgagagaggtccagagaaagaa 6244
Qy 6061 gttgcaaggttctgtgagtgagtcgaactggcctcgtagaagtagtgagaaaa 6120
Db 6245 gttgcaaggttctgtgagtgagtcgaactggcctcgtagaagtagtgagaaaa 6304
Qy 6121 tatgctgtaactatagtgagagcaaaagcaagctctctacagagcattgtatc 6180
Db 6305 tatgctgtaactatagtgagagcaaaagcaagctctctacagagcattgtatc 6364
Qy 6181 gggggggccctcggtgtgtcttgtagtaaacccacagagatgagatcccaagccgg 6240
Db 6365 gggggggccctcggtgtgtcttgtagtaaacccacagagatgagatcccaagccgg 6424
Qy 6241 cggctcttgtagaattgtgacctaaagtgtgtcaagagagggagagtagtgcttaca 6300
Db 6425 cggctcttgtagaattgtgacctaaagtgtgtcaagagagggagagtagtgcttaca 6484
Qy 6301 tctcaatagtagaagaatgtgaagctcttgtagtaaacccacagagatgagatcccaagccgg 6360
Db 6485 tctcaatagtagaagaatgtgaagctcttgtagtaaacccacagagatgagatcccaagccgg 6544
Qy 6361 aggttcaggtgcttgtagcaggtgtccagacatctaaataaggttgtagatgtatataca 6420
Db 6545 aggttcaggtgcttgtagcaggtgtccagacatctaaataaggttgtagatgtatataca 6604
Qy 6421 atagttgtagaataagcaaggtgtccaaacccgagctgtagagctgtccagatcttcttga 6480
Db 6605 atagttgtagaataagcaaggtgtccaaacccgagctgtagagctgtccagatcttcttga 6664
Qy 6481 ctgtgctcttgtagaaggtgtcttaaaagagaaacacccgagacatgtagaataacagctt 6540
Db 6665 ctgtgctcttgtagaaggtgtcttaaaagagaaacacccgagacatgtagaataacagctt 6724
Qy 6541 ccatctcatatctctctgtagcagatattcagatcctctccagagcaaaagcga 6600
Db 6725 ccatctcatatctctctgtagcagatattcagatcctctccagagcaaaagcga 6784
Qy 6601 ctccacataagaagactctgttcttcagacacacacttgacaaatatttgtaactt 6660
Db 6785 ctccacataagaagactctgttcttcagacacacacttgacaaatatttgtaactt 6844
Qy 6661 gccaaagagcaaaatgtagtgaaccacttaaaagacotcattacacaaaacagagaca 6720
Db 6845 gccaaagagcaaaatgtagtgaaccacttaaaagacotcattacacaaaacagagaca 6904
Qy 6721 gtagtgaagctgtgagttctacacattcttctacagagatgagaagtgagaagctat 6780
Db 6905 gtagtgaagctgtgagttctacacattcttctacagagatgagaagtgagaagctat 6964
Qy 6781 gtagtgaagctgtgagttctacacattcttctacagagatgagaagtgagaagctat 6840
Db 6965 gtagtgaagctgtgagttctacacattcttctacagagatgagaagtgagaagctat 6988

```

RESULT 12

AA506121 standard; cDNA; 9854 BP.

AA506121:

12-SEP-2001 (first entry)

Human ABC1 DNA sequence #2.

Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;

cardiovascular; neurological; Tangier disease; LCAT deficiency;

lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.

Homo sapiens.

Key Location/Qualifiers

298..7078

```

FT      /tag= a
ET      /product= "Human ABC1 protein"
XX      WO200130848-A2.
XX      03-MAY-2001.
XX      26-OCT-2000; 2000MO-EP10886.
XX      26-OCT-1999; 99EP-0402668.
XX      01-MAR-2000; 2000US-0186260.
XX      (AVENTIS PHARMA SA.
XX      Denelle P, Rosier-Montus M, Arnaud-Reguigne I, Prades C, Naudin L;
XX      Lemoine C, Duvenger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;
XX      Dean M;
XX      WPI: 2001-316327/33.
XX      P-PSDB; AAU02176.
XX      New human ABC1 nucleic acids and polypeptides for treating
XX      atherosclerosis, malaria and diabetes -
XX      Claim 1: Page 209-213; 368pp; English.
XX      The sequence represents the coding sequence #2 of human ABC1. The
XX      nucleic acid sequence, primers and probes derived from the ABC1 sequence,
XX      and polypeptides and vectors are useful for the prevention of
XX      atherosclerosis, in a subject affected by a dysfunction in the reverse
XX      transport of cholesterol. The polypeptide encoded by the ABC1 gene is
XX      useful for screening for an active ingredient for the prevention or
XX      treatment of a disease resulting from dysfunction in the reverse
XX      transport of cholesterol. The nucleic acids and polypeptides are also
XX      useful for treating and preventing cardiovascular and neurological
XX      pathologies, and other diseases e.g. Tangier disease, lecithin-
XX      cholesterol (LCAT) deficiency, malaria and diabetes.
XX      Sequence 9854 BP; 2665 A; 2219 C; 2334 G; 2635 T; 1 other:
SQ
Query Match      99.7%; Score 6784.8; DB 22; Length 9854;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6792; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 1 atggctgttgagctcagctgaggtgtgtgtgtggaagaacctcacttcagagaaga 60
Db 298 atggctgttgagctcagctgaggtgtgtgtgtggaagaacctcacttcagagaaga 357
Qy 61 caaacatgtcagctgttactggaagtgagctgtgctctatattcttctgtatcgtatc 120
Db 358 caaacatgtcagctgtgctggaagtgagctgtgctctatattcttctgtatcgtatc 417
Qy 121 tctgttgagctgagctacacacacacacacacacacacacacacacacacacacacac 180
Db 418 tctgttgagctgagctacacacacacacacacacacacacacacacacacacacacac 477
Qy 181 atgcccctgaggaacacactctcttggtgtcaggggtatctgttaatgccaaacccc 240
Db 478 atgcccctgaggaacacactctcttggtgtcaggggtatctgttaatgccaaacccc 537
Qy 241 tgttcgtagccgagctcctggtgagagctcccgaggtgttggaaactttaacaatcc 300
Db 538 tgttcgtagccgagctcctggtgagagctcccgaggtgttggaaactttaacaatcc 597
Qy 301 atgtgagctgcgtgtctgagatgagctcgagaggtctttatcacagccagaagacacc 360
Db 598 atgtgagctgcgtgtctgagatgagctcgagaggtctttatcacagccagaagacacc 657
Qy 361 agcatgaagagatgagcaagttctgagaacattacagcagatcaagaatccagctaca 420
Db 658 agcatgaagagatgagcaagttctgagaacattacagcagatcaagaatccagctaca 717

```


Db	2878	accgaagctcactggtgttctggccgaggaagtgatgtagaagagccaccctgtgtccaaacag	2937
Oy	2641	aagaagatgctagaacatctcatgtagaaggaacccaccacttgaaagcttgagctgtgtcc	2700
Db	2938	aagagatatacgaacatctcatgtagagaggaacccaccacttgaaagcttgagctgtgtcc	2997
Oy	2701	atcagaacactgtgtaaaagctctacagagatgagatgaaggttgagcttgatgtgcttgca	2760
Db	2998	atcagaacactgtgtaaaagctctacagagatgagatgaaggttgagcttgatgtgcttgca	3057
Oy	2761	ctgaaattttttatggggccagatcaactctctctctctggccacaatgagagcgaggaaagag	2820
Db	3058	ctgaaattttttatggggccagatcaactctctctctctggccacaatgagagcgaggaaagag	3117
Oy	2821	accacacatgcaatccatgcaacgggtgtgtcccccgaacctccgggacacgcgtctacatccg	2880
Db	3118	accacacatgcaatccatgcaacgggtgtgtcccccgaacctccgggacacgcgtctacatccg	3177
Oy	2881	ggaaaagacatctgcctctcgagatgagacacatcccgagagaacctgggggctgtctcccaag	2940
Db	3178	ggaaaagacatctgcctctcgagatgagacacatcccgagagaacctgggggctgtgtcccaag	3237
Oy	2941	cataaagctgtgctttgacatgctgactgtgtagaagaacacatctgtgtctatgtcccgcttg	3000
Db	3238	cataaagctgtgctttgacatgctgactgtgtagaagaacacatctgtgtctatgtcccgcttg	3297
Oy	3001	aaaagagctctctggagaagcagctgtaagcgcgagatgagatgagcgcggagatgttggt	3060
Db	3298	aaaagagctctctcgaaagacacgctgtaagcgcgagatgagatgagcgcggagatgttggt	3357
Oy	3061	ttgacataaagcaaaagctbtaaaagcaaaacaaagcagctgttcaaggttggaatgacagaaag	3120
Db	3358	ttgacataaagcaaaagctbtaaaagcaaaacaaagcagctgttcaaggttggaatgacagaaag	3417
Oy	3121	ctatctgtgagccttgagccttgtgtcggggagatctaagttgttcattctcgatgtgaacccaca	3180
Db	3418	ctatctgtgagccttgcgcttgtgtcggggagatctaagttgttcattctcgatgtgaacccaca	3477
Oy	3181	gctgtgtgagacccctactcccgccaggggaatagtgagctgtcgtcgtcgtgaatataccgacaa	3240
Db	3478	gctgtgtgtgagacccctactcccgccaggggaatagtgagctgtcgtcgtcgtgaatataccgacaa	3537
Oy	3241	ggccgacacattatctctctctacacacacatagatgtagaagcagagctcccttggggagag	3300
Db	3538	ggccgacacattatctctctctacacacacatagatgtagaagcagagctcccttggggagag	3597
Oy	3301	attggacataatctccatgtagagagctgtgtcgtgtgtgtggtctccctctttcttaagaac	3360
Db	3598	attggacataatctccatgtagagagctgtgtcgtgtgtgtggtctccctctttcttaagaac	3657
Oy	3361	cagctgtggagacagagctactactcttgacccctgtgtcaagaagaatgttgaaatccctccatgt	3420
Db	3658	cagctgtggagacagagctactactcttgacccctgtgtcaagaagaatgttgaaatccctccatgt	3717
Oy	3421	tccttgagaanaaagatgtagacactgtgttcatacctggaanaaaggaagacaggtttcttcag	3480
Db	3718	tccttgagaanaaagatgtagacactgtgttcatacctggaanaaaggaagacaggtttcttcag	3777
Oy	3481	agcaagttctgtagtctgagcccttgagcagcgacatgtagagatgtagacgcgtgacatcgatgtc	3540
Db	3778	agcaagttctgtagtctgagcccttgagcagcgacatgtagagatgtagacgcgtgacatcgatgtc	3837
Oy	3541	tctgtcatctccaactctatcaggaagcattgtgtctgtaagcccggtctgtgtgaagacata	3600
Db	3838	tctgtcatctccaactctatcaggaagcattgtgtctgtaagcccggtctgtgtgaagacata	3897
Oy	3601	gggcatgagctgtgacattgtctgtccatatatgaaagctbtaaaagcgagccctttgtgaa	3660
Db	3898	gggcatgagctgtgacattgtctgtccatatatgaaagctbtaaaagcgagccctttgtgaa	3957
Oy	3661	ctctttcaatgagatgtgataacgggctctctagaacctggggcatcttctaagtatagacatcca	3720
Db	3958	ctctttcaatgagatgtgataacgggctctctagaacctggggcatcttctaagtatagacatcca	4017

XX Human: cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX Homo sapiens.
XX W0200157190-A2.
XX 09-AUG-2001.
XX 05-FEB-2001; 2001WO-US04098.
XX 03-FEB-2000; 2000US-0496914.
XX 27-APR-2000; 2000US-0560875.
XX 20-JUN-2000; 2000US-0598075.
XX 19-JUL-2000; 2000US-0620323.
XX 01-SEP-2000; 2000US-0654936.
XX 15-SEP-2000; 2000US-0663561.
XX 20-OCT-2000; 2000US-0693325.
XX 30-NOV-2000; 2000US-0728422.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX WPI; 2001-476283/51.
XX P-PSDB; AAM78550.
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX Claim 1; Page 1086-1096; 6221pp; English.
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78123-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX Sequence 7281 BP; 1831 A; 1773 C; 1915 G; 1762 T; 0 other:
SQ
Query Match 99.7%; Score 6783.2; DB 22; Length 7281;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6791; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
OY 1 atgctgttggtcctcagctgagttgctgtgtggaagaacctcactttcagaagaaga 60
DB 342 atgctgttggtcctcagctgagttgctgtgtggaagaacctcactttcagaagaaga 401
OY 61 caacatgctcagctgttactggaagtgcctgctctattattcttcctgactgctgac 120
DB 402 caacatgctcagctgttactggaagtgcctgctctattattcttcctgactgctgac 461
OY 121 tctgttgctgagctacccaccctatgaaacaatgacatgacatttccaaataagacc 180
DB 462 tctgttgctgagctacccaccctatgaaacaatgacatgacatttccaaataagacc 521
OY 181 atgaccttcaggaacaacttccttgggttcagggaattatctgttaatgccaaacccc 240
|||||

DB 522 atgaccttcaggaacaacttccttgggttcagggaattatctgttaatgccaaacccc 581
OY 241 ttttccgttacccagctcctggtgaggtcccggaatttttgaaacttaacaatcc 300
DB 582 ttttccgttacccagctcctggtgaggtcccggaatttttgaaacttaacaatcc 641
OY 301 atttggtcgtcgtgttttcagatgctcgtgaggtctctttatataccagaagaacacc 360
DB 642 atttggtcgtcgtgttttcagatgctcgtgaggtctctttatataccagaagaacacc 701
OY 361 agcatgaagaagacatgcgaagaattctggaacattacagcagatcaagaatccagctca 420
DB 702 agcatgaagaagacatgcgaagaattctggaacattacagcagatcaagaatccagctca 761
OY 421 aacttgaagcttcaagatttctgtgtggaacaatgaacaactctgtggttccatatacc 480
DB 762 aacttgaagcttcaagatttctgtgtggaacaatgaacaactctgtggttccatatacc 821
OY 481 aactctctctcccaagctactgtggaagaatgctggaaggtctgatactctccac 540
DB 822 aactctctctcccaagctactgtggaagaatgctggaaggtctgatactctccac 881
OY 541 aaggtatttttgcaaggtctacagttacatttgacaagctgtgtcaatgtatcaaatca 600
DB 882 aaggtatttttgcaaggtctacagttacatttgacaagctgtgtcaatgtatcaaatca 941
OY 601 gaagagatgatacactgtgtggaagaagaatttctgaggttttgggtctcaagaagag 660
DB 942 gaagagatgatacactgtgtggaagaagaatttctgaggttttgggtctcaagaagag 1001
OY 661 aacttgctgcagcagagagatgactgtgttccaacatgagacatctctgaacatccctg 720
DB 1002 aacttgctgcagcagagagatgactgtgttccaacatgagacatctctgaacatccctg 1061
OY 721 agaacataactctacatctccctcccgagcagagagctgtgagccacaataaaca 780
DB 1062 agaacataactctacatctccctcccgagcagagagctgtgagccacaataaaca 1121
OY 781 ttctcgtatgcttcttgagctcctggtccagagctgttcaagatgagaagctgtgagctac 840
DB 1122 ttctcgtatgcttcttgagctcctggtccagagctgttcaagatgagaagctgtgagctac 1181
OY 841 atgcgaagaggtgtgatttctgacaaatgtgaacagctccagctctccacccaatcc 900
DB 1182 atgcgaagaggtgtgatttctgacaaatgtgaacagctccagctctccacccaatcc 1241
OY 901 taccaggtgtgtcctgatttctgtcgcgggcatcccgagggagggggtctgagaagtcag 960
DB 1242 taccaggtgtgtcctgatttctgtcgcgggcatcccgagggagggggtctgagaagtcag 1301
OY 961 tctctcaactggtatgagacaacaactacaagccctcttggaggtcaatgtgactgag 1020
DB 1302 tctctcaactggtatgagacaacaactacaagccctcttggaggtcaatgtgactgag 1361
OY 1021 gaagatgctgaacactctctatgacaactctacaaccccttactgcaatgattgtgag 1080
DB 1362 gaagatgctgaacactctctatgacaactctacaaccccttactgcaatgattgtgag 1421
OY 1081 aatttgaggtctgattctcttcccgatctatctggaagctctggaagcgtctgctgtt 1140
DB 1422 aatttgaggtctgattctcttcccgatctatctggaagctctggaagcgtctgctgtt 1481
OY 1141 ggaagaatctcttatacactgacatccagcacaaggtctatgctgtgagtgaac 1200
DB 1482 ggaagaatctcttatacactgacatccagcacaaggtctatgctgtgagtgaac 1541
OY 1201 aagacattccaggaagctcgtgttccatgactctggaaggtctggtggaaggaactcaac 1260
DB 1542 aagacattccaggaagctcgtgttccatgactctggaaggtctggtggaaggaactcaac 1601
OY 1261 cccaagatctgaccttcattggaagaacagcagaagaatgtgacctgtccgagtgtgtt 1320
DB 1602 cccaagatctgaccttcattggaagaacagcagaagaatgtgacctgtccgagtgtgtt 1661
|||||

QY 1321 gacagcagggacaatgacacacattttgggaacagcagtttgatggtcttaagtggagacgc 1380
|||||
Db 1662 gacagcagggacaatgacacacattttgggaacagcagtttgatggtcttaagtggagacgc 1721
QY 1381 caagacatctgtgctgtttttggccaagcacccagagagatgctcagctcagtaagtgttct 1440
|||||
Db 1722 caagacatctgtgctgtttttggccaagcacccagagagatgctcagctcagtaagtgttct 1781
QY 1441 gtttacaacttgagagaagcttccaacagactaaccaagccaatcccgacacatctgcg 1500
|||||
Db 1782 gtttacaacttgagagaagcttccaacagactaaccaagccaatcccgacacatctgcg 1841
QY 1501 ttcatgagatgtgtcaaccttgaaacagcttagaaccatagccaacgaanaatcgtgcctac 1560
|||||
Db 1842 ttcatgagatgtgtcaaccttgaaacagcttagaaccatagccaacgaanaatcgtgcctac 1901
QY 1561 aacaagtccaatgagagctgtgagatgagagaagttctgtgctgtgtatgtgttcaactgga 1620
|||||
Db 1902 aacaagtccaatgagagctgtgagatgagagaagttctgtgctgtgtatgtgttcaactgga 1961
QY 1621 attactccagcagcagcttagagctgtgcctccatctatgtcaagtacaagaatccgaatgacatc 1680
|||||
Db 1962 attactccagcagcagcttagagctgtgcctccatctatgtcaagtacaagaatccgaatgacatc 2021
QY 1681 gacaatgtgagagagacaataaataacaggaatgaggtactgtggagacccctgtctcagact 1740
|||||
Db 2022 gacaatgtgagagagacaataaataacaggaatgaggtactgtggagacccctgtctcagact 2081
QY 1741 gacccctttgagagacatgtggtatcgtctgaggggcttgcctactctgacagatgtgtg 1800
|||||
Db 2082 gacccctttgagagacatgtggtatcgtctgaggggcttgcctactctgacagatgtgtg 2141
QY 1801 gggcagagcaatcatcagagctgtctgacggcagccggaagaacagtggttcatatgtgaa 1860
|||||
Db 2142 gggcagagcaatcatcagagctgtctgacggcagccggaagaacagtggttcatatgtgaa 2201
QY 1861 cagatgacctatccctgttgaactgtatgacatcttctgtcgggtgtatgagccgtgtcaatg 1920
|||||
Db 2202 cagatgacctatccctgttgaactgtatgacatcttctgtcgggtgtatgagccgtgtcaatg 2261
QY 1921 cccctcttcatgagcctgtgcctgagtttactacagtgagctgtgtatcatcaagaagcagctg 1980
|||||
Db 2262 cccctcttcatgagcctgtgcctgagtttactacagtgagctgtgtatcatcaagaagcagctg 2321
QY 1981 tatgagaaggaagcagcgtctgaaagaacacatgcgacatcatgagcctgtgacaacagcata 2040
|||||
Db 2322 tatgagaaggaagcagcgtctgaaagaacacatgcgacatcatgagcctgtgacaacagcata 2381
QY 2041 cctctgtttagctgtgttcaattagtagcctcatctcctctctgtgtgagcgtgcgctgcta 2100
|||||
Db 2382 cctctgtttagctgtgttcaattagtagcctcatctcctctctgtgtgagcgtgcgctgcta 2441
QY 2101 gttgtcatctgaaagttaagaaacctgtgtcctacacagtgatctccaaaggtgtgtttgtc 2160
|||||
Db 2442 gttgtcatctgaaagttaagaaacctgtgtcctacacagtgatctccaaaggtgtgtttgtc 2501
QY 2161 ttctcgttcgt 2220
|||||
Db 2502 ttctcgttcgt 2561
QY 2221 tccagagaacacactgagcagcagcctgtgagggacatcatcttcaacagctgttactctccc 2280
|||||
Db 2562 tccagagaacacactgagcagcagcctgtgagggacatcatcttcaacagcgtgttactctccc 2621
QY 2281 taagtctgt 2340
|||||
Db 2622 taagtctgt 2681
QY 2341 ctgctgtctcctgt 2400
|||||
Db 2682 ctgctgtctcctgt 2741

QY 2401 ggcattggagtgcaagtggagacaacctgtttgagagctcctgtggaaggaatggtcttcaat 2460
|||||
Db 2742 ggcattggagtgcaagtggagacaacctgtttgagagctcctgtggaaggaatggtcttcaat 2801
QY 2461 ctcaacacattgcatctccatgatagtctgttttgaacacctctctatctgtgtgtgtgtgtgtgtgt 2520
|||||
Db 2802 ctcaacacattgcatctccatgatagtctgttttgaacacctctctatctgtgtgtgtgtgtgtgtgt 2861
QY 2521 tacatttgagctgtctcttccagcagataggaatctccaaagccctgtgttttctctgtc 2580
|||||
Db 2862 tacatttgagctgtctcttccagcagataggaatctccaaagccctgtgttttctctgtc 2921
QY 2581 accaagtctcactgt 2640
|||||
Db 2922 accaagtctcactgt 2981
QY 2641 aaggaatgtcaagaatcttgataggaaggaaccccaacttgaagctgtggtgtgtc 2700
|||||
Db 2982 aaggaatgtcaagaatcttgataggaaggaaccccaacttgaagctgtggtgtgtc 3041
QY 2701 attcagaacctgtgtataaagtctaacgagatggaatggaagggtgtgtgtgtgtgtgtgtgtgtgtgtgt 2760
|||||
Db 3042 attcagaacctgtgtataaagtctaacgagatggaatggaagggtgtgtgtgtgtgtgtgtgtgtgtgtgt 3101
QY 2761 ctggaattttatgaggggccaagatcactctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2820
|||||
Db 3102 ctggaattttatgaggggccaagatcactctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3161
QY 2821 accacacatgtcaaatccctgagccgggtgttctcccccagccctcggagcccgctacatctgt 2880
|||||
Db 3162 accacacatgtcaaatccctgagccgggtgttctcccccagccctcggagcccgctacatctgt 3221
QY 2881 ggaataaagacatctgctctgtgagatgagacacatcccgagacaacctgtgtgtgtgtgtgtgtgtgt 2940
|||||
Db 3222 ggaataaagacatctgctctgtgagatgagacacatcccgagacaacctgtgtgtgtgtgtgtgtgtgt 3281
QY 2941 cataagctgt 3000
|||||
Db 3282 cataagctgt 3341
QY 3001 aaagggctctctgtgagaagcagctgtgaaagcgtgagatgagacagatactgtgacctgtgtgtgtgt 3060
|||||
Db 3342 aaagggctctctgtgagaagcagctgtgaaagcgtgagatgagacagatactgtgacctgtgtgtgtgt 3401
QY 3061 ttgcacatcaagcagcgtctgaaagaacaaacagccacgtctcaggtgtgaaatgcagagaaga 3120
|||||
Db 3402 ttgcacatcaagcagcgtctgaaagaacaaacagccacgtctcaggtgtgaaatgcagagaaga 3461
QY 3121 ctatctgtgacctgt 3180
|||||
Db 3462 ctatctgtgacctgt 3521
QY 3181 gctgt 3240
|||||
Db 3522 gctgt 3581
QY 3241 ggcgcgacacatctatctctctacacacacatggaatggaagcggaagctctctgtgaaataacgacaa 3300
|||||
Db 3582 ggcgcgacacatctatctctctacacacacatggaatggaagcggaagctctctgtgaaataacgacaa 3641
QY 3301 attgcacatactccacatgaggaagctgt 3360
|||||
Db 3642 attgcacatactccacatgaggaagctgt 3701
QY 3361 cagctgtggaacagcgtctacactcagcctgt 3420
|||||
Db 3702 cagctgtggaacagcgtctacactcagcctgt 3761
QY 3421 tccctgagaagaagatgagacagctgtgtcatatcctgtgaaagaaggaagcgtgttctcag 3480
|||||
Db 3762 tccctgagaagaagatgagacagctgtgtcatatcctgtgaaagaaggaagcgtgttctcag 3821
QY 3481 agcagttctcgt 3540

|||||
Db 3822 agcagttcgtatcgtgccttggcagcgacatagatgacacgcctgacatcgtatc 3881
QY 3541 tctgtatctccaacctatcaaggagatgtgtctgaagcccgctgggtgaaacata 3600
Db 3882 tctgtatctccaacctatcaaggagatgtgtctgaagcccgctgggtgaaacata 3941
QY 3601 gggcatgagctgacatgtgtctgcataatgaagctgctaaggagggagccttgtgaa 3660
Db 3942 gggcatgagctgacatgtgtctgcataatgaagctgctaaggagggagccttgtgaa 4001
QY 3661 ctcttcatagaattgtagacggcgtctccagacctgggcatcttctagtatgacatca 3720
Db 4002 ctcttcatagaattgtagacggcgtctccagacctgggcatcttctagtatgacatca 4061
QY 3721 gagaagaccttggaagaattctctcaagtgccgaagagtgagggtgtagatcgtag 3780
Db 4062 gagaagaccttggaagaattctctcaagtgccgaagagtgagggtgtagatcgtag 4121
QY 3781 acctcagatgtagccttgcagcaagacgaaacaggcggtccctcggggacagcagagc 3840
Db 4122 acctcagatgtagccttgcagcaagacgaaacaggcggtccctcggggacagcagagc 4181
QY 3841 tgtcttcgcccgttcaactgaatgtagtctgtgtaacaaatgattctgacatgaccca 3900
Db 4182 tgtcttcgcccgttcaactgaatgtagtctgtgtaacaaatgattctgacatgaccca 4241
QY 3901 gaatccagagagacagactgtctcagtgagatgtagtggaagaaggctctaccaggtgaa 3960
Db 4242 gaatccagagagacagactgtctcagtgagatgtagtggaagaaggctctaccaggtgaa 4301
QY 3961 ggtctggaacttacaagacaagatttggccttggtagaagaagctgtaattcc 4020
Db 4302 ggtctggaacttacaagacaagatttggccttggtagaagaagctgtaattcc 4361
QY 4021 agacggagtcggaagaatttcttgctcagatgtctctgcagcgtgtgttctgtcatc 4080
Db 4362 agacggagtcggaagaatttcttgctcagatgtctctgcagcgtgtgttctgtcatc 4421
QY 4081 ggccttgtgtcagcctgtatcgtgcacaccttggcaagtaaccagcctgtgaattcag 4140
Db 4422 ggccttgtgtcagcctgtatcgtgcacaccttggcaagtaaccagcctgtgaattcag 4481
QY 4141 cccctgtagtgaacaagacgtagacattgttcaagaatgtagtccctgaagacacggga 4200
Db 4482 cccctgtagtgaacaagacgtagacattgttcaagaatgtagtccctgaagacacggga 4541
QY 4201 accctggaactcttaaacgacctcaaccaagacctggtctcgggagcccgctgtatgaa 4260
Db 4542 accctggaactcttaaacgacctcaaccaagacctggtctcgggagcccgctgtatgaa 4601
QY 4261 ggaaaacccaatcccagacaagccttgcagcgcaaggaggaagagtgagccactcccca 4320
Db 4602 ggaaaacccaatcccagacaagccttgcagcgcaaggaggaagagtgagccactcccca 4661
QY 4321 gtccccaagacatcatgtagcctctccagaaatgtagaactgtagcaaatgtagaacccttca 4380
Db 4662 gtccccaagacatcatgtagcctctccagaaatgtagaactgtagcaaatgtagaacccttca 4721
QY 4381 cctgtatgcagtgtagcagcgacaataatcaagaagaatgctgcctgtgtgtccccaagg 4440
Db 4722 cctgtatgcagtgtagcagcgacaataatcaagaagaatgctgcctgtgtgtccccaagg 4781
QY 4441 gcaagggggggtcgtcctctccacaagaagaacaacatcagatatccctccagagccgtg 4500
Db 4782 gcaagggggggtcgtcctctccacaagaagaacaacatcagatatccctccagagccgtg 4841
QY 4501 acaggaagaacaacatttcggaattatctgtggaagacglatgtgcagatcatalagccaaagc 4560
Db 4842 acaggaagaacaacatttcggaattatctgtggaagacglatgtgcagatcatalagccaaagc 4901
QY 4561 ttaagaagaagatcctgggtgaatggaattagatgtatggtggtcttccctgggtgtcagt 4620
|||||

Db 4902 ttaagaagaagatcctgggtgtagatgatttagtgaatggtggtccttccctgggtgtcagt 4961
QY 4621 aataactaaagcaactctcctccaggtcaagaagttaattatgccaaccaaaatgaagaagaa 4680
Db 4962 aataactaaagcaactctcctccaggtcaagaagttaattatgccaaccaaaatgaagaagaa 5021
QY 4681 cccctaaagcttgccaagaagacagctctgcagatcgattctcccaacagcttgggaagattc 4740
Db 5022 cccctaaagcttgccaagaagacagctctgcagatcgattctcccaacagcttgggaagattc 5081
QY 4741 atgacagagactggaacacagaataatgtlcaaggtgtgtgtlcaataaacaagggtgcgat 4800
Db 5082 atgacagagactggaacacagaataatgtlcaaggtgtgtgtlcaataaacaagggtgcgat 5141
QY 4801 gcaatcagctcttccctgaatgtcatlcaacaatgccaattctccgggccaactgcaagaag 4860
Db 5142 gcaatcagctcttccctgaatgtcatlcaacaatgccaattctccgggccaactgcaagaag 5201
QY 4861 ggaagaaaccttagacatattgaaattactgtcttcaatctcaatccctgaatccacaag 4920
Db 5202 ggaagaaaccttagacatattgaaattactgtcttcaatctcaatccctgaatccacaag 5261
QY 4921 cagcagctctcagaaggtggtctgtatgaccacatcagtgatgttccctgtgtccatctgt 4980
Db 5262 cagcagctctcagaaggtggtctgtatgaccacatcagtgatgttccctgtgtgtccatctgt 5321
QY 4981 gtatcttggcaatgtccttgcctccagccagccttgtcgtatctccatccagagagcg 5040
Db 5322 gtatcttggcaatgtccttgcctccagccagccttgtcgtatctccatccagagagcg 5381
QY 5041 gtccagcaagcaaaaacaccttgagttcatlcaacagtggaagtgaagcctgtcatcactggtc 5100
Db 5382 gtccagcaagcaaaaacaccttgagttcatlcaacagtggaagtgaagcctgtcatcactggtc 5441
QY 5101 tccaatttggctcgggataatgtgcaaatcagttgtccctgcgcaacatggtatataatc 5160
Db 5442 tccaatttggctcgggataatgtgcaaatcagttgtccctgcgcaacatggtatataatc 5501
QY 5161 ttcatctgctccagcagaagttccatgtgtctcccaaccaatctgctgtgtagccctt 5220
Db 5502 ttcatctgctccagcagaagttccatgtgtctcccaaccaatctgctgtgtagccctt 5561
QY 5221 ctacttctgtatgtgtgtgtatcaatcaactcttcatatgtaaccagcctctgtgtctc 5280
Db 5562 ctacttctgtatgtgtgtgtatcaatcaactcttcatatgtaaccagcctctgtgtctc 5621
QY 5281 aagatccccaagcaagcctatgtgtgtgtccacaagcgtgaaccttcatatgtaaat 5340
Db 5622 aagatccccaagcaagcctatgtgtgtgtccacaagcgtgaaccttcatatgtaaat 5681
QY 5341 ggcagcgtggccaaccttggctgtagagctgttaccgcgaataaagctgaataatcaat 5400
Db 5682 ggcagcgtggccaaccttggctgtagagctgttaccgcgaataaagctgaataatcaat 5741
QY 5401 gatacctgaagtcctgtgtcttcatcttccacatcttggcttggaagaggtctatc 5460
Db 5742 gatacctgaagtcctgtgtcttcatcttccacatcttggcttggaagaggtctatc 5801
QY 5461 gacatgtgtaaaaaacgggaatgagctgtatgccttggaaaggttttggggagatcgctt 5520
Db 5802 gacatgtgtaaaaaacgggaatgagctgtatgccttggaaaggttttggggagatcgctt 5861
QY 5521 ggttcacatattcttggagctgtgtggagagaaacctcttcgcatgtgcgttgaaagg 5580
Db 5862 ggttcacatattcttggagctgtgtggagagaaacctcttcgcatgtgcgttgaaagg 5921
QY 5581 gtgtgttcttccctcatctattgttctgatacagttacagattcttcatcgccagacct 5640
Db 5922 gtgtgttcttccctcatctattgttctgatacagttacagattcttcatcgccagacct 5981
QY 5641 gtaaatcgaagctatctctgtgaatgtagatgaaatgtggaagcttggagcggaagaagcag 5700
Db 5982 gtaaatcgaagctatctctgtgaatgtagatgaaatgtggaagcttggagcggaagaagcag 6041
|||||

QY 5701 agaattcttgatgtgagccgaatgacatcttgaataaacaaggatgacgaagata 5760
 |||||
 Db 6042 agaattcttgatgtgagccgaatgacatcttgaataaacaaggatgacgaagata 6101
 QY 5761 tatagaaggaagcggagcctgctgttgacagattgtgtgacatctctgtgtgag 5820
 |||||
 Db 6102 tatagaaggaagcggagcctgctgttgacagattgtgtgacatctctgtgtgag 6161
 QY 5821 tgccttggcctcctggaggttaattgggctggaataatcatcaattcaagaatgtaaca 5880
 |||||
 Db 6162 tgccttggcctcctggaggttaattgggctggaataatcatcaattcaagaatgtaaca 6221
 QY 5881 gggagataccctgttaccagaagagatgcttctcctaacaataatgataatcaaac 5940
 |||||
 Db 6222 gggagataccctgttaccagaagagatgcttctcctaacaataatgataatcaaac 6281
 QY 5941 atccagaagtatatagaacatgagctactgctcctcagtttgatgcatcacagctg 6000
 |||||
 Db 6282 atccagaagtatatagaacatgagctactgctcctcagtttgatgcatcacagctg 6341
 QY 6001 ttgacttggagagaacacgttgagttcttctgaccttttgaagagagctccagaagaaga 6060
 |||||
 Db 6342 ttgacttggagagaacacgttgagttcttctgaccttttgaagagagctccagaagaaga 6401
 QY 6061 gttggcaaggttgggtgagtgagcagatctcgaaactgggctcgtggaatgagagaanaa 6120
 |||||
 Db 6402 gttggcaaggttgggtgagtgagcagatctcgaaactgggctcgtggaatgagagaanaa 6461
 QY 6121 tatgctggaataatagttgagggcaacaacgaagctctctacagccatgctttgac 6180
 |||||
 Db 6462 tatgctggaataatagttgagggcaacaacgaagctctctacagccatgctttgac 6521
 QY 6181 ggcgggctcctctgtgtgttcttgatgaaccacacagcagatgcatcccaaacccgg 6240
 |||||
 Db 6522 ggcgggctcctctgtgtgttcttgatgaaccacacagcagatgcatcccaaacccgg 6581
 QY 6241 cggttcttgggaattgtgctcctaagtggttgcgaaggagggagatcagtagtctta 6300
 |||||
 Db 6582 cggttcttgggaattgtgctcctaagtggttgcgaaggagggagatcagtagtctta 6641
 QY 6301 tctcatagatggaagaatgtaagctcttgcactagaatgcaatcatggttcaatga 6360
 |||||
 Db 6642 tctcatagatggaagaatgtaagctcttgcactagaatgcaatcatggttcaatga 6701
 QY 6361 aggttcaggtgctcctggcaggtgctcgaacatctaaanaataggttggagatggtataca 6420
 |||||
 Db 6702 aggttcaggtgctcctggcaggtgctcgaacatctaaanaataggttggagatggtataca 6761
 QY 6421 atagttgacgaatagcaggtgacaccccgacctggaagcctgtccagatttcttga 6480
 |||||
 Db 6762 atagttgacgaatagcaggtgacaccccgacctggaagcctgtccagatttcttga 6821
 QY 6481 ctgtcatctctggaagtgttcttaaaagaagaacacccggaacatctcacaatcacagctt 6540
 |||||
 Db 6822 ctgtcatctctggaagtgttcttaaaagaagaacacccggaacatctcacaatcacagctt 6881
 QY 6541 caatttcatatctctcctggcaggaatattcagcatctctccagagagaanaagcga 6600
 |||||
 Db 6882 caatttcatatctctcctggcaggaatattcagcatctctccagagagaanaagcga 6941
 QY 6601 ctccacatagaagactactcgttctcagaacaacttggccaagtattgtgaacttt 6660
 |||||
 Db 6942 ctccacatagaagactactcgttctcagaacaacttggccaagtattgtgaacttt 7001
 QY 6661 gccaaagcacaagtatgatacacttaaaagacactctcattacacaanaacagaga 6720
 |||||
 Db 7002 gccaaagcacaagtatgatacacttaaaagacactctcattacacaanaacagaga 7061
 QY 6721 gtagtgagcgttggcaggtctcacatcttctacagatgagaaagtgaagaagactat 6780
 |||||
 Db 7062 gtagtgagcgttggcaggtctcacatcttctacagatgagaaagtgaagaagactat 7121

QY 6781 gtagagaatctctgttcatacgg 6804
 |||||
 Db 7122 gtagagaatctctgttcatacgg 7145

RESULT 14
 ABA09200
 ID ABA09200 standard; cDNA; 7086 BP.
 XX
 AC ABA09200;
 XX
 DT 11-JAN-2002 (first entry)
 XX
 DE Human ABCA1 homologue-encoding cDNA, SEQ ID NO:976.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; anti-inflammatory;
 KW antiasthmatic; antiarthritis; haemostatic; antiarteriosclerotic;
 KW cytosstatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnerary; antiulcer; ss.
 XX
 XX Homo sapiens.
 OS
 PN W0200157188-A2.
 XX
 PD 09-AUG-2001.
 XX
 PE 05-FEB-2001; 2001WO-US03800.
 XX
 PR 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 XX
 PA (HXSF-) HXSFO INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WP1: 2001-457740/49.
 XX
 PT P-PSDB; ABB11956.
 PT Human proteins and DNA encoding sequences useful for preventing,
 PT treating or ameliorating a medical condition in a mammalian subject
 PT e.g. arthritis and cancer -
 XX
 PS Claim 1; Page 833-835; 1963pp; English.
 XX

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09374 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; haematopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include

QY 4021 agacgagatcggaagatcttctgcatgctgctgacgctgttctgcat 4080
|||||
Db 4324 agacgagatcggaagatcttctgcatgctgctgacgctgttctgcat 4383
QY 4081 gacctgtgtacgctgtacgctgtgacaccccttggcaagtaaccagcctgtgaactcaag 4140
|||||
Db 4384 gacctgtgtacgctgtacgctgtgacaccccttggcaagtaaccagcctgtgaactcaag 4443
QY 4141 cctgtgtatcaacgaaagatcacatctgtcagcatatgctcctcgaggaacaggga 4200
|||||
Db 4444 cctgtgtatcaacgaaagatcacatctgtcagcatatgctcctcgaggaacaggga 4503
QY 4201 acccttgaaactttaagcctccaacgaacccctgtgtcgggaacccgctgtatgaa 4260
|||||
Db 4504 acccttgaaactttaagcctccaacgaacccctgtgtcgggaacccgctgtatgaa 4563
QY 4261 ggaatacccaatcccaagacacgctgtccagcagggaggaagatgagcaactgccca 4320
4564 ggaatacccaatcccaagacacgctgtccagcagggaggaagatgagcaactgccca 4623
QY 4321 gtcccccagcaatcatatgaaactctccaagaatgggaactggacaatgcagaaaccttca 4380
|||||
Db 4624 gtcccccagcaatcatatgaaactctccaagaatgggaactggacaatgcagaaaccttca 4683
QY 4381 cctgtacatgctgtacgagcagcaaaatcaagaagaatgctgtgtgtgtcccccagg 4440
4684 cctgtacatgctgtacgagcagcaaaatcaagaagaatgctgtgtgtgtcccccagg 4743
QY 4441 gcaagggggctgctcctccacaaagaaacaaacacgacagatctccttcaggaactg 4500
|||||
Db 4744 gcaagggggctgctcctccacaaagaaacaaacacgacagatctccttcaggaactg 4803
QY 4501 acaggaagaacattcggatatactgtggaagacgtatgtgcagatacgaacaaagc 4560
|||||
Db 4804 acaggaagaacattcggatatactgtggaagacgtatgtgcagatacgaacaaagc 4863
QY 4561 ttaaaagaacaaagtctgggtgaaatgagtttaagtatggcgcttctccctgggtgtgcat 4620
4864 ttaaaagaacaaagtctgggtgaaatgagtttaagtatggcgcttctccctgggtgtgcat 4923
QY 4621 aatacccaagcaactctcctccagatcaagaagttaatgatgcatacacaacaaatgaaaga 4680
4924 aatacccaagcaactctcctccagatcaagaagttaatgatgcatacacaacaaatgaaaga 4983
QY 4681 caactaaagctggcgaagacagttctgcagatcgatcttccaacagcttgggaagatt 4740
4984 caactaaagctggcgaagacagttctgcagatcgatcttccaacagcttgggaagatt 5043
QY 4741 atgacagagctggacacccgaataatgtcaaggtgtgttcaataacaaaggtgtgcat 4800
5044 atgacagagctggacacccgaataatgtcaaggtgtgttcaataacaaaggtgtgcat 5103
QY 4801 gcaatagcctcttcttgatgatacacaacatgcatctcccgggccaactgcgaaga 4860
5104 gcaatagcctcttcttgatgatacacaacatgcatctcccgggccaactgcgaaga 5163
QY 4861 ggaagaaacccatgacatataatgaatgaatgcttcaatcaatccctgtgaatcacaaga 4920
5164 ggaagaaacccatgacatataatgaatgaatgcttcaatcaatccctgtgaatcacaaga 5223
QY 4921 caagacactcctcagaaggtgtgtgatgacacacatgagttgagttctgttctgcatctt 4980
5224 caagacactcctcagaaggtgtgtgatgacacacatgagttgagttctgttctgcatctt 5283
QY 4981 gtaactcttgcaatgtcctctgtcccaagcagctgtgtcgtatctccgtgtccaggaacgg 5040
5284 gtaactcttgcaatgtcctctgtgtcccaagcagctgtgtcgtatctccgtgtccaggaacgg 5343
QY 5041 gtaacgaagcaaaacacactgcagttcatcatgtgaggtgaagcctgtcatctacgtgttc 5100
5344 gtaacgaagcaaaacacactgcagttcatcatgtgaggtgaagcctgtcatctacgtgttc 5403
Db

QY 5101 tctaatttctgtggaatgataatgaatgaatgtgtccctgtccacactgtgcatatcatc 5160
|||||
Db 5404 tctaatttctgtggaatgataatgaatgaatgtgtccctgtccacactgtgcatatcatc 5463
QY 5161 ttaatctgtctccagcagaagatctctatgtgttcccaacaaatcgtcgtgtgcatagccct 5220
5464 ttaatctgtctccagcagaagatctctatgtgttcccaacaaatcgtcgtgtgcatagccct 5523
QY 5221 ctacttctgtgtatgtgtgttcaatcaacactctcaatgtatccagcctcctgtgtgtc 5280
5524 ctacttctgtgtatgtgtgttcaatcaacactctcaatgtatccagcctcctgtgtgtc 5583
Db 5584 aagatccccagcaacagcctatgt 5643
QY 5341 ggcagcgtgtgcaacactgt 5400
5644 ggcagcgtgtgcaacactgt 5703
QY 5401 gatactcgtgaagctgt 5460
5704 gatactcgtgaagctgt 5763
Db 5461 gacatgtgtgaataacccaagcaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5520
5764 gacatgtgtgaataacccaagcaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5823
QY 5521 gtgtacatatacttctgt 5580
5824 gtgtacatatacttctgt 5883
QY 5581 gt 5640
5884 gt 5943
QY 5641 gtaaatgtcaaaagctatcctcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5700
5944 gtaaatgtcaaaagctatcctcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6003
Db 5701 agaatcttctgt 5760
6004 agaatcttctgt 6063
QY 5761 tataagaagaagcgaagacccgt 5820
6064 tataagaagaagcgaagacccgt 6123
QY 5821 tgccttgggtcctcctgt 5880
6124 tgccttgggtcctcctgt 6183
Db 5881 ggaagataacacatgtatcagaagagatgtcttcttcaacaaatagatatacacaac 5940
6184 ggaagataacacatgtatcagaagagatgtcttcttcaacaaatagatatacacaac 6243
QY 5941 atccatgaagatcatcaaaacatgt 6000
6244 atccatgaagatcatcaaaacatgt 6303
Db 6001 ttgactgtggaagaaacacgt 6060
6304 ttgactgtggaagaaacacgt 6363
QY 6061 gtgtgcaaggt 6120
6364 gtgtgcaaggt 6423
Db 6121 tatgtgtgtatataatgt 6180
6424 tatgtgtgtatataatgt 6483
QY 6181 ggcgggctcctcgt 6240


```

Db      6484  ggcgggacctcctcgtgtgttctcgtatgaaccacacagcagatcccaagcccg 6543
Qy      6241  cggctcttggaattgtgcccctaagtgttcaagagagagagatcaatgagctaca 6300
Db      6544  cggctcttggaattgtgcccctaagtgttcaagagagagagatcaatgagctaca 6603
Qy      6301  tctcatagatggaagaatgaaagctcttgcacatagatgagcaatcagtcaatgga 6360
Db      6504  tctcatagatggaagaatgaaagctcttgcacatagatgagcaatcagtcaatgga 6663
Qy      6361  aggttcaggtccttggaatgagcagatcctcaaaaataggttgagatggtttaca 6420
Db      6664  aggttcaggtccttggaatgagcagatcctcaaaaataggttgagatggtttaca 6723
Qy      6421  atagttgacgaatagcaaggttccaaaccgagcttgaaagctgtccagatcttcttga 6480
Db      6724  atagttgacgaatagcaaggttccaaaccgagcttgaaagctgtccagatcttcttga 6783
Qy      6481  ctggcatttctggaagtgttctaaagaagaacaccgagacattgtacataccgctt 6540
Db      6784  ctggcatttctggaagtgttctaaagaagaacaccgagacattgtacataccgctt 6843
Qy      6541  ccatcttcattatctctcgcgcagagatatacagatcctcctccagagcaaaagcga 6600
Db      6844  ccatcttcattatctctcgcgcagagatatacagatcctcctccagagcaaaagcga 6903
Qy      6601  ctccacataagaactactctgtttctcagaacaacttgacccaatattgtgaactt 6660
Db      6904  ctccacataagaactactctgtttctcagaacaacttgacccaatattgtgaactt 6963
Qy      6661  gccaaagaccaaagtgatgagccacttaaaagacctccattacacaaaacagaca 6720
Db      6964  gccaaagaccaaagtgatgagccacttaaaagacctccattacacaaaacagaca 7023
Qy      6721  gtagtgagcgttgcaagttctacacatcttctcagagatgagaagtgaaagaactat 6780
Db      7024  gtagtgagcgttgcaagttctacacatcttctcagagatgagaagtgaaagaactat 7083
Qy      6781  gta 6783
Db      7084  gta 7086

RESULT 15
AAK52667
ID      AAK52667 standard; cDNA; 7086 BP.
XX
AC      AAK52667;
XX
DT      06-NOV-2001 (first entry)
XX
DE      Human polynucleotide SEQ ID NO 2196.
XX
KW      Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW      vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW      tissue growth factor; immunomodulatory; cancer; leukaemia;
KW      nervous system disorder; arthritis; inflammation; ss.
XX
OS      Homo sapiens.
XX
PN      WO200157190-A2.
XX
PD      09-AUG-2001.
XX
PF      05-FEB-2001; 2001WO-US04098.
XX
PR      03-FEB-2000; 2000US-0496914.
PR      27-APR-2000; 2000US-0560875.
PR      20-JUN-2000; 2000US-0598075.
PR      19-JUL-2000; 2000US-0620325.
PR      01-SEP-2000; 2000US-0654936.
PR      15-SEP-2000; 2000US-0663561.

```

```

PR      20-OCT-2000; 2000US-0693325.
PR      30-NOV-2000; 2000US-0728422.
XX
PA      (HYSE-) HYSEQ INC.
XX
PI      Tang YT, Liu C, Dmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI      Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI      Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR      WPI; 2001-476283/51.
DR      P-PSDB; AAM79534.
XX
PT      Nucleic acids encoding polypeptides with cytokine-like activities,
PT      useful in diagnosis and gene therapy -
XX
PS      Claim 1; Page 4558-4560; 6221pp; English.
XX
CC      The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC      encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC      cytokine, cell proliferation or cell differentiation or which may induce
CC      production of other cytokines in other cell populations. The
CC      polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC      peptide therapy. The polypeptides have various cytokine-like activities,
CC      e.g. stem cell growth factor activity, haematopoiesis regulating
CC      activity, tissue growth factor activity, immunomodulatory activity and
CC      activin/inhibin activity and may be useful in the diagnosis and/or
CC      treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC      inflammation.
CC      Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC      (AAM80020) are omitted as the relevant pages from the sequence listing
CC      were missing at the time of publication.
XX
SQ      Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;

```

```

Query Match      99.4%; Score 6762.2; DB 22; Length 7086;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6770; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy      1  atggcttggcctcagctgaagttgtgtgtggaagaaccctcatcagaagaaga 60
Db      304  atggcttggcctcagctgaagttgtgtgtggaagaaccctcatcagaagaaga 363
Qy      61  caaactgctcagctgttactggaagtggcctgacctattatcttctcgtatcgtatc 120
Db      364  caaactgctcagctgttactggaagtggcctgacctattatcttctcgtatcgtatc 423
Qy      121  tctgttcgctgagctaccacacctatgaacaacatgaatgccatttccaataaagcc 180
Db      424  tctgttcgctgagctaccacacctatgaacaacatgaatgccatttccaataaagcc 483
Qy      181  atgcccctgcaggaacacttcttggtgtcagaggaattatcgttaatgccaacaacccc 240
Db      484  atgcccctgcaggaacacttcttggtgtcagaggaattatcgttaatgccaacaacccc 543
Qy      241  tgttcctgtacccgactcctgaggagagctcccgagttgttgaaacttaacaatcc 300
Db      544  tgttcctgtacccgactcctgaggagagctcccgagttgttgaaacttaacaatcc 603
Qy      301  atttggtcgcctgttctcagatgctcggaggtcttttatatacaccagaagaagacc 360
Db      604  atttggtcgcctgttctcagatgctcggaggtcttttatatacaccagaagaagacc 663
Qy      361  agcatgaagacatgcgcaagttctggaacatctacagacagatcaagaatcagctca 420
Db      664  agcatgaagacatgcgcaagttctggaacatctacagacagatcaagaatcagctca 723
Qy      421  aacttgaagctcaagatctcctgtgtgacaatgaacacttctctggttccatatcac 480
Db      724  aacttgaagctcaagatctcctgtgtgacaatgaacacttctctggttccatatcac 783
Qy      481  aacctctctccaaagtacactgtgacaagaatgcttgagggtgtgcatcttcacac 540

```


Db 784 aacctctctcccaagaatctactgtgacagaatgctgagggctgatactctccac 843
QY 541 aaggaatttggcaaggtaccaggtatattgcaaggtcgtgcaatgatacaaatca 600
Db 844 aaggaatttggcaaggtaccaggtatattgcaaggtcgtgcaatgatacaaatca 903
QY 601 gaagagatgatacaactgtgacccaagaagtcttgagcttctgagcttcccaaggag 660
Db 904 gaagagatgatacaactgtgacccaagaagtcttgagcttctgagcttcccaaggag 963
QY 661 aaactggtcgcagcagcagagacttctgctccaacatgacatccctgaacatccctg 720
Db 964 aaactggtcgcagcagcagagacttctgctccaacatgacatccctgaacatccctg 1023
QY 721 agaaactaaactactactctccctcccgagcaagagcgtgctgaaagcccaaaaaa 780
Db 1024 agaaactaaactactactctccctcccgagcaagagcgtgctgaaagcccaaaaaa 1083
QY 781 ttgctgcatagtcttggaactctgcccagagcgtgttcaagatgagaagcttgagtgac 840
Db 1084 ttgctgcatagtcttggaactctgcccagagcgtgttcaagatgagaagcgtgagtgac 1143
QY 841 atgcagcagagagtgatgttcttgaccaaagtgaacagctccagctccccaacaaatc 900
Db 1144 atgcagcagagagtgatgttcttgaccaaagtgaacagctccagctccccaacaaatc 1203
QY 901 taccagcgtgtgtctcgtatgtctgcgggcatcccgagggagggggtcgtgaatacaag 960
Db 1204 taccagcgtgtgtctcgtatgtctgcgggcatcccgagggagggggtcgtgaatacaag 1263
QY 961 tctcccaactgtgtatgagaacaacaactacaagaacccctcttgagggcaatgagcactag 1020
Db 1264 tctcccaactgtgtatgagaacaacaactacaagaacccctcttgagggcaatgagcactag 1323
QY 1021 gaagatgtcgaacactctatagacaactctacaactctactctgacatgatttgaag 1080
Db 1324 gaagatgtcgaacactctatagacaactctacaactctactctgacatgatttgaag 1383
QY 1081 aatttgaggtctagtcctcttcccgcatctatctgaaagcctgaaacccgtgctgtc 1140
Db 1384 aatttgaggtctagtcctcttcccgcatctatctgaaagcctgaaacccgtgctgtc 1443
QY 1141 gggaagatccgttatacaacttgacactccagcccaagcaggtacatgctgaggttgac 1200
Db 1444 gggaagatccgttatacaacttgacactccagcccaagcaggtacatgctgaggttgac 1503
QY 1201 aagacactccaggaactggtgtgttccatgatactgaaagcagatgtggaggaactcagc 1260
Db 1504 aagacactccaggaactggtgtgttccatgatactgaaagcagatgtggaggaactcagc 1563
QY 1261 cccaagatctggaactcttatgagaagaacccaagaatgagacactgttccgagatgtgtg 1320
Db 1564 cccaagatctggaactcttatgagaagaacccaagaatgagacactgttccgagatgtgtg 1623
QY 1321 gacagcagggacaatgacaactcttgaggaaacagcagcttgagtgcttgaatgacaac 1380
Db 1624 gacagcagggacaatgacaactcttgaggaaacagcagcttgagtgcttgaatgacaac 1683
QY 1381 caagacatcgtgtgttcttggccaagcaccagaagatgtccagtaatgtgtctc 1440
Db 1684 caagacatcgtgtgttcttggccaagcaccagaagatgtccagtaatgtgtctc 1743
QY 1441 ggtgtacactggagaagacttcaacagagataacagcagcaatccggacatctcgtgc 1500
Db 1744 ggtgtacactggagaagacttcaacagagataacagcagcaatccggacatctcgtgc 1803
QY 1501 ttcatgtgagtggttcaacactgacaagctatagaccatagacaagaagctgtgtcatc 1560
Db 1804 ttcatgtgagtggttcaacactgacaagctatagaccatagacaagaagctgtgtcatc 1863
QY 1561 aacaagatcagagcgtgtgtgaatgagaggaagctctgagctgtatctgttcaactgga 1620
Db 1864 aacaagatcagagcgtgtgtgtgaatgagaggaagctctgagctgtatctgttcaactgga 1923

QY 1621 attactccagcagcatgtgagctgcccacatcatgtcaagtacaaagatccgaatgagacat 1680
Db 1924 attactccagcagcagcatgtgagctgcccacatcatgtcaagtacaaagatccgaatgagacat 1983
QY 1681 gacaaatgtgagagagacaataaaatcaagatgagatgagatgagacactgtctcagact 1740
Db 1984 gacaaatgtgagagagacaataaaatcaagatgagatgagatgagatgagacactgtctcagact 2043
QY 1741 gaccccttgagagacatgagctgagctgagggggtctgagcctacttgacagatgtgtg 1800
Db 2044 gaccccttgagagacatgagctgagctgagggggtctgagcctacttgacagatgtgtg 2103
QY 1801 gacgagagcaatcatcaaggtggtgagcagccagagaagaagaactgtgtctatagca 1860
Db 2104 gacgagagcaatcatcaaggtggtgagcagccagagaagaagaactgtgtctatagca 2163
QY 1861 cagatgcccataccctgttactgttgaatgacatcttctgagggtgaatgagccggtcatg 1920
Db 2164 cagatgcccataccctgttactgttgaatgacatcttctgagggtgaatgagccggtcatg 2223
QY 1921 cccctcttcatgacgctgagcctgagatcttactcaagtgagctgtgatcatcaaggacatg 1980
Db 2224 cccctcttcatgacgctgagcctgagatcttactcaagtgagctgtgtgatcatcaaggacatg 2283
QY 1981 tatgagaagagagcagcgtgtaagaagacatgcggaatcaatgagcctggaacaacagata 2040
Db 2284 tatgagaagagagcagcgtgtaagaagacatgcggaatcaatgagcctggaacaacagata 2243
QY 2041 ctctgtttagctgtgtcatatagtagctcatctctctctctgtgtgagcgtgagcgtgta 2100
Db 2344 ctctgtttagctgtgtcatatagtagctcatctctctctctgtgtgagcgtgagcgtgta 2403
QY 2101 gttgtcatctctgaaagttaagaaacctgtgctcctacagtgatcccaagcgtgtgtgttc 2160
Db 2404 gttgtcatctctgaaagttaagaaacctgtgctcctacagtgatcccaagcgtgtgtgttc 2463
QY 2161 ttccgttcggt 2220
Db 2464 ttccgttcggt 2523
QY 2221 tccagagcccaactctgagcagcagcctgtgaggagcatcatctacttcaacgctgtaccc 2280
Db 2524 tccagagcccaactctgagcagcagcctgtgaggagcatcatctacttcaacgctgtaccc 2583
QY 2281 taagctcgt 2340
Db 2584 taagctcgt 2643
QY 2341 ctgctgtctcctgt 2400
Db 2644 ctgctgtctcctgt 2703
QY 2401 ggcacttgagtgacgtgagcaaacctgttgaagatccctgtgagaggaatgagcttcaat 2460
Db 2704 ggcacttgagtgacgtgagcaaacctgttgaagatccctgtgagaggaatgagcttcaat 2763
QY 2461 ctcaacacttgcatactcatagatgctgttgaacaactctctcatataggggtgagatgactg 2520
Db 2764 ctcaacacttgcatactcatagatgctgttgaacaactctctcatataggggtgagatgactg 2623
QY 2521 tacattgagcgtgtcttccagcagctacgaaatcccaagccctgtatcttctcctg 2580
Db 2824 tacattgagcgtgtcttccagcagctacgaaatcccaagccctgtatcttctcctg 2683
QY 2581 accaagtctactgtgttggcagaaagtgaatgaagaagcaacccctgtgtcccaaccag 2640
Db 2884 accaagtctactgtgttggcagaaagtgaatgaagaagcaacccctgtgtcccaaccag 2943
QY 2641 aagaagatgttaagaatctgtcatgtgagaggaagaacccaacttgaagcgtggcgtgtcc 2700
Db 2944 aagaagatgttaagaatctgtcatgtgagaggaagaacccaacttgaagcgtggcgtgtcc 3003

QY	2701	atccaagaactcgtgtcaaaagctctacccgagatvgagagvggtctgcgatvgccctvgca	2760
Db	3004	atccaagaacctcgtgtcaaaagagctctaccgagatvgagagatgaaagtggtctgcgtatvgccctvgca	3063
QY	2761	ctgaattttttctgvgggcccgacatcaacctctctctctgvgccacaatvgagacgvggagagagc	2820
Db	3064	ctgaattttttctgvgggcccgacatcaacctctctctctgvgccacaatvgagacgvggagagagc	3123
QY	2821	accacaatgftcaatcctcgaccgggttggttcctcccgacctcgggacccgctcaacctc	2880
Db	3124	accacaatgftcaatcctcgaccgggttggttcctcccgacctcgggacccgctcaacctc	3183
QY	2881	ggaaaaagacatctgctctctgtagatvgagacaacatcccgccagaaacctcgggtctgtctccag	2940
Db	3184	ggaaaaagacatctgctctctgtagatvgagacaacatcccgccagaaacctcgggtctgtctccag	3243
QY	2941	cataaagctgctgttttgacatgctgacgtgtcgaagaacaatctggtttctatgctccgcttg	3000
Db	3244	cataaagctgctgttttgacatgctgacgtgtcgaagaacaatctggtttctatgctccgcttg	3303
QY	3001	aaagvgctctctctgagaaagcagctggaagvcgvgagatvgagacagatvggcccctvgatgtgt	3060
Db	3304	aaagvgctctctctgagaaagcagctggaagvcgvgagatvgagacagatvggcccctvgatgtgt	3363
QY	3061	ttgccaatcaagcaagcctgcaaaaagcaaaaacaagccaagcttccgggtgagaaatgcaagaaag	3120
Db	3364	ttgccaatcaagcaagcctgcaaaaagcaaaaacaagccaagcttccgggtgagaaatgcaagaaag	3423
QY	3121	ctatctctggtccttggtcccttgctgcggvggagatctaaggttgtaattctctgtagtaaccaca	3180
Db	3424	ctatctctggtccttggtcccttgctgcggvggagatctaaggttgtaattctctgtagtaaccaca	3483
QY	3181	gctgtgtgvgaccccttaccctcccgacaaggagatctvgagagctgctgctgaataataccagaa	3240
Db	3484	gctgtgtgvgaccccttaccctcccgacaaggagatctvgagagctgctgctgaataataccagaa	3543
QY	3241	ggccgacacattatctctctctacacaacacatgtagtaagcggagacgtccctgvgggagag	3300
Db	3544	ggccgacacattatctctctctacacaacacatgtagtaagcggagacgtccctgvgggagag	3603
QY	3301	attgcacatcatctcccatctgagaaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	3360
Db	3604	attgcacatcatctcccatctgagaaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	3663
QY	3361	cagctcgtggaacaggtctactactcctcgaccttgytcaagaagaagtgtgaaatccctccctcagt	3420
Db	3664	cagctcgtggaacaggtctactactcctcgaccttgytcaagaagaagtgtgaaatccctccctcagt	3723
QY	3421	ttccctcgagaaacgttagttagcactgtgtatcaacctgtaaaaagagagacagtgtttctccag	3480
Db	3724	ttccctcgagaaacgttagttagcactgtgtatcaacctgtaaaaagagagacagtgtttctccag	3783
QY	3481	agcagcttctgtatgtctgcccgtgvgccagccagccatggaagatgaaacgctgacacatcgatctc	3540
Db	3784	agcagcttctgtatgtctgcccgtgvgccagccagccatggaagatgaaacgctgacacatcgatctc	3843
QY	3541	tctgtctatctccaaacctcaatcaggaagcagtggtctgaaagcccggtctgvggaagacata	3600
Db	3844	tctgtctatctccaaacctcaatcaggaagcagtggtctgaaagcccggtctgvggaagacata	3903
QY	3601	gggacataagcctgacactctgtgtgtcgcacatgtaagcctgctcaagagagggagcccttggtgaa	3660
Db	3904	gggacataagcctgacactctgtgtgtcgcacatgtaagcctgctcaagagagggagcccttggtgaa	3963
QY	3661	ctcttcaatgagatgtgatgagcccggtctcaagcccggtgatttcaatgtatgacatca	3720
Db	3964	ctcttcaatgagatgtgatgagcccggtctcaagcccggtgatttcaatgtatgacatca	4023
QY	3721	gagacgagcccttgaaagaaatattccctcaagvggtccgaaagagagtggtgtgagtgctgag	3780
Db	4024	gagacgagcccttgaaagaaatattccctcaagvggtccgaaagagagtggtgtgagtgctgag	4083
QY	3781	accccaagatgttaaccttgccagaaagacgaaacacagcvggtccctctcggggagacagacagc	3840

Db	4084	accctcaagtctgttacctctgtccacgaacgaacgaacaaacagggcgctctcgggagacgaagcagac	4143
Qy	3841	tgctctgcgcgcgttcaactggaagatgagatgcgtgcgacccaatgattcttgcataacaccca	3900
Db	4144	tgctctgcgcgcgttcaactggaagatgagatgcgtgcgacccaatgattcttgcataacaccca	4203
Qy	3901	gaatccagaagacgaagacttgctccagtctgggaatgatatgcgaagaaggtctctacaggtgaa	3960
Db	4204	gaatccagaagacgaagacttgctccagtctgggaatgatatgataaggaaggtctctacaggtgaa	4263
Qy	3961	gactggaactatcacagccaacagtttgctgcgccttcttggaagaagactgtctaaattcc	4020
Db	4264	gactggaactatcacagccaacagtttgctgcgccttcttggaagaagactgtctaaattcc	4323
Qy	4021	agaacgagtcgggaagaagatttltgtccagatgtctctgcagctgtgttctgtccatt	4080
Db	4324	agaacgagtcgggaagaagatttltgtccagatgtctctgcagctgtgttctgtccatt	4383
Qy	4081	ggcccttgcttcacgcgtgacatcggtgcacaccccttggaaatccccagccttggaactttag	4140
Db	4384	ggcccttgcttcacgcgtgacatcggtgcacaccccttggaaatccccagccttggaactttag	4443
Qy	4141	cccttgatgtacacgaacgaactacacatttgttaacgaatgattgtctctgtaggaacagga	4200
Db	4444	cccttgatgtacacgaacgaactacacatttgttaacgaatgattgtctctgtaggaacagga	4503
Qy	4201	accctggaaactcttaaaagccctacccaagaacccctgcttgggaacccgctgttatgaa	4260
Db	4504	accctggaaactcttaaaagccctacccaagaacccctgcttgggaacccgctgttatgaa	4563
Qy	4261	ggaaaccccaatccccagaacagccctgcgaagcagggaagaagaatgtgacacatgccca	4320
Db	4564	ggaaaccccaatccccagaacagccctgcgaagcagggaagaagaatgtgacacacatgccca	4623
Qy	4321	gttcccaagaccatcatgtgacatctctccagaatgtggaaactgtgacaaatgcagaacccctca	4380
Db	4624	gttcccaagaccatcatgtgacatctctccagaatgtggaaactgtgacaaatgcagaacccctca	4683
Qy	4381	cctgtacatgcagctgttagcagcgaacaaatcaagaagaatgctccgtgtgtctcccaagg	4440
Db	4684	cctgtacatgcagctgttagcagcgaacaaatcaagaagaatgctccgtgtgtctcccaagg	4743
Qy	4441	gcaagggggctgtgcctcctccacaagaagaacaacaacatgcagatatcccttcagaacctg	4500
Db	4744	gcaagggggctgtgcctcctccacaagaagaacaacaacatgcagatatcccttcagaacctg	4803
Qy	4501	acagaagaagaacatttggattctctgtgtgaagaagtatgtacagatatatgccaagaac	4560
Db	4804	acagaagaagaacatttggattctctgtgtgaagaagtatgtacagatatatgccaagaac	4863
Qy	4561	ttaagaacaaagactctgtgtgaatgatttagttagttagttagttagttagttagttagttagt	4620
Db	4864	ttaagaacaaagactctgtgtgaatgatttagttagttagttagttagttagttagttagttagt	4923
Qy	4621	aatactcaagcacttccctccggagtcaagaagttaatgtatgtccatcaacaacaatgaagaa	4680
Db	4924	aatactcaagcacttccctccggagtcaagaagttaatgtatgtccatcaacaacaatgaagaa	4983
Qy	4681	caacctaagaactgtgcgaagcagttctgcagatcagattctctcaacagcttggaagattt	4740
Db	4984	caacctaagaactgtgcgaagcagttctgcagatcagattctctcaacagcttggaagattt	5043
Qy	4741	atgacaagactgtgacaccaaataatgttcaaggtgtgtgttcaataacaagaagctgtgcat	4800
Db	5044	atgacaagactgtgacaccaaataatgttcaaggtgtgtgttcaataacaagaagctgtgcat	5103
Qy	4801	gcaatcagctcttctccgaatgtcatcaacaatgcatcttccggccaacactgcaaaag	4860
Db	5104	gcaatcagctcttctccgaatgtcatcaacaatgcatcttccggccaacactgcaaaag	5163
Qy	4861	ggagagaaccccttagccattttagaatctatgtcttcaatacaatccctgaatctcaacag	4920

Db 5164 ggagagaacctagccatlatggaatlaactgcttccaatccatccctgatacccaag 5223
QY 4921 cagcagctctcaagagtgctctgatagacacatagagtgatgctctgttccatctgt 4980
Db 5224 cagcagctctccagagtgctctgatagacacatagagtgatgctctgttccatctgt 5283
QY 4981 gtcacatcttgcaatgctctctgctccagcagctctgtcgtatctccatccagagctg 5040
Db 5284 gtcacatcttgcaatgctctctgctccagcagctctgtcgtatctccatccagagctg 5343
QY 5041 gtcacagaagcaaaacacacctgcatlcatcaagtgagtgaaagctgtlcatctactgctc 5100
Db 5344 gtcacagaagcaaaacacacctgcatlcatcaagtgagtgaaagctgtlcatctactgctc 5403
QY 5101 tctaatcttgctggaatgtaagtaacgttgcctccgcaacgttgatatactc 5160
Db 5404 tctaatcttgctggaatgtaagtaacgttgcctccgcaacgttgatatactc 5463
QY 5161 ttcactgctctccagcagaagtcctatgtgtcctccaccaaactgtgctgtagccctt 5220
Db 5464 ttcactgctctccagcagaagtcctatgtgtcctccaccaaactgtgctgtagccctt 5523
QY 5221 ctaacttgctgtaagtggttgatcaatccacacctcctcatgtaacagcctctgtgttc 5280
Db 5524 ctaacttgctgtaagtggttgatcaatccacacctcctcatgtaacagcctctgtgttc 5583
QY 5281 aagatccccaagcaacagcctatgtgtgtcctcaacagcgtgtaacacctctcatatggtcaat 5340
Db 5584 aagatccccaagcaacagcctatgtgtgtcctcaacagcgtgtaacacctctcatatggtcaat 5643
QY 5341 ggcagcgtgcccacacctgtgtctggaagctgttccacgcaaaataagctgtaataataat 5400
Db 5644 ggcagcgtgcccacacctgtgtctggaagctgttccacgcaaaataagctgtaataataat 5703
QY 5401 gataccctgaagctcgtgttcttgatcttccacacatcttgcctggaagcgggctcctc 5460
Db 5704 gataccctgaagctcgtgttcttgatcttccacacatcttgcctggaagcgggctcctc 5763
QY 5461 gacatggtgtaaaaaacacagcaatgctgctgacccctgtaaaagcttctggaagaaacgcgttt 5520
Db 5764 gacatggtgtaaaaaacacagcaatgctgctgacccctgtaaaagcttctggaagaaacgcgttt 5823
QY 5521 ggtgtaacattatctcttggaagctgtgtggaacgaacacctctcgcaatgagccgtggaaggg 5580
Db 5824 ggtgtaacattatctcttggaagctgtgtggaacgaacacctctcgcaatgagccgtggaaggg 5883
QY 5581 gttggttctctccatcaactgtctcgtatccagtaacagattctctcatcagggcccaagcct 5640
Db 5884 gttggttctctccatcaactgtctcgtatccagtaacagattctctcatcagggcccaagcct 5943
QY 5641 gtaaatgcaaaagctatctctctcgtgaatgaaatgaaatgtaagatgtaagcggaagaaacag 5700
Db 5944 gtaaatgcaaaagctatctctctcgtgaatgaaatgaaatgtaagatgtaagcggaagaaacag 6003
QY 5701 agaattcttgatgtgtggaagcgcaaatgacactcttagaataatcaagaggtggaacgaata 5760
Db 6004 agaattcttgatgtgtggaagcgcaaatgacactcttagaataatcaagaggtggaacgaata 6063
QY 5761 tatagaaggaagcggaagcctgctgttgacaagatttgcgtggaagctctccctcggtgag 5820
Db 6064 tatagaaggaagcggaagcctgctgttgacaagatttgcgtggaagctctccctcggtgag 6123
QY 5821 tgccttgagctcctggaagttaatlgggctggaataatcatcaacttcaagaatgttaaca 5880
Db 6124 tgccttgagctcctggaagttaatlgggctggaataatcatcaacttcaagaatgttaaca 6183
QY 5881 ggaagatccacatgttaccagaagagatgcttcccttaacaaataagtatctatcaaac 5940
Db 6184 ggaagatccacatgttaccagaagagatgcttcccttaacaaataagtatctatcaaac 6243
QY 5941 atccatgaagtaacatggaacatggtactgacctgaagtttgaatgcatcacaagagctg 6000
Db 6244 atccatgaagtaacatggaacatggtactgacctgaagtttgaatgcatcacaagagctg 6303

QY 6001 ttgactggagagaacacggtggaattcttgcctcttgagaggaagtcaccaagaagaa 6060
Db 6304 ttgactggagagaacacggtggaattcttgcctcttgagaggaagtcaccaagaagaa 6363
QY 6061 gttggcaaggttggatggatggcgatccggaactggcgctctggaagatggaagaaaaa 6120
Db 6364 gttggcaaggttggatggatggcgatccggaactggcgctctggaagatggaagaaaaa 6423
QY 6121 tatgttgtaactaagtggaagcaacaacgcaagctctcttaacacacatggtttgatc 6180
Db 6424 tatgttgtaactaagtggaagcaacaacgcaagctctcttaacacacatggtttgatc 6483
QY 6181 ggcgggctcctctgtgtgttcttgatgaacccaacacagcagatgatacccaagccgg 6240
Db 6484 ggcgggctcctctgtgtgttcttgatgaacccaacacagcagatgatacccaagccgg 6543
QY 6241 cgttctcttggaattgtgcccctaagtggtgtcaagaaggggagatcagatggttaca 6300
Db 6544 cgttctcttggaattgtgcccctaagtggtgtcaagaaggggagatcagatggttaca 6603
QY 6301 tctcataagtatggaagaaatgtaagctcttgcactaagaaatggaatcaatggtcaatgga 6360
Db 6604 tctcataagtatggaagaaatgtaagctcttgcactaagaaatggaatcaatggtcaatgga 6663
QY 6361 aggttcaaggtgctctggcagatgtccagcatcttaaaaaataagtttggagatggtataca 6420
Db 6664 aggttcaaggtgctctggcagatgtccagcatcttaaaaaataagtttggagatggtataca 6723
QY 6421 atagttgtaacgaatagcagaggtccaaacccggaacctgaagcctgtccaggaattcttga 6480
Db 6724 atagttgtaacgaatagcagaggtccaaacccggaacctgaagcctgtccaggaattcttga 6783
QY 6481 ctggcatcttccgtggaagtgttcttaaaagaaacacccggaacatgctataatccagctt 6540
Db 6784 ctggcatcttccgtggaagtgttcttaaaagaaacacccggaacatgctataatccagctt 6843
QY 6541 ccaatctcatatctctctcgtgcagagatatcagatctctccgaagggcaaaaagcga 6600
Db 6844 ccaatctcatatctctctcgtgcagagatatcagatctctccgaagggcaaaaagcga 6903
QY 6601 ctccacatagaagactactctgttcttccagacaacacttgaaccaagtatttgaactt 6660
Db 6904 ctccacatagaagactactctgttcttccagacaacacttgaaccaagtatttgaactt 6963
QY 6661 gccaaaggaccaaagtgatgatagacacttaaaagacctctcatatacaaaaacagaca 6720
Db 6964 gccaaaggaccaaagtgatgatagacacttaaaagacctctcatatacaaaaacagaca 7023
QY 6721 gtagtgagcgttgcaattctcacaatcttcttaagatgagaagaatggaagaagctat 6780
Db 7024 gtagtgagcgttgcaattctcacaatcttcttaagatgagaagaatggaagaagctat 7083
QY 6781 gta 6783
Db 7084 gta 7086

Search completed: September 14, 2002, 08:00:35
Job time: 73347 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2002, 07:22:46 ; Search time 20132.5 Seconds
(without alignments)
7072.350 Million cell updates/sec

Title: US-09-595-526b-1_COPY_291_7094
Perfect score: 6804
Sequence: 1 atgctgtgtgtgctcagct.....gaagaatcctgttcatacgg 6804

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_hg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_da.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vl.*
30: em_hg_hum.*
31: em_hg_inv.*
32: em_hg_other.*
33: em_hg_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
------------	-------------	-------	--------	-------	-------------

1	6804	100.0	10442	6	AX060713	AX060713 Sequence
2	6804	100.0	10442	6	AX060892	AX060892 Sequence
3	6804	100.0	10442	9	AF285167	AF285167 Homo sapi
4	6802.4	100.0	10474	6	AX060719	AX060719 Sequence
5	6802.4	100.0	10474	6	AX060721	AX060721 Sequence
6	6802.4	100.0	10474	6	AX060898	AX060898 Sequence
7	6802.4	100.0	10474	6	AX060900	AX060900 Sequence
8	6796	99.9	7860	6	AX092594	AX092594 Sequence
9	6788	99.8	7260	6	AX253452	AX253452 Sequence
10	6784.8	99.7	9741	6	AX127830	AX127830 Sequence
11	6784.8	99.7	9741	6	AX139817	AX139817 Sequence
12	6784.8	99.7	9741	6	AX351038	AX351038 Sequence
13	6784.8	99.7	9854	6	AX127831	AX127831 Sequence
14	6784.8	99.7	9854	6	AX139818	AX139818 Sequence
15	6771.6	99.5	7862	6	AX135712	AX135712 Sequence
16	6770.8	99.5	7862	6	AX135712	AX135712 Sequence
17	6728	98.9	6880	6	AX253450	AX253450 Sequence
18	6728	98.9	6880	6	HSAD012376	HSAD012376 Homo sapi
19	6728	98.9	9497	6	AX059973	AX059973 Sequence
20	6728	98.9	9497	6	AF165281	AF165281 Homo sapi
21	6714	98.7	9495	6	AX059978	AX059978 Sequence
22	6609.2	97.1	7878	10	MMAR01	MMAR01 Mus muscu
23	5596.2	82.2	7074	5	AF362377	AF362377 Bos tauru
24	4347.6	63.9	7298	4	AF001945	AF001945 Homo sapi
25	1931.6	28.4	7709	4	BTU90126	BTU90126 Homo sapi
26	1928.8	28.3	7268	10	MMAR000149	MMAR000149 Mus muscu
27	1928.8	28.3	7323	9	BD005026	BD005026 Genes rel
28	1926.8	28.3	5097	6	AK027864	AK027864 Homo sapi
29	1922.8	28.3	5097	6	AK027864	AK027864 Homo sapi
30	1922.8	28.3	5097	6	AF328787	AF328787 Homo sapi
31	1918.8	28.2	7276	9	AF328787	AF328787 Homo sapi
32	1742.2	25.6	6704	9	AB055390	AB055390 Homo sapi
33	1735.8	25.5	6027	9	AX320364	AX320364 Sequence
34	1735.8	25.5	6432	6	AX202218	AX202218 Sequence
35	1735.8	25.5	6522	6	AX202218	AX202218 Sequence
36	1735.8	25.5	6588	6	AF250238	AF250238 Homo sapi
37	1735.8	25.5	6588	6	AX320362	AX320362 Sequence
38	1696	24.9	6607	6	AX080493	AX080493 Sequence
39	1696	24.9	6607	10	AF287141	AF287141 Mus muscu
40	1531.6	22.5	5762	6	AX080462	AX080462 Sequence
41	1465	21.5	5669	6	AX202220	AX202220 Sequence
42	985	14.5	7305	6	AX235953	AX235953 Sequence
43	985	14.5	7482	9	AF327657	AF327657 Homo sapi
44	985	14.5	8056	9	AF178941	AF178941 Homo sapi
45	985	14.5	8195	6	AX235951	AX235951 Sequence

ALIGNMENTS

RESULT 1	AX060713	10442 bp	DNA	linear	PAT 22-JAN-2001
LOCUS	AX060713	Sequence 1 from Patent WO0078972.			
DEFINITION	AX060713				
ACCESSION	AX060713.1	GI:12406103			
VERSION					
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 10442)				
AUTHORS	Lawn, R.M., Wade, D. and Garvin, M.				
TITLE	Regulation with binding cassette transporter protein abcl				
JOURNAL	Patent: WO 0078972-A 1 28-DEC-2000;				
FEATURES	CV THERAPEUTICS, INC. (US)				
source	location/Qualifiers				
	1..10442				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
BASE COUNT	2898 a 2297 c 2408 g 2835 t				
ORIGIN					
					4 others

QY 4321 gtcccccagacatcagagctctccagaatgggaactggaacatgcaagacctca 4380
|||||
Db 4611 gttccccagaccatcatgatgaccttccagaaatgggaactggacaaatccacttca 4670
|||||
QY 4381 cctgcatgcagttgtagcagcagcaaaaatcaagaagatgctgctgtgtgtcccccagg 4440
|||||
Db 4671 cctgcatgcagttgtagcagcagcaaaaatcaagaagatgctgctgtgtgtcccccagg 4730
|||||
QY 4441 gcaagggggctgctcctcccaaaaacaaacactgcaatcatalcctccagagctg 4500
|||||
Db 4731 gcaggggggctgctcctcccaaaaacaaacactgcaatcatalcctccagagctg 4790
|||||
QY 4501 acaagaaagaacatttgatattctgtgaaagcgtatgagcagatcagacaaagc 4560
|||||
Db 4791 acaggaataaaatttgcgattatctgtgaaagcgtatgagcagatcagacaaagc 4850
|||||
QY 4561 ttaagaacaagaatctgggtgaatgagtttagatgagcggcttctccctgggtgag 4620
|||||
Db 4851 tttaagaacaagaatctgggtgaatgagtttagatgagcggcttctccctgggtgag 4910
|||||
QY 4621 aatctcaagacattcctccgagtcgaagagttatgagtcgcatcaaaatgaagaa 4680
|||||
Db 4911 aatctcaagacattcctccgagtcgaagagttatgagtcgcatcaaaatgaagaa 4970
|||||
QY 4681 caccataagctgagcgaagagacagttctgagatcgattctcccaagcttgggaagtt 4740
|||||
Db 4971 caccataagctgagcgaagagacagttctgagatcgattctcccaagcttgggaagtt 5030
|||||
QY 4741 atgacagagctgagcgaagcgaagaataatgtaaggtgtgtgtcaatacaaggctgag 4800
|||||
Db 5031 atgacagagctgagcgaagcgaagaataatgtaaggtgtgtgtcaatacaaggctgag 5090
|||||
QY 4801 gcaatcagctcttccctggaatgtaacaaatggcaattctccgggcaacccgtgcaag 4860
|||||
Db 5091 gcaatcagctcttccctggaatgtaacaaatggcaattctccgggcaacccgtgcaag 5150
|||||
QY 4861 ggaagaagaacctagacatctatggaatctgcttcaatcatccctgaaatccacaa 4920
|||||
Db 5151 ggaagaagaacctagacatctatggaatctgcttcaatcatccctgaaatccacaa 5210
|||||
QY 4921 cagcagctctcagaagtggtgctgtagacacacatcagtgagtgctgtgtgtcaatctgt 4980
|||||
Db 5211 cagcagctctcagaagtggtgctgtagacacacatcagtgagtgctgtgtgtcaatctgt 5270
|||||
QY 4981 gtaactcttgcaatgltcctcgtcccaagcagcttgtgctatctccgtagcagaagcg 5040
|||||
Db 5271 gtaactcttgcaatgltcctcgtcccaagcagcttgtgctatctccgtagcagaagcg 5330
|||||
QY 5041 gtaagaagaagaac 5100
|||||
Db 5331 gtaagaagaagaac 5390
|||||
QY 5101 tctaatcttctcgggatatgtaacttaagtgttccctggcaacatgtaactatcatc 5160
|||||
Db 5391 tctaatcttctcgggatatgtaacttaagtgttccctggcaacatgtaactatcatc 5450
|||||
QY 5161 ttaactctgcttcagagaagaagtcctatgtgtcctccacacacacacacacacacac 5220
|||||
Db 5451 ttaactctgcttcagagaagaagtcctatgtgtcctccacacacacacacacacacac 5510
|||||
QY 5221 ctactcttctgtagtggt 5280
|||||
Db 5511 ctactcttctgtagtggt 5570
|||||
QY 5281 aagatcccaagcaac 5340
|||||
Db 5571 aagatcccaagcaac 5630
|||||
QY 5341 ggcagagtgagcgaactgt 5400
|||||
Db 5631 ggcagagtgagcgaactgt 5690
|||||

QY 5401 gatatccgaagtcggt 5460
|||||
Db 5691 gatatccgaagtcggt 5750
|||||
QY 5461 gacatggtgaaaaaaccaggaatgagtgagtgccctggaaggtgtgtgtgtgtgtgtgt 5520
|||||
Db 5751 gacatggtgaaaaaaccaggaatgagtgagtgccctggaaggtgtgtgtgtgtgtgtgt 5810
|||||
QY 5521 ggtccacatctctggaactgt 5580
|||||
Db 5811 ggtccacatctctggaactgt 5870
|||||
QY 5581 ggt 5640
|||||
Db 5871 ggt 5930
|||||
QY 5641 gtaaatgcaagaatctctcctcctcctcctcctcctcctcctcctcctcctcctcct 5700
|||||
Db 5931 gtaaatgcaagaatctctcctcctcctcctcctcctcctcctcctcctcctcctcct 5990
|||||
QY 5701 agaatcttgatggt 5760
|||||
Db 5991 agaatcttgatggt 6050
|||||
QY 5761 tataagaagaagcgggaagcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5820
|||||
Db 6051 tataagaagaagcgggaagcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6110
|||||
QY 5821 tgccttgagctcctggaatgtaatgagctgtgaaatacaacttcaagaatgttaaca 5880
|||||
Db 6111 tgccttgagctcctggaatgtaatgagctgtgaaatacaacttcaagaatgttaaca 6170
|||||
QY 5881 ggaagatacaactgttcaacagagagatgcttctccttcaaaaaatagatcttcaaac 5940
|||||
Db 6171 ggaagatacaactgttcaacagagagatgcttctccttcaaaaaatagatcttcaaac 6230
|||||
QY 5941 atccatgaaatcatcagaacaatgggctgagctgctcctggtttagatcaacagagctg 6000
|||||
Db 6231 atccatgaaatcatcagaacaatgggctgagctgctcctggtttagatcaacagagctg 6290
|||||
QY 6001 ttgactgggaagaacacagtggaagcttcttcccttgggaaggagctcccaagaagaag 6060
|||||
Db 6291 ttgactgggaagaacacagtggaagcttcttcccttgggaaggagctcccaagaagaag 6350
|||||
QY 6061 gttggaaggt 6120
|||||
Db 6351 gttggaaggt 6410
|||||
QY 6121 tatgtgttaactatagtgagggcaacaacgcaagcctctacagcatgagcttgatc 6180
|||||
Db 6411 tatgtgttaactatagtgagggcaacaacgcaagcctctctacagcatgagcttgatc 6470
|||||
QY 6181 ggcgggctcctgt 6240
|||||
Db 6471 ggcgggctcctgt 6300
|||||
QY 6241 cgggtctgt 6300
|||||
Db 6531 cgggtctgt 6390
|||||
QY 6301 tctcatagtatgagaagaatggaagcctcttgcactgagatggaacatcagtgtaactgga 6360
|||||
Db 6591 tctcatagtatgagaagaatggaagcctcttgcactgagatggaacatcagtgtaactgga 6650
|||||
QY 6361 aggttcaggt 6420
|||||
Db 6651 aggttcaggt 6710
|||||
QY 6421 ataagttgaagaatgagcaggtgtccaaaccggaactggaagccttccaagatcttcttga 6480
|||||
Db 6711 ataagttgaagaatgagcaggtgtccaaaccggaactggaagccttccaagatcttcttga 6770
|||||
QY 6481 ctgcaattcctgtgaagtggttctaaagaagaacacccggaacatgtctaatcacagct 6540
|||||

|||||
Db 6771 CTTGGATTTCGGAGGTTCTTAAGAGAAACACCGGACATGCTACATACCACTT 6830
Qy 6541 ccattccattatctctctcgccagagatctccatccctccagagcaaaagcga 6600
|||||
Db 6831 CCATCTTCATTATCTTCTGCGCGAGATTTACGATCCCTCCAGAGCAAAAAGCGA 6890
Qy 6601 ctccacatagaagactactctgttcttcagacaacacttgcaagatatttgyaacttc 6660
|||||
Db 6891 CTCACATAGAGACTACTCTGTTCTTCAGACAAACACTTGGACAAATTTGTGAACCTT 6950
Qy 6661 gccaaagccaaagatgatgatgacactaaagaacctctattacacaaaacagaca 6720
|||||
Db 6951 GCCAAGAGACCAAGATGATGATGACCATTTAAAGACCTCTTATACCAAAAACCAACA 7010
Qy 6721 gtagtgcagctgtcagcttctcacatcttcttcacagagatgaaagtgaagaaagctat 6780
|||||
Db 7011 GTAGTGGAGCTTGCACTTCTCATCTTTCTACAGATGAGAAAGTGAAGAAAGCTAT 7070
Qy 6781 gtagaagaatccgttcatacgg 6804
|||||
Db 7071 GTATGAAGATCTGTCATACGG 7094

RESULT 2
AX060892 10442 bp DNA linear PAT 22-JAN-2001
LOCUS AX060892 1 from Patent W00078971.
DEFINITION Sequence 1 from Patent W00078971.
ACCESSION AX060892
VERSION AX060892.1 GI:12406270
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10442)
AUTHORS Law, R.M., Wade, D., Oram, J.F. and Garvin, M.
TITLE Atp binding cassette transporter protein abcl1 polypeptides
JOURNAL Patent: WO 0078971-A 1 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
source location/Qualifiers
1..10442
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2898 a 2297 c 2408 g 2835 t 4 others
ORIGIN

Query Match 100.0%; Score 6804; DB 6; Length 10442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|||||
Db 591 ATTGGCTCGCTGCTGTCTTCAGATGCTCGAGGCTCTTTATACACCCAGAAAGACCC 650
Qy 361 agcatgaaggacatgycgaagcttcctgagaacattacagcaatcaagaatccagctca 420
|||||
Db 651 AGCATGAAGAGACATCGCAAAAGTTCTGAGAACATTACAGCATCAAGAAATCCAGCTCA 710
Qy 421 aacttgaagcttcaagattctctgtgtgagaaatgaacacctctctgtgttccatctac 480
|||||
Db 711 AACTTGAAAGCTTCAAGATTCTCTGCTGGACAAATAAACCTTCTGTGGTTCATATAC 770
Qy 481 aacctctctcccaagcttacttctgtggaacaaga tgcgtgaaggtgtatgtcatctccac 540
|||||
Db 771 AACCTCTCTCTCCCAAGCTACTACTGTGACAAAGATGCTGAGGCTGATGTCATTTCTCC 830
Qy 541 aagtaatttttgcgaaggtctaccagttacatttgacaagctgtctcaatgtataaaatca 600
|||||
Db 831 AAGGTAATTTTTCGAAGGCTACCCAGTTTACATTTGACAAAGTGTGCAATGATCAAAATCA 890
Qy 601 gaagagatgattcaactgtgtgagcaagaagttcttgagcttctgtgcttaccagaagag 660
|||||
Db 891 GAGAGATATTTCAACTTGTGTGACCAAGATTTCTGAGCTTTGTGGCTTACCAAAAGAG 950
Qy 661 aaactgtctgcagcagagcagagtaactgttcccaacatgacatccgtgaagccaatccgt 720
|||||
Db 951 AAACCTGCTGCAGCAGAGGAGTACTGTTCCAAACATGACATCTGAAGCCAAATCTG 1010
Qy 721 agacaactaaactctacatctccctcccgagcagaagcgtgtgttgagccacaanaaca 780
|||||
Db 1011 AGAACCTTAACCTTACATCTCTCCGAGCAAGAGGAGGCTGAGAGCCACAAACA 1070
Qy 781 ttgctcatagctcttgagacatcttgcccaagagcgtgttcaacatgagagcttgagtgac 840
|||||
Db 1071 TTCTCTCATAGTCTTGCGACTGTGGCCAGAGAGCTGTTCACATGAGAAAGCTGGAGTAC 1130
Qy 841 atgcgacagagtgatgttcttgacaactgtgaacagctccagctctccaccaaatc 900
|||||
Db 1131 ATGCGACAGAGAGTGTGTTCTTGACCAATGTGAACACACTCCAGCTCTCCACCAATC 1190
Qy 901 taccagcgtgtgtctgtatcttctgcgggacatcccgagagaggggctgaagatacaag 960
|||||
Db 1191 TACCAGGCTGTGTCTGTGTTGTCTGCGGGATCCCGAGGAGGGGGCTGAAGATCAAG 1250
Qy 961 tctctaactgtatgaggaacaacaactcaaaagccctcttggaggaatgtgcactgag 1020
|||||
Db 1251 TCTCTCACTGATGAGAACAACTACAAAGCCCTTGTGAGGCAATGCGACTGAG 1310
Qy 1021 gaagatgctgaaacctcttatgacaactctacaactctctactgtaatgatttatgaag 1080
|||||
Db 1311 GAAGATGCTGAACCTTCTATGACAACTCTACACTCTTACTGCAATGATTTGATGAAG 1370
Qy 1081 aatttgagctagctctctctccgcatctatctgaaagctctgaaagccgctgctgt 1140
|||||
Db 1371 AATTGGAGCTAGTCTCTCTTCCCGCATTTATCTGGAAGAGCTGAACCCGCTGCTT 1430
Qy 1141 gggagaagctctgtataacctgacactccagccacaagcagtgcatgtgtgagtgaaac 1200
|||||
Db 1431 GGGAGAATCTGTATACACTGACCTCCAGCCACAGGCAAGCATGATGCTGAAGTGAAC 1490
Qy 1201 aagagcttccaggaactgt 1260
|||||
Db 1491 AAGACCTTCCAGGAACCTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1550
Qy 1261 cccaagatctgacacttcatgagaaacaagcaagaatgagacctgtgcogagtgtgtgt 1320
|||||
Db 1551 CCCAAGATCTGGAACCTTCAATGAGAACAGCAAGAAATGACCTTGTCCGATGCTGTG 1610
Qy 1321 gacagcaggaacaatgacacacttcttggaacagcagttgagtggttattgagcaac 1380
|||||
Db 1611 GACAGCAGGAGCAATGACCACTTTTGGGAACACCAATGATGAGCTTGAATGGACAGCC 1670
Qy 1381 caagacatctgtgcttcttgagcaagccccaagagatgtccagtaattgtct 1440
|||||

Db 1671 CAAGACATCGTGGCTTTTGGCCAAGCACCCAGAGATGTCCAGTCAATGCTTCT 1730
Qy 1441 gtgtacaacctggagaagtttcaacgagactaaccaaggcaatcccgacatattcgc 1500
Db 1731 GTGTACACCTGGGAGAAAGCTTTCACAGAGACTAACACAGGCAATCCGAGCAATCTCC 1790
Qy 1501 ttcatgagtggtgtcaaacgtaaacagcttagaacccatagcaacagaatctggtctatc 1560
Db 1791 TTTGATGAGGTGTCAACCTGGAACCAAGCTAAGAACCATATGCAACAGAACTTGCTCATC 1850
Qy 1561 aacaagtcgaagagctgtgtgagtagaagaaagttctggtctgtatgtgttcatgga 1620
Db 1851 AACAACTGCATGAGAGCTGTGTGATGAGAGAAATTCGTGGGTGTGTGTCTCACTGGA 1910
Qy 1621 attaccgaagcgagctgtgagctgccccatgttcaagtagaagaatccgaatgacatt 1680
Db 1911 ATTACTCCAGGAGCAATGAGCTGCCCCATCATGTCAATACAGATCCAGATGACATT 1970
Qy 1681 gacaatgtgagagagaacaataaatacaagatgtggttactgtggaacctgtctcgaagt 1740
Db 1971 GACAAATGTGAGAGAGCAATAATAATCAAGATGGTACTGTGGAGACCTGTCTCGAGCT 2030
Qy 1741 gaacctttgagagacatcggtacgtctgtggtggggtctgcctacttgcaagatgtgt 1800
Db 2031 GACCCCTTTGAGAGACATCGCGGTACGTCTGGGGGGCTTGCCTACTTGCAGATGTGTG 2090
Qy 1801 gaagcaagcaatcaatcagaggtgtgtgagagcgacaggaagaagaacgtgttcatatgcaa 1860
Db 2091 GACAGAGCAATCATCAGGTGCTGTGACGGGACACGAGAAAGAAATGCTGTCTATATGCAA 2150
Qy 1861 cagatgtccatccctgtttagatgtgacatcttctgtggtgtgtagagccgtgcaatg 1920
Db 2151 CAGATGCCCTATCCCTGTACGTGTGATGACATCTTCTGGGTGATGAGCCGGTCATNG 2210
Qy 1921 ccccttcatagagctgtgctgagctggttactactgaagtgtgtatcaagaagatgtgt 1980
Db 2211 CCCCTTTATGACGCTGTGCTGTGATTAATCTGAGGTGTGATCATGAAGGCACTGTG 2270
Qy 1981 tatgagaagagagcagcgtctgaagaagacatgtcgatcatgtggtcgtgacaacagcata 2040
Db 2271 TATGAGAAGAGAGCAGCGCTGAAGACACATGCGGATCATGTGGCTGTGACACAGCTA 2330
Qy 2041 cctgtgttagctgtgtatctagtagcctcatctctctgtgtgtgtgtgtgtgtgtgt 2100
Db 2331 CTCTGTGTGTAGCTGTCTATTTAGTACCTCATCTCTCTGTGTGTGTGTGTGTGTGT 2390
Qy 2101 gtgtcatcctgaagttgaagaacctgtgtccctacagtagtcccaaggtgtgtgtgtgt 2160
Db 2391 GTGTGTATCTTAAGTTAGAAACCTGTGCTTACAGTGTGATCCAGGTGTGTGTGTGT 2450
Qy 2161 ttctgtcctgt 2220
Db 2451 TTTCTGTCTGT 2510
Qy 2221 tccaaagcaaacctgtgagcagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2280
Db 2511 TCCAAAGCAACCTGTGAGCAGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2570
Qy 2281 taagctgt 2340
Db 2571 TACGTCTGT 2630
Qy 2341 ctgtgtctcctgt 2400
Db 2631 CTGTGTCTCTGT 2690
Qy 2401 ggaattgtgagtgagtgagacaactgttgaagctcctgtgtgtgtgtgtgtgtgtgtgtgt 2460
Db 2691 GGAATGTGAGTGAGTGAGACAACCTGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2750
Qy 2461 ctcaaaccttgatctcgaatgt 2520
Db 2751 CTCACCACTTGATCTCATGT 2810
Qy 2521 taactgagctgtcttccagccagtagaaltcccaagccctgtgtatttctctgtc 2580
Db 2811 TACATTTGAGGCTGTCTTCCAGGCCAGTACGGAATTCACAGGCTGTGTGTGTGTGTGTGT 2870
Qy 2581 accaagctctactgt 2640
Db 2871 ACCAAGTCTCTGT 2930
Qy 2641 aagaatgtcaagaatctgcatgtgagagagaaaccccaactggaagctgtgtgtgtgtgtgt 2700
Db 2931 AAGAGAAATGTCAAGAAATGTGATGTGAGAGAGAACCCACCACTTGAAGCTGTGTGTGTGT 2990
Qy 2701 attcaagaacctgttgaagttcagagatgtgagatgtgagatgtgtgtgtgtgtgtgtgtgt 2760
Db 2991 ATTCAAGAACTGT 3050
Qy 2761 ctgaatttttgaagggccagatcacctctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2820
Db 3051 CTGAATTTTGTGAGGGCCAGATCACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3110
Qy 2821 accacacatgtcaatcctgtgagcgggtgttcccccagacctgtgtgtgtgtgtgtgtgtgtgt 2880
Db 3111 ACCACCAATGTCAATCTGACCGGTTGTTCOCOCAGACTGTGTGTGTGTGTGTGTGTGTGTGT 3170
Qy 2881 ggaagaagacatgt 2940
Db 3171 GGAAGAAAGCATTTCTGT 3230
Qy 2941 cataagctgt 3000
Db 3231 CATACGTGCTGT 3290
Qy 3001 aaaggtctctctgtgaagcagcgt 3060
Db 3291 AAAGGCTCTCTGTGAAGCAGCAGTGAAGCGGAGATGAGCAGATGTGCGCTGTGTGTGTGT 3350
Qy 3061 ttgcatcaagcaagcgt 3120
Db 3351 TTTGCCATCAAGCAGCTGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 3410
Qy 3121 ctatctgt 3180
Db 3411 CTATCTGTGCTGT 3470
Qy 3181 gt 3240
Db 3471 GT 3530
Qy 3241 ggcgcacacattatctctctctac 3300
Db 3531 GCGCGCACCATTTATCTCTTACACACACATGTGATGAAGCGGACCTCTGTGTGTGTGTGTGT 3590
Qy 3301 attgcaatcatctccatgt 3360
Db 3591 ATTGCCATCATCTCCATGTGGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3650
Qy 3361 caagctgt 3420
Db 3651 CAGCTGTGGAAGCAGCTACCTGTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3710
Qy 3421 tccctgtgaagaacagtagtagcaactgtgtcatcacttaaaagagagagagagagagagagag 3480
Db 3711 TCTGTGAGAAAGAGTAGTAGCACTGTGTATACCTGTAAGAAAGAGAGAGAGAGAGAGAGAG 3770
Qy 3481 agcagatctgt 3540
Db 3771 AGCAGTTGT 3830
Qy 3541 tctgtcatctcaaacctcaaggaagcagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3600
Db 3831 TCTGTATCTCAACCTCATCAGGAAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3890

Dh 6051 TATAGAAAGGAGCGAGCCTGCTGTGACAGATTTGCGTGGGCTTCTCTCGGTGAG 6110
Qy 5821 tgcttgggcccctgggagatgtaatggggcgtggaataatcacaacttcaagatgttaaca 5880
Dh 6111 TGGCTTTGGGCTCCGAGGATTAATGGGGCTGGAAATCATCACTTTCAAGATGTTTAA 6170
Qy 5881 ggaatccacactgttaccagagagatgcttcttcaacaaaataglatctataaac 5940
Dh 6171 GGAATACCACTGTTACCAAGAGATGCTTTCTTTACAAAATATATCTTATCAAC 6230
Qy 5941 atccatgaatgatacagacaatgggactgacctcagttgatagtcacaagagctg 6000
Dh 6231 ATCCATGAAGTACATGAGAACATGGGCTACTGGCCCTCAGTTGATGTCATCAGAGAGCTG 6290
Qy 6001 ttgactgggagagagacacgtggagttcttggcccttttgagagagagtcaccaagaagaa 6060
Dh 6291 TTGACTGGGAGAGAACACGTGGAGTTCTTGGCCCTTTTGAGAGAGAGTCCACAGAAAGAA 6350
Qy 6061 gttgcaagatgtgtgagtgagcgatctggaataactgggacctgtgaagatgagaagaaaa 6120
Dh 6351 GTTGGCAAGGTTGGTGAGTGGCGGATTCGAAACCTGGGCTCGTGAAGTATGGAGAGAAAA 6410
Qy 6121 taatgtgtaactactagtgagagcaacaacagcaagctctctacaagccatgcttgatc 6180
Dh 6411 TATGCTGTAAGTATAGTGGAGCAACAAACGCAAGCTCTCTACAGCAATGGCTTTGATC 6470
Qy 6181 ggcggggccctctgtgtgttcttgatgaaacccacacagagatgatacccaagcccg 6240
Dh 6471 GGGGGGCTCTCTGCTGGTGTGGATGAGAACCCACACAGATGATCCCAAGCCCGG 6530
Qy 6241 cggctctgtggaatgtgcccctaaagtgtgtcaagaagggagatcagtaagtcttaca 6300
Dh 6531 CGGTTCTGTGGAATGTTGCCCTAAGTGTGTCAAGAGAGGGGAGATCAGTAGTCTTAA 6590
Qy 6301 tctcaatgataaggagaatgtgaagctcttgcactagatgagcaatcaatgagatgga 6360
Dh 6591 TCCATAGTATGGAAGAAATGTGAAGCTTTGACATAGATGCAATCATGTCATGCA 6650
Qy 6361 aggttcagagctctggcagctgtccacatctaaataaagtgttgagatgagttataa 6420
Dh 6651 AGGTTCAAGGCTTGGCAGATGTCAGCATCTTAAATAATGATGGAATGTTATTA 6710
Qy 6421 atagttgacgaatagcaaggttccacacccggaacttgaagctgtccagatcttctga 6480
Dh 6711 ATAGTGTGAGCAATAGCAGGCTCCACCGAGCTTAACCTCTCCAGATTTCTTTGA 6770
Qy 6481 ctgcatctcccggaagtggttctaaagagaacacccggaacatgctacatacagact 6540
Dh 6771 CTTCGATTTCTGGAAGTGTCTTAAAGAGAAACACCGAGCATGCTACATATCAGCTT 6830
Qy 6541 ccaatctcaatctctctgccaagatatcagatctctcccaagggcaaaaagcga 6600
Dh 6831 CCATCTTCAATATCTCTGCGCAGATATTCAGCATCTCTCCAGAGCAAAAAGCA 6890
Qy 6601 ctccacatagaagactactctgttctcagacaacacttgaacaaatgttgtaactt 6660
Dh 6891 CTCACATATGAAAGACTACTCTGTTCTCAGACAACACTTGACCAAGTATTTGTAACCTT 6950
Qy 6661 gccaaagaccagaagatgatacacttaaaagacctctatctcaaaaaaacagaca 6720
Dh 6951 GCCAAGGACCAAGATGATGATGACCACTTAAAGACCTCTCTTACACAAAACAGACA 7010
Qy 6721 gtagtgaagctgtcagttctcacaatcttctcagagatgagaagatgaagaagacat 6780
Dh 7011 GTAGTGAAGCTGTGCACTTCTCAGATCTTTCTTACAGGATGAGAAAGTGAAGAGCTAT 7070
Qy 6781 gtagaagaatccgttcaacag 6804
Dh 7071 GTATGAAGATCTGTTCTATACGG 7094

RESULT 3
AF285167

LOCUS AF285167 10442 bp mRNA linear PRI 09-AUG-2000
DEFINITION Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA,
complete cds.
ACCESSION AF285167
VERSION AF285167.1 GI:9751518
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 10442)
Schwartz, K., Lawn, R.M., and Wade, D.P.
ABCA1 gene expression and apoA-I-mediated cholesterol efflux are
regulated by LXR
JOURNAL
2 (bases 1 to 10442)
Lawn, R.M., Wade, D.P., Garvin, M.R., Wang, X., Schwartz, K.,
Porter, J.G., Sellmeyer, J., Vaughan, A.M., and Oram, J.F.
Direct Submission
Submitted (06-JUL-2000) Discovery Research, CV Therapeutics Inc.,
3172 Porter Drive, Palo Alto, CA 94304, USA
FEATURES
source
1..10442
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/map="q31"
/cell_type="fibroblast"
/tissue_type="skin"
1..10442
/gene="ABCA1"
291..7076
/gene="ABCA1"
/codon_start=1
/product="ATP-binding cassette transporter 1"
/protein_id="AAP8175.1"
/db_xref="GI:9751518"

/translation="MNCWPDQLRLKLNLTERRRQCQLLEAVPLFTLLISVRL
SYPRVEQHECHFPNKAAGTLPWVGIIICANNPCFRYPGGAAGVGVNFKSIV
ARLSPDRRLLYSOKDTSKMDKRLVRLTQQLKSSSLKLDQFLVDNEFGSLYH
NLSPKSTVDKMLRADVILKHFVLOGVGLHLSLGSSEEMQLDQDQEVSLGTP
KERLAAERVLRSNMDIKPLIPLTINLSTSPSPKELAEAKTLLSLGTLADLPSMR
SNMDQREVFLLNNVSSSSSTIYQAVRSIVCGHEGGGLKLSLMTEDNNVLALE
GGNGEDBATFTYDNTSTPYCNDLMLNLSPLSLRLIMALKPLGLKLLYPDPAT
ROYVAELNKAFTFOELAVFHDEGMWELSPKWTFMNSOEMDLVRLMLDSRNDHWE
QQLDGLDNTADIVAFELAKHEDVQSSNSVYTWRAFNEDNOLITIRSPMECVLN
KLPIPIATEVWLINKSMELDERFMAGIYVETGTPQSLPLPHVKKIKIMDIDNERT
NLIKDGWDGPRADPEMDRKYVWGGFAVLQDVBAITRVLTGPEKTKGYMOQRY
PCYVDITFLPMSRSMPLDKTLANIYSAVITIKGIYEKARKETRMIGDNLSTLM
FSWFISLIPFLVSGILVYLKLNMLPYSQSVFVFLVFAVVTIIQCLISTLF
SRNLAAACGIIIFLLYLPLVLCVAMQVYGTFLKIFASLSPVAFVGCYFALFE
EOGIGVQWMDLFPSPVEDGFLNLTISIIMLDTFLGYMTWYIEAVFGQYGIPLPW
YFPCRTSYMGESDEKSHPSNOKRMSICMEEBETHLKLGVISIONLVKYVRODKV
AVDGLALNFEYGOITSLFNGAGKGTSTSIILGLPPTSGATIIIGKDIRSEMTIR
ONIGVCPQHNHVLFDMLTVEHITMFEYARKLGSSEKHYKARMDMALDYGKPSKLKST
SOLSGMOKRLSVALAFVGSKYIIDEPTAGVDRSRNGIELLTKTRKGTITLST
HMDHEDVDJDRITATISGKLCVSSLELKMOLGTYLLTLKHKDVBSLSLSSNNS
STVSYLKKEDEVSSSDAGLSGDSHDLTIDVSAISMLIRKHVSEARVLSDICHEL
TYVLPYPAKKEGAFVELFHEIDRLSDLGISYSISLLEBFLKVAEESGVATS
DGLTPARNRRAFGDKOSCLRPTEEDADPDSDIDPSRETDLSGMDGVSQYK
GMRLOQOOVALIMKRLILARSRRKFFQIYVLPVAVCIALVPSIYPRPKYSLE
LOPMWNEQYTVPSNDAPEDTGTIELNALITDPGRTGCMGNTIPIDPCOAGEEEN
TTAPVQTTIMDLFQNGMTWNPSPACQSSDKIKMLPVCPPAGAGLPPQKONTA
DILODTLGRNLSIDYLVKTYVQILAKSLKKIWNVERKGGFLGVSNTALDPPSOEVN
DAIQOMKRLKSLAKSDSADRFNLNSLRFGTGDTRNNVYVFNNGKGMHAIISFLAVIN
NALIRANLOKGENPSHYGITAFFNHPNLTKOOLSEVALMTTSDVLSYFANFVS
PASEVVEILOERYSAKHLOFTISGVKPYVIMSNVYMCNAYVAVTLYITITFOO
KSYVSTNLPYVALILLIYGNSITPLMTPASVYKIPSTAYVILSVNLTGINSVA
TYVLELFTDNKLNINDILKSVFLFPHFCILRGLLIDVKNQAMADALERGEENKFS
PLSWDLVGNRLPAAVAVGVFLIYVLIQYRPIRPPVNAKSLINDEDEVERERO
RLIDGGQNDIIEIKELTKIYRRKRPAVDRCVGIPECEGGLGVAGKGSFTFKM
LNGDTVTITGDAFLNNKNSITLSNIHEHOMGVCPOFDATITELTGREHVEFPALIRGY
PKEVKGVEWMAIRKLGLVYKGEKTAGNNSGKNKKSLTAMLLIGPPVYFLDEPTTG

BASE COUNT	2898 a	2297 c	2408 g	2835 t	4 others
ORIGIN	MDPRARRIMNCALSYKBERSVLTLSHMEGCPALCTRMALNVGPRCLGSVOHLK NRFGGITIVRLINGSNPDLKPVQDFEGFALPESGVILKEHRMLDYOQPSLSLARI FSLSOSKKRLHIEDYSVSQTLDDVFNFAFDQSDHDLKDSLAKKQAVDVAVLTL SFIDKEKESYV"				

Query Match	100.0%;	Score 6804;	DB 9;	Length 10442;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 6804;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	atgctctgttgcgctcgaagctgaggtctgtgctgtgtgtggaagacccctaccccttcgaagaagaa	60
Db	291	ATGGCTTGTGGGCTCAGCTGAGTGGTGGCTGGTGGGAAGAACCTTCACCTTTCAGAAAGAA	350
QY	61	caaaactgtcaagtctactgtgaagtagtcctgagctcattactctccatcccgatc	120
Db	351	CAAAcATGTCAGTGTACTGTAGGAGGGCTGGCTCTATTATTCCTTCGATCTCGATC	410
QY	121	tcgttcgcgtgagcaccaccacctataaacaatgaatgcatttccaaataaagcc	180
Db	411	TCGTTCGCGTGAAGCTATGCCACCGATGAACAACATGATGCATTTTCCAAATAAAGCC	470
QY	181	atgcctctgcaggaacacttcccttgggttcagggtatctctgtaatgcacaacccc	240
Db	471	ATGCCCTCTGCAGGAACACTTCTCTGGGTTCAGGGGATTAATCTAATGGCAACACCC	530
QY	241	tgtttcggttaaccgcgctctctgggaaggtctcccgagttgtgttgaacttaacaaatcc	300
Db	531	TGTTTCGGTATCCCGACTCTCGGGAGGCTCCCGAGTTGTTGGAAACTTAAACAAATCC	590
QY	301	atgtgctgcgcgtcttctcagatgctctggaagctctcttatacaagccgaagaagacc	360
Db	591	ATGTGGCTGCCTGTTCTCAGATGCTCGAGAGCTTCTTTATACAGCCAAAGAACACC	650
QY	361	agcctgaagaacatgcgcaaaagtctcgaaacaattacagcgagatcaagaataatcaagctca	420
Db	651	AGCATGAAGGACATGCGCCAAAGTTCTGGAACATTAACAGCATCAAAATATCCAGCTCA	710
QY	421	aacttgaagctcaagaatttcctcgtgtgagcaatgtgaacctctcgtgttccctatatac	480
Db	711	AACTTGAAGCTCAAGATTTCTCGTGTGGACATTAAGAACCTTCTGGGTTCCGTATATCAC	770
QY	481	aaactctctctcccaagttctactgtgtgcaagaatgctgagggctgatatctctccac	540
Db	771	AACTCTCTCTCCCAAGTCTACTGTGTGGACATGATCTGTAGGGCTGATGTATTTCTCCAC	830
QY	541	aaggtatatttgcgaagctacacagttacagtttgcacaagttctgtaaatgtgaataaata	600
Db	831	AAGGATTTTGGCAAGGCTACAGATTACATTTGACAAAGTCTGTGCAATGTGATCAAAATCA	890
QY	601	gaagatgatatacaacttgtgtgaccaagaagttctcgaagtttctgtgtgtccataccaagag	660
Db	891	GAAGAGATGATTCAACTTGGTGACAAAGAAAGTTTGTGACTTTGTGGCCTACCAAAGAG	950
QY	661	aaactgctgcagcagagcgagtaacttcgttcccaaatgaaatccctgaagccaactcgt	720
Db	951	AAACTGCTGCAGCAGACGAGTGATCTTGTCCAAATGGAATCTCTGAAGCAATCTCTG	1010
QY	721	agaacaactaaactacatctccctccctccgagaagaagctctgcgtgaagcccaaaaaca	780
Db	1011	AGAAcATTAACCTTACTATCTCCCTTCCGAGCAAGGACTGGCTGAAGCCCAAAAACA	1070
QY	781	ttgtctgcatagtccttgggaactctgcccaggaagctgttcaagcatgagaagctgtgagtgac	840
Db	1071	TTCGTGCATATCTTTGGGACTCTGGCCCAAGACTGTTTCAGATGAGAGCTGAGGTGAC	1130
QY	841	atgcgaagagggatgtatttcttcaacaatgttgaacagctccgaagctccctccacccaatc	900
Db	1131	ATGCGcAGAGAGGTATGTTTCTTACCAATGTGAACAGCTCCAGCTCTCCACCAACATTC	1190
QY	901	taccagagctgtgtctgtattgtctcggggacatcccgaggagggggtctgaagaataag	960

[illegible]

Db 2271 TATGAGAGAGGACGCTGTAAGAGACCATGCGATCATGCGCTTGACAAACAGATA 2330
QY 2041 ctctggttctgcttgcttcatatgaagctcaatctctctctcttgtagcgctgagctgta 2100
Db 2331 CTCTGGTTTAAAGCTGGTTTCAATAGAGCTCATCTCTCTCTCTCTCTCTCTCTCTCTCT 2390
QY 2101 gtgtcatctccgaagttaggaaacctgtgcccatacagttatcccaagcgtggtgttctc 2160
Db 2391 GTGGTCACTCTGAAAGTTAGAAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2450
QY 2161 tctctgctgctgttctgctgtgtgacaaatctctgcaatgctctctctctctctctctc 2220
Db 2451 TTCTCTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2510
QY 2221 tccagagcccaactgtgaggaagcctgtgtgaggaatcatatctctctctctctctctc 2280
Db 2511 TCCAGAGCCCAACCTGGAGAGCCTGTGGGGGATCATCTCTCTCTCTCTCTCTCTCTCT 2570
QY 2281 taagctctgtgtgtgcatgaggaactagctgtggtctcaactcaagaatctctctctag 2340
Db 2571 TAGGTCTGTGTGTGGCATGGAGACTAGTGGGCTTCACTCAAGATCTTCTGCTTACG 2630
QY 2341 ctgctgtctctctgtgcttcttggttctgctgtgagtaacttgcccttcttgagagag 2400
Db 2631 CTGCTGTCTCTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 2690
QY 2401 ggcattggaatgtagtggagcaaacctgtttagagatccgtgtgaggaagaatgttctca 2460
Db 2691 GGCATTGGAATGCAAGTGGAGCAACCTGTGTGTGAGTCTGTGTGAGGAAATGGCTTCA 2750
QY 2461 ctcaacacttgaatctcatalgtatgtctgttgacacttctctctctctctctctctg 2520
Db 2751 CTCACCACTTCGATCTCCATGATGCTGTGTGACACCTTCTCTATGGGTGATGACTG 2810
QY 2521 taattgaggtctctctctccagagcaagtaacgaatcccaagccctgtglatctcttc 2580
Db 2811 TACATTGAGGCTGTCTTCTCCAGGCCAGTACGGAATCCAGGCCCTGTGATTTTCC 2870
QY 2581 accaactccactggtgtgttgagaggaatgtatggaagaagcaacccctgttctcaacag 2640
Db 2871 ACCAATCTCTACTGCTTTTGGCGAGAAATGTATGAAAGAGCCACCTGTGTTCCAA 2930
QY 2641 aagagaatgtcagaaatctgtcatalgtgagaggaaccacccacttgaagctgtgctgc 2700
Db 2931 AAGAGAAATGTCAAGAAATCTGCATGGAGAGAACCCACCTTGAAGTGGGCTGTG 2990
QY 2701 attcgaacacctgttaaatcttaacgagatgagatggaatgtgtgtgtgtgtgtgtg 2760
Db 2991 ATTCAAAACCTGGTAAAGTCTACCGAGATGGATGAAGTGGCTGTGATGGCTGGCA 3050
QY 2761 ctgaattcttaagagggcagatcaactctctctctgagcaatgagagcgagagagag 2820
Db 3051 CTGAATTTTATAGAGGGCCAGATCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3110
QY 2821 accacactgtcaatccctgacccggtgtgtctcccccagacctcgggacacccctacatctc 2880
Db 3111 ACCACCATGTCAATCTGACCGGTTGTTCCTCCCGACTGGGACCGCCCTACATCTCTG 3170
QY 2881 ggaagaagacattcgtctgtgagatgagcaacatccgagcaaacctgtgggtgtgtctcc 2940
Db 3171 GGAAGAAAGACATTGCTGTGAGATGAGCAACATCCCGGCAAACTGGGGTCTGTGCCAG 3230
QY 2941 cataagctgtgtgttgatagatgtgtgtgtgagaagaacatctgttctatgcccgtctg 3000
Db 3231 CATTAACGTGCTGTGTGAATGTGTGTGTGTGAAGAACATCTGTGTGTGTGTGTGTGTG 3290
QY 3001 aaaaggctctctgagaagcaagtgagagcgagatgtagagagatgagccctgtagtgtgt 3060
Db 3291 AAAGGGCTCTCTGAAGACAGCTGAAGCGGAGATGAGCGAGATGGCCCTGATGTGTGT 3350
QY 3061 ttgcatcaagaagaatgtgaaagcaaaacagcaagctgtgcaagtgtagatgtagaagaag 3120
Db 3351 TTGGCATCAAGCAAGCTGAAGAAAGCAAAACAGCCAGCTGTGAGGTGGAATGCAAGAAAG 3410
QY 3121 cctatctgtgcttggcttctgctggtgagatcgaagtgtgcatctgtatgaaccaca 3180
Db 3411 CTATCTGTGGCTTGTGGCTTGTGGGGGATCTAAGTTGTATCTGTGATGAACCCCA 3470
QY 3181 gctgtgtgtgagcccttaactcccgaggggaatagtagagctgtgtgtgtgtgtgtgt 3240
Db 3471 GCTGTGTGTGTGAGCCCTTACTCCCGAGGGGAATATGGAGCTGTGCTGTGAATACCGAA 3530
QY 3241 ggcgcacacattatctctctcaacacacacacacacacacacacacacacacacac 3300
Db 3531 GGCCTGACCATTTATCTCTCTCTCAACACCAATGATGAAGCGGAGCTCTGGGGAGAG 3590
QY 3301 attgcaatcattctccatgaggaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3360
Db 3591 ATTGCCATCATCTCCCATGGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3650
QY 3361 cagctggggaagaagctactactactactactactactactactactactactactact 3420
Db 3651 CAGCTGGGAACAAGCTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 3710
QY 3421 tctgtcagaagaagtagtagacatgtgtcatcactgtgaaagaagagagagagagagag 3480
Db 3711 TCTCTGACAAACAGTAGTAGACACTGTGTCTATCTGAAAAAGAGAGAGAGAGAGAGAG 3770
QY 3481 agcagttctgt 3540
Db 3771 AGCAATTTCTGATGT 3830
QY 3541 tctgtctatctcaacactctcaataggaagcatgtgtgtgtgtgtgtgtgtgtgtgtgt 3600
Db 3831 TCTGTATCTCAACCTCATATAGGAAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3890
QY 3601 ggcagtagctgacatctgt 3660
Db 3891 GGGCATGAGCTGACCTATGT 3950
QY 3661 ctcttcaatgagatgtatgacagcgtctcagaacctgtgcaatcttctgtatgtgtgtgt 3720
Db 3951 CTCTTTCTATGAGATGT 4010
QY 3721 gagaagacctggaagaatataatctcaaggtgtgtgtgtgtgtgtgtgtgtgtgtgt 3780
Db 4011 GAGACGACCTGGAAGAAATTTCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4070
QY 3781 acctcaagatgttactctgt 3840
Db 4071 ACCTCAGATGT 4130
QY 3841 tgtctgt 3900
Db 4131 TGTCTTGT 4190
QY 3901 gaatccag 3960
Db 4191 GAATCCAG 4250
QY 3961 ggtctggaacttaacacagcaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4020
Db 4251 GGCTGGAACCTTACACAGCAAGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4310
QY 4021 agacgagatgtgaaagagatcttctgtcaagatgtgtgtgtgtgtgtgtgtgtgtgt 4080
Db 4311 AGACGGAGTGGAAAGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4370
QY 4081 ggcctgt 4140
Db 4371 GCGCTTGT 4430
QY 4141 cctgtgagtagaagaagaagtagacacattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4200
Db 4431 CCTGTGATGTACAGCAAGTAGTACATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4490

4201 accctgaactcttaacgcccctaccaaagaccgtgctcgaggaccgctgtaga 4260
4491 ACCCTGAACCTCTTAACGCCCTCACCAAGACCTGCTTGGGCCCCGCTGATGGAA 4550
4261 ggaaccccaatccagacacgcccctgacgagggaggaagagtgcacactgccca 4320
4551 GGAACCCCAATCCCAACACAGCCCTCCAGCGAGGAGAGAGTGCACACTGCCCA 4610
4321 gtcccccagacacatcagacctctccagaatgggaactggacaatgcagaccctca 4380
4611 GTTCCCAAGACATCATGAGACCTCTTCCAGAAATGGGAACATGACATGAGAACTCTCA 4670
4381 cccgcatgcccagtgtagcagcgcaaaatcaagaagatctcgtgtgtgtcccccagg 4440
4671 CCGCATGCTGAGTGTAGACGACGCAAAATCAAGAAAGATGCTGCTGTGTCCCGACGG 4730
4441 gcaaggagggtgctcctcccaaaaacaaacacacacacacacacacacacacacac 4500
4731 GCAAGGGGGCTGCTCCTCCACAAAGAAACAAACACATGCAATATCTTCAAGACCTG 4790
4501 acagaagaacacatctcgaatctcgtgtagaagcgtatgtgcagatcagccaaagc 4560
4791 ACAGAAGAAACATTTGCGATATCTGTGAGAGACGATATGCGAGATCATAGCCAAAGC 4850
4561 ttaagaacaaagtctgggtggaatgagtttagttagtggggcttccctgggtgctagt 4620
4851 TTAAAGAACAAAGATGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATG 4910
4621 aatactcaaacacttccctcgaatcagaatgaatgaatgaatgaatgaatgaatgaat 4680
4911 AATACTCAACACTTCTCTCGAGTCAAGAGTTAATGATGATGATGATGATGATGATGATG 4970
4681 caactaaagctggcgaagacagttctcagatcgatcttcaacacgcttgggaattt 4740
4971 CACTTAAAGCTGGCAAGGACAGTTCGAGATCGATTTCTCAACAGCTTGGGAAATTT 5030
4741 atacaagacttgacaccaaataatgtaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4800
5031 ATGACAGGACTGGACACCAAAATATGTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5090
4801 gcaatcagctcttccctgaatgtaacatgaatgaatgaatgaatgaatgaatgaatga 4860
5091 GCAATCAGCTCTTCTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5150
4861 ggagagaacacctgacctatggaatcagcttcaatcattccctggaatctcacaag 4920
5151 GGAGAGAACCCTTACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5210
4921 cagcagctccagaggtggtcctgtagaacacatcagtgatgtctgtgtgtgtgtgtgtgt 4980
5211 CAGCAGCTCTCAGAGGTGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 5270
4981 gtcaatcttgaatgctcctgctccagcagcttgcgtatcctgatalccaggaagcgg 5040
5271 GTCAATCTTTCGAATGCTCTGCTCCAGCCAGCTTTGCTATTCCTGATCCAGTCCAGAGCG 5330
5041 gtcaagaagaacaaacccctgcaatcagtagagtagagtagagtagagtagagtagagtag 5100
5331 GTCAAGCAAGCAAAACCTGCACTCATGATGATGATGATGATGATGATGATGATGATGATG 5390
5101 tctaatttctgtagatagtggaatagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5160
5391 TCTAATTTTGTCTGGATATGTGCAATTAGCTGTCTCCCTCCACACTGGTCAATATCATC 5450
5161 ttaactgtctcagcagaagctcctatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5220
5451 TTCAATCTGCTTCCAGCAAAATCTCATGATGATGATGATGATGATGATGATGATGATGATG 5510
5221 ctacttctgt 5280
5511 CTACTTTTGT 5570
5281 aagatcccccagacagcctatgt 5340

5571 AAGATCCCAAGACAGCTATGT 5630
5341 ggcagctgtgccacttgt 5400
5631 GGCAGCTGTGCCACTTGT 5690
5401 gatatacgaagctgt 5460
5691 GATATCTGGAAGTCCGT 5750
5461 gacatgtgaaacaaacaggaacatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5520
5751 GACATGTGAAACAAACAGGACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5810
5521 gtgtacatatacttgggaactgt 5580
5811 GTGTACCATATATCTTGGGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5870
5581 gt 5640
5871 GT 5930
5641 gtaaatgcaagcctatccctcgaatgtagaagatgtagaagatgtagaagatgtagaag 5700
5931 GTAATGCAAAAGCTATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 5990
5701 agaattcttgatgt 5760
5991 AGAATTTTGT 6050
5761 tatagaagaacggaagcctgt 5820
6051 TATAGAGAACGGAAGCTCTCTGTGACAGATTTGCTGTGTGTGTGTGTGTGTGTGTGTGT 6110
5821 tgccttgggtccttgggaatgtagaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5880
6111 TCGTTGGGCTCCTGGAGATTAATGGGCTGGAATATCATCAATCTTCAAGTGTTAACA 6170
5881 ggaataacacactgttacaagaagaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5940
6171 GGAGATACACCTGTACCGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6230
5941 atccatgaagatcatcagacatggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6000
6231 ATCCATGAAGTACATGAGAACATGGGCTTACTGCCATGTTGATGCCATCACAGAGCTG 6290
6001 ttgaactggagaagaacgltgagttccttgccttcttgaagaagtcaccagaagaaga 6060
6291 TTGACTGGAGAGAACACGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6350
6061 gttagaagaagttgt 6120
6351 GTTGGCAAGT 6410
6121 tatgtcgttaactatagtgtaggaagaacaaacgaagctctctacacagatggtgtgtgt 6180
6411 TATGCTGTGATCATATGT 6470
6181 ggcgggctccctgt 6240
6471 GGGGGGCTCTCTGT 6530
6241 cgttcttctgtgaatgt 6300
6531 CGGTTTGT 6590
6301 tctcatagataggaagaatgtgaagctcttgacttagaaggcaatcaatggtgtgtgtgt 6360
6591 TCTCATAGATAGGAAGAATGTGAAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6650
6361 aggttcaagtgcttggcaggt 6420


```
Db 6651 AGGTTACAGTCCCTTGGCAGTGTCCAGCATCTAAATAATAGTTTGGAGATGGTTATACA 67110
QY 6421 atagttgacgaatagcaagggtcccaaccggagctgaagctgtgccagatltcttga 6480
Db 6711 ATAGTTGACGAATAGCAGGGGTCCACCCGGACTGAAGCCTGTCCAGGATTTCTTTGA 6770
QY 6481 cttagcttctggaagtgttcttaagaagaacaaccggagaactgtctacataccagctt 6540
Db 6771 CTTCATTTCTCTGGAAGTGTCTAAAGAGAAACACCGGAACATGCTACATATCCACCTT 6830
QY 6541 ccacttcattatcttctctgcccagatatctcagcatcctctccagagcaaaacgca 6600
Db 6831 CCATCTTCATATCTCTCTGTGGCCAGATATTCAGCATCTCTCTCCAGACAAAACGCA 6890
QY 6601 ctccacatagaagaactactctgttctccagaacaactgtgccaagtattgtgaactt 6660
Db 6891 CTCACATAGAGACTACTCTGTCTTCACAAACACTTGACCAACTGATTTGTGAATCTT 6950
QY 6661 gccaaagaccaaaagtgaatgatacacttaaaagacctcattacacaaaaccagaca 6720
Db 6951 GCCAAGGACCAAGTATGATGATGACACTTAAAGACCTCTCATTTACCAAAAACGACACA 7010
QY 6721 gtagtggacgttgcagttctccacatcttctctacagatgagaagtgaaagtgaaagctat 6780
Db 7011 GTACTGGACGTTGCAGTTCTCACATCTTTCTTACAGGATGAGAAAGTGAAGAAAGCTAT 7070
QY 6781 gtagaagaatccctgtctacacg 6804
Db 7071 GTATGAAGAAATCCTGTTTCATACGG 7094

RESULT 4
LOCUS AX060719 10474 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 7 from Patent WO0078972.
ACCESSION AX060719
VERSION AX060719.1 GI:12406108
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn,R.M., Wade,D. and Garvin,M.
TITLE Regulation with binding cassette transporter protein abcl
JOURNAL Patent: WO 0078972-A 7 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
source location/Qualifiers
1..10474
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2906 a 2305 c 2416 g 2843 t 4 others
ORIGIN

Query Match 100.0%; Score 6802.4; DB 6; Length 10474;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6803; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 atgagctgttgagctcagctgaagtgctgctgtggaagaactccttcgaagaaga 60
Db 323 ATGGCTTGTGGCTCAGCTGAGGTGTGCTGTGGAAGAACCTCCTTTCAGAAAGAA 382
QY 61 caaacaatgcagctgttactgaagtgcctgacctctatctctctcctgctgctatc 120
Db 383 CAAACATGTCAGCTGTACTGGAAGTGGCTGCTCTATTATATCTTCTGATCCGATC 442
QY 121 tctgttcgctgagctacccacccctatgaacaacatgatgcattcttcaataaagcc 180
Db 443 TCTGTTCGGCTGAGTACCCACCTATGAACAACATGAAATGCCATTTCCTCAATTAAGCC 502
QY 181 atgacctcgaaggaactcctctggtgtcaggggattatctgaatgccaacacccc 240
|||||

Db 503 ATGCCCTTGACAGAACACTTCTTGCTGAGGGGATTATCTGTAAATGCCAACAAACCC 562
QY 241 tcttcgcttaccagactcctcctggaagctcccggaagtgttggaactttaaacaacc 300
Db 563 TGTTCCTGTACCCGACTCTCTGGGAGGCTCCCGAGTGTGTGGAACCTTTACAAATTC 622
QY 301 atttggtcgcctgttctcagaatgctcgaagcttcttatacagccagaagaacac 360
Db 623 ATTTGGCTCGCCTGTTCAGATGCTCGAGAGCTTCTTTTATACAGCCAGAAAGACAC 682
QY 361 agcatgaagaatcgcgaagaatcttgaaacattacagccagatcaagaatccaagcca 420
Db 683 AGCATGAAGAAATGGCGCAAACTTCTGAGAACATTTACAGCATGATGAAGAAATTCAGCTCA 742
QY 421 aacttgaagcttcaagatctcctggttggaacaaatgaacacttctcctggttctcatalcac 480
Db 743 AACTGGAAGCTTCAGATTTCTCGGTGAGCAATGAACACTTCTGTGGTCTCTATATAC 802
QY 481 aaactctctctccaaagtctactgttgacaagaatgctgagaggtcgtatctccac 540
Db 803 AACCTCTCTCTCCAAAGTCTACTGTGACAAAGATGCGAGGCTGATGTCATTCTCCAC 862
QY 541 aaggtatttttcaagagctacagattacattgaacaagctgtgcaatgataatca 600
Db 863 AAGGTATTTTTCAGAGGCTACCAAGTTACATTGACAACTGTGTGCAATGATCAAAATCA 922
QY 601 gaagagatgaltcaactgtgtgacaaagaattctgagcttgtgtgcttaccaaagag 660
Db 923 GAAGAGATGATTTCAACTGTGTGACCAAGATTTCTGAGCTTGTGGCTACCAAGAG 982
QY 661 aaactggtcgaagcagaagcaggtactgttcccaacatggaacatccatgaacacactcgt 720
Db 983 AAACCTGCTGCGACGACGACGAGTAATCTGTTCACATGAGCAATCTGAAACCAATCTG 1042
QY 721 agaacactaaactctacatctccctcccgacaagagctgtgtgaaagccacaacaa 780
Db 1043 AGAACATAAATCTTACATCTCTCTCTCCGAGCAAGAGCTGGCTGAAGCCACAAAACA 1102
QY 781 ttgctgcatagttctggagctctgcccagagctgttccagatgagaagctgtgagac 840
Db 1103 TTGCTGCATAGCTTGTGGAGCTGTGGCCGACGAGAGCTGTTCACATGAGAAAGCTGAGTGC 1162
QY 841 atgcagcagagagtgatgttcttgcacaaatgtgacagctcagctccctccacccaatc 900
Db 1163 ATGCGACAGAGAGTATGTTTCTGTACCAATGGAACAGCTCAGCTCTCCACCCAAATC 1222
QY 901 taacagctgtgtctcgatgtgtctgctgctgagcaccgcgaagagggggctgtgaatcaag 960
Db 1223 TACCAAGCTGTGTCTCGTATTTGTGTGCGGCGCATCCGAGGAGGGGGCTGAAGATCAAG 1282
QY 961 tctctcaactgtatgaagagacaacaactacaagaagccctcttgaaggcaatgagactgag 1020
Db 1283 TCTCTCAACTGTGTATGAGGACAACTACAAACCCCTCTTTGAGGCAATGGACTGAG 1342
QY 1021 gaagatgttgaacactctatagacaactctacaactccttacttgcataatgtatgaag 1080
Db 1343 GAAGATGCTGAACCTCTGTATGACAACTCTACAACTCTCTTACTGCAATGATTTGATGAAG 1402
QY 1081 aatttgaggtctagttctcttctcccgatattctcgaagaagctcgaagccgctgtcgtt 1140
Db 1403 AATTGGAGTCTAGTCCCTTCCGATTAATCTGGAAGGCTGGAAGCCGCTCTCTGTT 1462
QY 1141 ggaagaatccctgtatacaccctgacacccacgaagagaggtcatgagctgtgagagac 1200
Db 1463 GGGAAAGATCCGTATACACCTGACACTCCAGCCCAAGGCAAGGTGATGCTGAGGTGAAC 1522
QY 1201 aagaacctcagaagactgtgtgttccatgatalcttgaaagcaltgttggaaggaactcagc 1260
Db 1523 AAGACCTTCCAGAACTGGCTGTGTTCATGATGTGGAAGGCAATGAGGAACTCAGC 1582
QY 1261 cccaagatctggaactcctcattgaggaagaacagccaagaatgtgaactgttccgagatgctgtg 1320
Db 1583 CCCAAGATCTGAGCTTTCATGAGAAACAGCCAAAGAAATGAGACCTTGTCCGATGCTGTG 1642
```

QY 1321 gacagcaggaacatgacacatttgggaacagcagtgtgacttagattgacagcc 1380
|||||
DB 1643 GACAGCAGGAGCAATGACCACTTTTGGGAACAGCAGTTGGATGGCTTAGATTGACAGCC 1702
|||||
QY 1361 caagacatcgttggcgttttggcaagcaaccagagatgtccagtcagtaatgtttc 1440
|||||
DB 1703 CAAGCAATCGTGGGCTTTTGGCCAGACCCAGAGATGTCAGTCCAGTAATGGTTCT 1762
|||||
QY 1441 gttgacacctggagagaagcttcaacagagactaacagagcaatccagacatactcc 1500
|||||
DB 1763 GTGTACCTCGAGAGAAAGCTTTTCAACAGACACTAACCGCAATCCGGACCATATCTCCG 1822
|||||
QY 1501 ttcatgagatgtgtcaacactgaaacagctagaaccataagcaagaagcttggctc 1560
|||||
DB 1823 TTCCATGGAGTGTGTCACCACTGACCAAGCTAGAACCCATAGCAACAGAACTGTGCTCATC 1882
|||||
QY 1561 aacaagtcacatggagagctgtgtatgagagagaagtttggctgtattgtttcaactgga 1620
|||||
DB 1883 AACCAAGTCATGAGAGCTGCTGATGAGAGAAAGTTCTGGCTGGTATGTTCACTGGA 1942
|||||
QY 1621 attactcagcagcagcattgagctgtgcccacatgtcaagtaacagatccagatgacatt 1680
|||||
DB 1943 ATTACTCCAGGAGCATTTGAGCTGGCCCATCATGTCAAGTACAGATCCGATGAGACATT 2002
|||||
QY 1681 gacaaatgtggagaggaacaataaatacaagatgggttactgtggaccctgttccctcagact 1740
|||||
DB 2003 GACCAATGTGGAGAGCAAAATAAATCAAGATGGGTACTGGGACCCCTGTCTCGAGCT 2062
|||||
QY 1741 gaccccttggagagatgcgtgagctgtgggggggcttcgactacttcaagatgtgtg 1800
|||||
DB 2063 GACCCCTTGGAGAGATGGGTACCTGTGGGGGGCTTCGCCCTACTTGGGATGTGTTG 2122
|||||
QY 1801 gacagcgaacatcatcaagggtgtctgaacgggcaacggaaacactgtgtctataatgcaa 1860
|||||
DB 2123 GAGCAGGCAATCATCAGGGTGTCTGACGGGCAACGAGAAAGAACTGTGTTATGCA 2182
|||||
QY 1861 cagatgacctaccctgtttagcttgaagacatcttctgcgggtgtatgagacgggttcaa 1920
|||||
DB 2183 CAGATGCTCTATCCCTGTTACGTTGATGACATCTTCTGGGGTATGAGCCGGTCAATG 2242
|||||
QY 1921 ccccttcatagcgtgcgtcgtgatttactcagctgtgctgtatcatcaagggtcgtg 1980
|||||
DB 2243 CCCCTTCTATGACGCTGGCTGGATTTACTGAGTGGCTGTATCATCAAGGGCATCGG 2302
|||||
QY 1981 tatgagaagagagcagcgtctgaagaagacatgtcgatcatatggcctgtgaacagcata 2040
|||||
DB 2303 TATGAGAAAGAGGACGCGCTGAAGAGACCATGCGATCATGCGCTGGACAAACAGCAT 2362
|||||
QY 2041 cctcgttttagctgttcaatagcttagctcattctccttctgttgaagcgtgcgtgcta 2100
|||||
DB 2363 CTCTGTTAGCTGTTCAATGATAGCCCTCATTTCTTCTGTGAGCCCTGGCTGCTGCT 2422
|||||
QY 2101 gttgatacctctgaagtttagaagaacctgtctccctacagatgataccagcgtgtgttctc 2160
|||||
DB 2423 GGTGCTATCTGATAGTTAGGAAACCGTGCCTACAGATGATCCACAGCTGTGTTGTC 2482
|||||
QY 2161 ttcctgtccgtgttgcgtgtgtgaataacccgtcagtgcttccgtattagcaactcttc 2220
|||||
DB 2483 TTCTCTTCGCTGTTGCTGTGAGCAATCTGCAATGCTTCTGATTAAGCAACACTCTTC 2542
|||||
QY 2221 tccaagagcaacctgtgcaagacccgttggggatcatcatctacttcaacgtgttaccgtcc 2280
|||||
DB 2543 TCCAGAGCCAACTGCGACAGCCTGTGGGGCATCATCTACTTCAAGCTGTACCTGCC 2602
|||||
QY 2281 tacgtctgtgtgtgcatgagcaagactaagtgagcttcaacataaagatcttcgttagc 2340
|||||
DB 2603 TACGTCTGTGTGTGAGATGGAGACTAGTGGGCTTCACTCACTCAAGATCTTCCGTACG 2662
|||||
QY 2341 ctgctgttccctgtgtgcttttgggttggctgtgagtaacttggccctttttagagagcag 2400
|||||
DB 2663 CTGCTGTCTCTGTGCTTTTGGCTTGGCTGTGAGTACTTGCCTTTTGGAGGAGAG 2722

QY 2401 ggcattggagatgcagtgaggacaacactgtttgagagctcctgttggaggaatggttcaat 2460
|||||
DB 2723 GGCATTGGAGTGTGAGTGGGCAACCTGTTTGAAGTCTGTGGAGGAAATGGCTTCAAT 2782
|||||
QY 2461 ctcaacactctgacttccatgactgctgttgaacacttccctatgtgggttgaactgtg 2520
|||||
DB 2783 CTACACCACTTCATCTCCAGATGCTGTGACACTTCTCTGATGGGGTATGACCTGG 2842
|||||
QY 2521 tacattgagctgttcttccaaagccagtaagaaatcccaagccctgtgtatttctctgc 2580
|||||
DB 2843 TACATTGAGCTGTCTTCCAGGCCAGTACGGAATTCACAGGCCCTGTGATTTCTTCC 2902
|||||
QY 2581 accaagctcctacgtgttggcgaggaagatgataagaagccacacttggtttccaaacag 2640
|||||
DB 2903 ACCAAGTCTACTGTGTTTGGCGAGAAAGTATGATGAAGAGCCACCTGTGTTCAACCA 2962
|||||
QY 2641 aagagatgtcagaatctcatgagagaggaacccacacttgaagcttggcgtgtctc 2700
|||||
DB 2963 AAGGATGTCAAGAAATCTCATGAGAGAACCCACCTTGAAGCTGGGCTGTCC 3022
|||||
QY 2701 attcaagaacctgtataaagcttcaacagatgtggaatgaggtgtgtctgtatgtcgtgca 2760
|||||
DB 3023 ATTCAAGACCTGTGTAAGTCTACCGAGATGGATGAAGGTGGCTGTGATGGCTGGA 3082
|||||
QY 2761 ctgaaatttataagggccagatcaacttctcctgtgggccaacatgagcgggaaagacg 2820
|||||
DB 3083 CTGAATTTTATGAGGCGCAGATCACCTCTTCTGTGGCCACATGAGCGGGGAAGAGC 3142
|||||
QY 2821 accacacatgcaactcctgacccggtgttcccccgcgactcgggcaacgcctacactcgt 2880
|||||
DB 3143 ACCACCATGTCAACTGACCGGGGTGTCCCCCGACCTCGGGCAACCGCTTCATCTC 3202
|||||
QY 2881 ggaaaaaacatctgcctcttgatgagatgagacacatccggaagaaacttgggggtcttcccg 2940
|||||
DB 3203 GGAATAACATTCCTCTGTGATGAGACCATCCGGAGAACTGGGGCTGTCTCCACG 3262
|||||
QY 2941 cataagctgtcgttctgacatgctgactgtcgaagaacacatctgttctatgcccgcttg 3000
|||||
DB 3263 CATACGCTGCTGTTGACATGCTGACTGTGAAGAACATCTGCTGTTGCCCGCTTG 3322
|||||
QY 3001 aaaggctctctgaagacagctgaaagcggagatgtgaagcaatgtgcccgtgttgtgt 3060
|||||
DB 3323 AAAAGGCTCTCTGGAAGACAGTGAAGCGGAGATGAGAGAGATGCGCTGTGATGTTG 3382
|||||
QY 3061 ttgcataaagcaagctgaaagcaaaacaaagcagctgttcaagtgtgaatgtcagagaag 3120
|||||
DB 3383 TTGCCATTAACCAAGCTGAAGAAACCAAGCAACGCTGTGAGTGAATGACAGAGAA 3442
|||||
QY 3121 ctactgtgctctgtgccttgtctcggggatctaagttgtcaltctgtatgaaccaca 3180
|||||
DB 3443 CTATCTGTGGCTTGGCTTGTGCGGGGATCTAAGGTTGTCATTTGATGAACCCACA 3502
|||||
QY 3181 gctgtgtgtgacacttactcccgaggggaatataggagctgctgtcgaatccggaca 3240
|||||
DB 3503 GCTGTTGTGACCTTACTTCCGAGGGGAATATGGAAGCTGCTGTGAATATCCGACAA 3562
|||||
QY 3241 ggcgcacacattatctcttcaacaacacatgatatgaagcggcgtccctggggagagc 3300
|||||
DB 3563 GCGCGCACCATTAATTTCTCTACACACACACATGATGAAGCGAGACGTCCTGGGGACAG 3622
|||||
QY 3301 attgcacatctctccatlggaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3360
|||||
DB 3623 ATTGCCATCATCTCCATGGGAAGCTGTGCTGTGGCTCTCTCTCTCTCTCTCTCTCT 3682
|||||
QY 3361 cagctgggaagaagcttactactgacttggttcaagaagaatgtggaatccctccctcagt 3420
|||||
DB 3683 CAGCTGGGAACAGGCTTACTTACCTGTGACTTGGTCAAGAAAGTGTGGAATCTCTCTCAGT 3742
|||||
QY 3421 tctcgaagaacagtagtagcactgtgtcactacacttgaaaaaagagagcaggttctcag 3480
|||||
DB 3743 TCTCTCAAGAAACAGTAGAGACACTGTGTCAATACCTGAAGAAAGAGAGACAGTGTTCAG 3802
|||||
QY 3481 agcagttctgactgtgccttggcagagcaatgagagtgacaagctgtgacacatcgtatgtc 3540

Db	3803	ACCAGTTCTGATGCTGGCGCTGGACGAGCAGCATGAGAGTGACACGCTGCACATTCAGATGTC	3862
OY	3541	tctgtatctccaactcatcagaagaatgltgtgaagcccgctgtgtgaagacta	3600
Db	3863	TCTGCTATCTCCAACTTCATDAGGAACATGTCTTGAAACCCGGCTGGTGGAAACATA	3922
OY	3601	gggcatgtgactgaactatgtgtgtccatatgaagctgtctaaagaaggaaccttttgaa	3660
Db	3923	GGGCAATGAGCTGACCTATGTGCTCCATATGAAGTGCTAAAGAGGAGACCTTTGTGGAA	3982
OY	3661	cccttcaatgatgatgaagccgctctcaagctgtggcattctagtatgaatccta	3720
Db	3983	CTCTTTCATGTGAGATTGATGACCGGCTCTCGACCTGGGATTTCAGTATGGCATCTCA	4042
OY	3721	gagacgaccctgggaagaataatctccaagtggtccgaagagatgtgggttgatgtctag	3780
Db	4043	GAGAGACCCCTGGAAAGAAATTTCTTAAGGTGGCCGAAAGAGATGGGGTGGATGTGAG	4102
OY	3781	acctgaatgtgtacctgtgccagaagaacgaagcgggctctcgggagacaagcaagc	3840
Db	4103	ACCTGAGATGTGACTTGTCCAGCAAGCAAGAAAGCGCGGGCTTGGGGACAGCAGAGC	4162
OY	3841	tgcttcgcccgttactatgaagtgtgtgtcgtgtatccaatgatcttgcacatagacca	3900
Db	4163	TGCTTTCACCCGTTCTACTGAAAGATGATGCTGCTGATCCAAATGATTCTGACATAGACCA	4222
OY	3901	gaatccagaagagaacagtctgtccagtgtgatgtgaatgtgaagaaggtctccacagtgtaa	3960
Db	4223	GAATCCAGAGAGACAGACTTGTCTAGTGGGATGAGTGGAAAGGTTCTACCAGTGAAA	4282
OY	3961	ggctgtgaaacttaacagcaacagtttgygccccttgttggaagagatgctaatgtgc	4020
Db	4283	GGCTGGAAACTTACACAGCAACAGTTGTGGCCCTTTGTGGAAAGACATGCTAATTGGC	4342
OY	4021	agaacgagtcggaagaatttttgcctcagattgtctctgcagctgtgttgttgcatt	4080
Db	4343	AGACGGAGTGGGAAAGATTTTTTGTCTCAGATTGTCTTGCCACGCTGTGTGTGCGATT	4402
OY	4081	ggccctgtgttcagctgtatcgtgtgccaccttttggaaaglaaccacagcttgaacttcag	4140
Db	4403	GCCCTTGTGTTCACCCCTGATGCTGTGCCACCTTTGGCAATCCCCAGCTGGAACCTTAG	4462
OY	4141	ccctgtgattgtacaacggagaagatcacattgttcagaaatgatgtccctcgaagaacggga	4200
Db	4463	CCCTGTGATGTAAACAGCAACGTACAAATTTGTACGAATGATGCTCTGGAAGAACGGGA	4522
OY	4201	acctgtgaactctaaacggccctcaccaagaacccctgtgttcggaaaccgctgtatgaa	4260
Db	4523	ACCTGTGAACCTTTAAAGCGCCCTCACCAAAAGACCTGGGTTGGGACCCGCTGTATGGAA	4582
OY	4261	ggaacccaatcccgagaacagccctctgcagcgaagtggaagatgtgaccaatgtcccca	4320
Db	4583	GGAAACCCAAATCCCAAGACAGCCCTCTCCAGGGAGGGGAGAAAGATGGACACACGTCCCA	4642
OY	4321	gttccccaagacataatgtgaacccctcttcacgaatgtggaactgtgaacatgtcaaaccttca	4380
Db	4643	GTTCGCCAGACATCATGAGACCTTTCCGAGATGGGAACGTGACATGTGCAACCCTTCA	4702
OY	4381	ccgtgatgtcagtgatgtacgacgagcaaaatcaagaagaatgtgtgcctgtgtgtcccccagg	4440
Db	4703	CCCTGCATGCCAGGTGTAGCAGCAGCAAAAATCAAGAGATGTGCTCTGTGTGCCCCAGGG	4762
OY	4441	ggcaggggggtgtgcctctccacaagaagaacaaacacttgaagtataccttgaagcctg	4500
Db	4763	GCAAGGGGGGCTGCTCTCTCCAAAGAAAGAAACAAACACTGGAGATTCCTTCAAGGACTTG	4822
OY	4501	acaggaagaacaattcggatatatcttgytgaagaacgtatgtgcagatcatagccaaagc	4560
Db	4823	ACAAGGAAGAAACATTTTCGATTTATCTGTGGAAAGACTGTATGCGATCATATGCCAAAGC	4882
OY	4561	ttaagaacaagaatctgggtgaatgaagtgttgatgtgacggcttttccctgggtgtcagt	4620

Db	4883	TTAAGAACAAATCTGGGTGAATGAGTTTAGATATGGGGGCTTTTCCGTGGTGCAT	494
QY	4621	aatactcaagcactctccgagfctcaagaagttaatgaatgcatacaacaatlgaaaga	4680
Db	4943	AATACTCAAGCACTTCCCTCCAGATCAAGAAATTTAATATCCCTCAACCAATGAAAGAA	5007
QY	4681	caactcaaaactcgccaagaagcaattctgcagatcgattctcaaaagcttggaaattt	4740
Db	5003	CACCTTAAGCTGGCCAAAGACAGTTCTGCAGATCGATTTTCTCAACAGCTTGGACATTT	5065
QY	4741	atgacaggactgagacaccagaataatgtaaggtygtgtcaatacaagaagcttgcac	4800
Db	5063	ATGACAGGACTGTGACACCAAGAAATTAATGTAAGGTGTGGTTCAATTAACAAGGCTGCAT	5122
QY	4801	ggaatcagactcttccttbaatgatacaaatgacattctccggccaactctgcaaaag	4866
Db	5123	GCATACAGCTCTTCTCGAAATGTATCAACAAATGCCATTTCTCGGGCCAACTCGCAAAAG	5183
QY	4861	ggaagagaacctagccaattatgaaattacatgcttcaatcatccctgtaactcccaag	4920
Db	5183	GGAGAGAACCCGAGCGAATTATGGAATTTACGTCTTCAATATCCCTGATCTCAACAG	5244
QY	4921	caggcaagctctcaagatgagctctgaatgacacatcagltgagatgcttgtccatctgt	4980
Db	5243	CAGCAGCTCTCAGAGGTGGCTCTCATATCCCAATCAATGATGATCCCTTGTGCATCTGT	5302
QY	4981	gfcacatttgcagatgctctctgctccgccaagatttggtaattctcttgatccaagaagg	5044
Db	5303	GTCACTTTTGCATATGTCTTGCTCCCGACCGACTTTGTGCTATTTCTGTATCCATCAAGAGGG	5362
QY	5041	gtcagcaaaagcaaaacacctgcagltcatcatagtgagatgaagctgtcaatacagctgc	5100
Db	5363	GTCAACAAAGCAAAACACCTGTCAATTCATCATGAGTGAAGTGAAGCTTGTCAATCTGGCTC	5422
QY	5101	tctaatttgccttgagatgtaatgaattgaattgtccctgcgaacctgttatcatc	5160
Db	5423	TCTAATTTTGTCTGGATATGTGCAATTTACGTTGTCCCTGCACACTGGTCAATTAATCATC	5482
QY	5161	ttcatctgcttcacagagaagctccatgtytctctccaacatctgctgtgtgaacctt	5220
Db	5483	TTCACTGCTCTTCCAGACGAGAGTCTATATGTCTCTCCACCAATCTGGCTGTGCTAACCTT	5542
QY	5221	ctaatttgcctgtatgagtgagtgtaatacaacatccatcaatgtaaccagctccttgtgttc	5280
Db	5543	CTACTTTTGTCTGTATGGGTGGTCAATTCACACCTCTCATGTACCAAGCCCTTTGTGTTC	5602
QY	5281	aagatccccaagaacagactatgtygtctcaacagagtgtaaccttcaatgtgacat	5340
Db	5603	AAGATCCCAACACAGCTTATGTGTGTCTCACAGGCTTAACCTCTTCAATTGTGCAATTAT	5662
QY	5341	ggcagcgttggcacacttgtgtctggaagctgttcaaccgaacaataagctgaataatcaat	5400
Db	5663	GGCAGCGTGGCACACTTTGTGTCTGGAGAGCTTTTACCGCAATTAACCTGAATTAATTCATAT	5722
QY	5401	gatactcgaagctcggtgtcttgatcttccaacatitttgccttggagcgaggctcatc	5460
Db	5723	GATATCTCGAAGTCCGTTGTTCTTGATCTTCCACATTTTGTGCTGGAGCAGGGCTCATTC	5782
QY	5461	gacatggttgaaaaaaacccaggaatgagctgtatgctccctggaaagglttgggaggaatcgctt	5520
Db	5783	GACATGTGTGAATAAACCCAGCAATGGCTGATGGCCCTTGAAAGGTTTGGGAGATATCGCTTT	5842
QY	5521	gtgtccaccattatcttgggaacttgttgggaagaaacactcttcgcacatgycgvtggaagg	5580
Db	5843	GTGTACACCAATTATCTTGGGACTTGTGGAGACAAACCTTTGGCCATGGCCGTGGAAGGG	5902
QY	5581	gttgggtctctccatlaactgtctgtacacgaataagatcttcatcaaggccaagact	5640
Db	5903	GTGGTGTCTTCTCTCATTTACTGTCTTGATCCAGTACAGATTTCTTATAGGCCCAAGACT	5962
QY	5641	gtaaatgcaaaagctatctctctgtgaatgaagaatgaagaatgtaagtcggaagaacag	5700
Db	5963	GTAATGTCAAAAGCTATCTCTCTGATGATGAATGAAGATGTGAGCGGGGAAGACAG	6022

QY 5701 agaattcttgaatgagggccgaatgacatcttagaatacaaggagttgacgaagata 5760
 |||||||
 Db 6023 AGAATCTTGATGATGGAGAGCCGAGATGACATCTTGAATATCAAGAGATTGACGAAGATA 6082
 QY 5761 tatagaaggaaggaagagctgtctgtgaagatttgctgagcaattctctgtgtag 5820
 |||||||
 Db 6083 TATAGAAGGAAGGAGGAGGCTGCTGTGACAGATTTGGGTGGGCAATTCCTCTGTGTAG 6142
 QY 5821 tgccttgaggtccctgggaatgagggctggaataatcaacttcaagatglttaaa 5880
 |||||||
 Db 6143 TGCTTTGGGCTCCTGGGAGTTATGGGGCGGAAATTCATCACTTCAAGATGTTAACA 6202
 QY 5881 ggaagatacaactgttaccagaagagatgcttcttcaaaaaaatgatatcttaacaac 5940
 |||||||
 Db 6203 GGAGATACCACTGTTACCAAGAGATGCTTCTTACAAAAATAGTATCTTATCAAC 6262
 QY 5941 atccatgaagtatcatcagaacatgggctacttgccctcaagttgatgccatcacagagctg 6000
 |||||||
 Db 6263 ATCCATGAATATACATCAAGAACATGGGCTACTGCCCTCAGTTTATGCCATCAGAGCTG 6322
 QY 6001 ttgacttggagagaacacgttgaatcttgccttcttgaagagagttcccaagaagaag 6060
 |||||||
 Db 6323 TTGACTGGAGAGAACACGTGAGATCTTGGCCCTTTGAGAGAGTCCAGAGAAAGAA 6382
 QY 6061 gttggcaagttgtgagtggtgagcttcggaataatgagctgtgagatgtagaagaaaa 6120
 |||||||
 Db 6383 GTTGGCAAGGTTGGTGAGTGCGCCATTCGGAAACTGGGCTCTGAAATGTGAGAAATA 6442
 QY 6121 tatctgttactactatgtgaggaacaacaagaagctctctcaagccatgagtttgatc 6180
 |||||||
 Db 6443 TATGCTGTGATCTATGATGAGGCAACAAACGCAAGCTCTTACAGCATGCGTTTGATC 6502
 QY 6181 ggcgggctccctgtgtgttcttgaatgaacccaacagagcatgagatcccaaaagccgg 6240
 |||||||
 Db 6503 GCGCGGCTCCTGCTGTGCTTCTGATGAACCCACACAGCATGATGCCAAAGCCCGG 6562
 QY 6241 cggctcttgggaatgtgcccctcaagtggttcaaggaagggagatgagtagtcttaca 6300
 |||||||
 Db 6563 CGGTTCTTGGGAATTTGCTCCCTTAAGTGTGTCAAGGAGGGAGATAGTAGTCTTACA 6622
 QY 6301 tctaatagatgagaatgtgaagctcttgcactagaatgagcaatcagatglttaatgga 6360
 |||||||
 Db 6623 TCTCATGATGATGAGAAATGTAAGATCTTGTGACATGAGATGCAATGATGATGA 6682
 QY 6361 aggttcaggtgcttggcagtggtccagcatctaaataatgagttgagatggttataca 6420
 |||||||
 Db 6683 AGGTTCAAGTGCTTGGCAGAGTCCACATCTAATAAATAGTGTGAGATGTTATACA 6742
 QY 6421 atagttgaagaatagcagggctccaccggagctgaagcctgtccagagatcttcttga 6480
 |||||||
 Db 6743 ATAGTTGATGACAAATAGCAGGGTCCAAACCGGACCTGAAAGCTGTCCAGATTTCTTGA 6802
 QY 6481 ctgcattctcctgggaatgtgtctaaagaagaacacccgaacatgltactaactacagct 6540
 |||||||
 Db 6803 CTGTGATTTCTTGGAAGTGTCTTAAGAAGAACACCGGAACATGCTAATACACAGCT 6862
 QY 6541 ccaatcttaattatcttctctggcagagatatcaagcatctctccagagcaaaaaagga 6600
 |||||||
 Db 6863 CCATCTTCATATCTTCTCTGCGCAGGATATTCAGCATCCCTCCCAAGAGCAAAAAACGA 6922
 QY 6601 ctcccaatagaagactactgtgttctcagaacaacacttgaacagatgltgtaactt 6660
 |||||||
 Db 6923 CTCCCATAGAGAGACTACTCTGTTTCTAGCAACACACTTGCACCAAGTATTTGTAACTTT 6982
 QY 6661 gccaaagaccaaatgtagatgataacttaaaagacactctcatatcacaaaaacagaca 6720
 |||||||
 Db 6983 GCCAAGAGCAAAAGTAGATGATGACCACTTAAGAAGCTCTCATTAACAAAAACAGACA 7042
 QY 6721 gtagtggacgttgcagttctcaacatcttcttcaagagatgagaagtagaagctat 6780
 |||||||
 Db 7043 GTAGTGGACGTTGACAGTTCTCAGATCTTCTACAGAGATGAGAAAGTGAAGAAAGCTAT 7102

QY 6781 gtagaagaatctgttcatagc 6804
 |||||||
 Db 7103 GTATGAGATCTCTTCTATACG 7126

RESULT 5
 AX060721 10474 bp DNA linear PAT 22-JAN-2001
 LOCUS Sequence 9 from Patent WO0078972.
 DEFINITION AX060721
 ACCESSION AX060721
 VERSION AX060721.1 GI:12406109
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 10474)
 AUTHORS Lawn, R.M., Wade, D. and Garvin, M.
 TITLE Regulation with binding cassette transporter protein abcl
 JOURNAL Patent: WO 0078972-A 9 28-DEC-2000;
 CV THERAPEUTICS, INC. (US)

FEATURES
 source location/Qualifiers
 1..10474
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 2907 a 2304 c 2415 g 2844 t 4 others
 ORIGIN

Query Match 100.0%; Score 6802.4; DB 6; Length 10474;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 6803; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 atggctgtgtgctcgaagtgagtggtgtgtgtgtggaagaaccttcacagagaaga 60
 |||||||
 Db 323 ATGGCTGTGTGGCTCCTCAGCTGAGGTTGCTGTGTGGAAGACCTTCTTCAAGAAAGA 382
 QY 61 caaacatgcaagctgttacttgaagtgagtggtgtgtgtgtgtgtgtgtgtgtgtgtgt 120
 |||||||
 Db 383 CAACAATGTCAGAGTGTACTGTGAAGTGGCTGGCTCTATTATCTCTGATCTGATC 442
 QY 121 tctgttcgctgagagctaccaccctatgaacaacatgaaatgacatcttccaaataagcc 180
 |||||||
 Db 443 TCTGTTCGGCTGAGTACCCACCTATGAACAACATGAATGCTATTTCCTCAATTAAGCC 502
 QY 181 atgccccttgcagaagacacttcttctgttcaagggagatctgttaatgccaacaacccc 240
 |||||||
 Db 503 ATGCCCTCTGCAGGAACACTTCTTGGGTTCAGGGATTAATCTGTATGCAACAAACCC 562
 QY 241 tgttccgttaccgactcctgtggagagctcccgagagtggttggaaacttcaacaatcc 300
 |||||||
 Db 563 TGTTTCGGTACCCGAGCTCCTGGGAGGCTCCCGAGTGTGGAATCTTAAACAAATCC 622
 QY 301 atgtgagctgcctgttctcagaatgctcggagagcttcttataagccagaagaagacac 360
 |||||||
 Db 623 ATGTGGCTCGCTGTTCTCAGATGCTCGAGGCTCTTTTATACGCCAGAAAGACACC 682
 QY 361 agcatgaagacatgagcgaagttctgagaacattcaagaagaatccagactca 420
 |||||||
 Db 683 AGCATGAAGACATGGCAGAAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA 742
 QY 421 aacttgaagttcaagaatctcgttggacaatgaaacacttcttgggttccataacac 480
 |||||||
 Db 743 AACTTGAAGCTTCAAGATTCTCGTGGACAAATGAACCTTCTGCTGGTCCATATCAC 802
 QY 481 aacctctctcccaagctactgttggacaagaatgctgaagggctgaatgcaatctccac 540
 |||||||
 Db 803 AACCTCTCTCCCAAGTCTACTGTGGACAAAGATCTGAGGCTGATGTATCTATCTCCAC 862
 QY 541 aaggaatttggaaaggctaccagttacatttgaagaagctgtgcaatgagatcaaatca 600
 |||||||
 Db 863 AAGGATTTTGGAGGCTACAGATTACATTGACAAAGTGTGCAATGATCAATAATCA 922

QY 601 gaagagatgatcaacttggtgaccagaagttcttgagcttctggtctacccaagag 660
Db 923 GAGAGATGATTCACCTGGTGACCACAAAGTTCTGTGGCTTGTGGCTACCAAGAG 982
QY 661 aaactggtcgaagcagacgagtaacttgctcacaatggacatccctgaagccaactctg 720
Db 983 AAACGGCTGACGACGACGACGACTTGTGTTCCAACTGACATCTGAAACCAATCCTG 1042
QY 721 agaacactaaactacatcctcctcctccgaagagagctggtctgaagccacaaaaa 780
Db 1043 AGAACACTAAACTCTACATCTCCCTCCGAGCAAGAGGTGGCTGAAGCCACAAAAACA 1102
QY 781 ttgctgaaatcttggtgaccttgccagagagctgtctgcaatgaaagctgagtgac 840
Db 1103 TTGCTGCAATGCTTGGGAGCTGGCCAGAGGCTGTTCACAGAGAAAGCTGAGAGAC 1162
QY 841 atgagacagaggtgagttcttcaccaatgtagaacagctcccaactcctccaccaatc 900
Db 1163 ATGGGACAGGAGGTGATGTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC 1222
QY 901 taacagagctgtctcgtlatgtctcgggacatcccgaggaggggggctgaagatcaag 960
Db 1223 TACAGAGCTGTGTCTCTATGTCTGGGGCATCCGAGGGAGGGGGCTGAAGATCAAG 1282
QY 961 tctctcaactgtatgaggaacaactacaaagccctcttggaagcaatgagctgag 1020
Db 1283 TCTCTCAACTGTGTATGAGACAACTACAAAGCCCTTGTGAGGCAATGAGCAGCTAG 1342
QY 1021 gaagaatcgaacactctatgaaactctacactcctactctgaatgtagatgaag 1080
Db 1343 GAAGATCTGAAACCTTCTATGACAACTTACAACTCCTTACTGCAATGATTTGATGAAG 1402
QY 1081 aatttgagcttaactcctctccgcatatctctgaaagctctgaagccgctgctcgt 1140
Db 1403 AATTGAGAGTCTACTCTCTTCCGATATCTGGAAGACCTCTGAAAGCCGCTGCTCTGT 1462
QY 1141 gggagaatcctglatacacttgacactccagccaagaagagctgagtgagtgagac 1200
Db 1463 GGGAGAGTCTGTATACACTGACACTCCAGCCACAAAGGAGGTGATGGCTGAGGTGAAC 1522
QY 1201 aagacctccagaagacgtgtgtgttccatgactctggaagcaatgtggaagaactcag 1260
Db 1523 AAGACCTTCCAGGAACCTGGCTGTGTTCATGATCTGAAAGCATGTGGGAGAACTCAG 1582
QY 1261 cccaagatcctgacactctgaggaacaagcaagaatggaactctgcagatgctgttg 1320
Db 1583 CCCAAGATCTGGAACCTTCATGAGAACAGCCAGAAATGAGACTTGTCCGATGCTGTG 1642
QY 1321 gacagcagggacaatgacactcttggaagcagagctgagtgagcttagatlgagacc 1380
Db 1643 GACAGCAGGGACAATGACCTTTTGGGAACACACTTGATGGCTTAAATGACAGCC 1702
QY 1381 caagacatcgtggtcttcttgccaagcaccagagagatgctcagatcagatgcttct 1440
Db 1703 CAGACATCTGTGCGCTTTTGGCCAAAGCACCAAGAGATGTCCAGTCCAGTATGTTT 1762
QY 1441 gtttacacctggaagagacttcaacgagactaaccaagcaatccggaacataltcgc 1500
Db 1763 GTGTACACCTGAGAGAAAGCTTCAACGAGACTAACCCAGGCAATCCGGACATATTCGC 1822
QY 1501 ttcaatgagtggttcaacctgaaacaagctagaaaccaatgacaagagatctggtctatc 1560
Db 1823 TTATGGAAGTGTCAACCTGAAACAGCTGAGAACCCATGCAACAACTTGTGGCTCAGC 1882
QY 1561 aacaagttcatggaagctgtgtagaggaagttcttggtcgtgtatgtgttcaactgga 1620
Db 1883 AACAACTTCATGGAGCTGCTGGATGAGAGAGTCTGTGGCTGTATTTGTTCACCTGGA 1942
QY 1621 attactccagagcagcatgtgagctgccaatcatgttcaagttacaagatccgaatggacat 1680
Db 1943 ATTACTCCAGGAGCAATGAGCTGCCCATCATGTCAATGATACAAAGATCCGATGACATTT 2002
QY 1681 gacaatgtgagaggaacaataaatacaagatgtgtatgtggaacctggtcctcagact 1740

Db 2003 GACAAATGTGAGAGGACCAATAAATCAAGGATGGTACTTGGACCTGTCTGAGCT 2062
QY 1741 gacctcttgaggaactgtgtaactgtctggggggtcttcgctactctgcaagatgtgtg 1800
Db 2063 GACCCCTTGGAGACATGTGTACGTCTGGGGGGCTTTCCTACTTGCAGATGTGGTG 2122
QY 1801 gaacaggaactacacaggtgtctgacggtcaccggaagaagaactggtgtctatgtcaa 1860
Db 2123 GACACGACCAATCATCAGGGTGTCTGACGGGACCCGAGAAAGAAACTGTGTCTATTTGCA 2182
QY 1861 cagatgccatccctcgttactgtagtacatctctcgtgggtgtagagccgtgcaatg 1920
Db 2183 CAGATGCCATTCCTTACCTGTGATGACATCTTTCGCGGGTATGAGCCGGTCAATG 2242
QY 1921 cccctctatagctgtgcctgattactaagtgtgtgtatcatcaagggatctg 1980
Db 2243 CCCCTTTCATGACGCTGGCTGATTTACTGATGCTGTGATCATCAAGGGCATTCGTG 2302
QY 1981 tatgaaagagagcagcgtgaaagacatgagatcatggtcctlgacaacagata 2040
Db 2303 TATGAAAGAGAGGACAGGCTGAAAGAACATCGGATCATGAGGCTTGACAAACGATA 2362
QY 2041 cctcgtttagctgttactatgtagctcatctcctctctgtgtagcgtggtcgtcta 2100
Db 2363 CTCTGTTTACCTGTCTATATAGTACCTCATCTCTCTTCTGTGAGCGCTGGCTGCTA 2422
QY 2101 gttgtatccttaagattgaaactgtctgcccctacagtgatccaggtgtgtgtct 2160
Db 2423 GTGTGATCCTTAAGTTAGAGAAACCTGCTCCCTTACAATGATCCAGAGGTGTGTGTC 2482
QY 2161 ttccgtctcgtgtgtgtgtgtgtagaaatcctgcagtgcttctctgtagaacactctc 2220
Db 2483 TTCTGCTCCGTGTGTGTGTGTGTGACAACTCTGAGTCTCTGATGACACACTCTTC 2542
QY 2221 tccagagcaactgtagcagcagcgtgtgaggagatcatctactcaagcttactctgcc 2280
Db 2543 TCCAGAGCCAACTGACAGACAGCCTGTGGGACATCATCTACTTACGCTTACTCTGCC 2602
QY 2281 taegtcctgtgtgtggaatggaagactacgtgtggtctcaactcaaatcttcagtc 2340
Db 2603 TACGTCTGT 2662
QY 2341 ctgctgtcctcgt 2400
Db 2663 CTGCTGTCTCTGT 2722
QY 2401 ggcattgtagtgcagtggaacaactgtlttagagctcgtgtggaagaatgagcttcaat 2460
Db 2723 GGCATTTGAGTGCAGGTGGGACAACTGTTTGAAGTCTGTGAGAGTGGCTTCAAT 2782
QY 2461 ctcaacacttgcactcctatgactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2520
Db 2783 CTCACCACTTGCATCTCATATGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2842
QY 2521 tacattgagctgtctctccagccagtlaggaatttccagggccctgtatttctctgc 2580
Db 2843 TACATTTAGGCTGTCTTCCAGGCCATGACGAATTCACAGCCCTGTGTATTTCTCTGC 2902
QY 2581 accaagttcactgtgtgtggaagaaagtatgtagaagagccacccctgtgttccaacag 2640
Db 2903 ACCAAGTCTCTACTGT 2962
QY 2641 aagaagatgtcaagaatctgtagaaggaagaaccccaacttgaagctggagctgtctc 2700
Db 2963 AAGGAATGTAGAAATCTGCATGTGAGAGAAACCCCACTTGAAGCTGGGCTGTCTCC 3022
QY 2701 attcagaacctgttaaaagtctacagagatgtagaagtggtgtgtgtgtgtgtgtgt 2760
Db 3023 ATTCCAGAACTGTATAAAGTCTACGAGATGGATGAAGTGGCTGTGTGTGTGTGTGTGT 3082
QY 2761 ctgaattttatgagggccagatcactcctcctctggtgcacaaatggaagcgggaaagc 2820

Db	3083	CTGATTTTTATGAGGGCCAGATTCACCTTCCTTGGGACCACAAATGAGCGGGGAAGACG	3142
Qy	2821	acccecatgtcaatccctgacccgggtgtgtcccccgaactcgggcaacgcgtcatcatctctg	2880
Db	3143	ACGACCATGTCAATCCTGACCGGGTTGTTCGCCCGACCTCGGGCACCGCCTCACTACCTG	3202
Qy	2881	ggaaagacatctgcctctgagatgagcaacatccggcagaacctgggggtctgtctcccaag	2940
Db	3203	GGAAAAACATTTGGCTCTAGATGAGCACCATCCGGCGAAACCTGGGGGTCTTCCCCAG	3262
Qy	2941	cataagtgctgtcttgaatctgtcagctgtcgaagaacacatctgttctctatgtcccgctg	3000
Db	3263	CATACACTGCTGTTTGACATGCTGACTGTGCAGAAACACATCTGCTTCTATGGCCGCTTG	3322
Qy	3001	aaagggctctctgagaagcagctgaaagccgagatgagacagatgtgccctggatgttgt	3060
Db	3323	AAAGGCGTCTCTGAGAAGACGTAAGGGGGGAGTGAAGACAGATGGCCCTGTGATGTTGGT	3382
Qy	3061	ttgcatcaagcaagctgtgaaagcaacaacacgcgctgttaagggtgaatgtcagagaag	3120
Db	3383	TTGGCATCAAGCAAGCTGAAAAACAAAACACCGCTGTGAGTGGGATGTCAGAGAAAG	3442
Qy	3121	ctatctgtggccttggccttgtctggggatctaaagttgtcatctctgatatgaccaca	3180
Db	3443	CTATCTGTGGCTGTGGCTTTGTGGGGGATTTAAGATTGTTCATTTCTGATGTAACCCACA	3502
Qy	3141	gctgtgtgtgaaccttaactcccgcaagggaataatgagagctgtcctctgaaataccgcaa	3240
Db	3503	GCTGTGTGGACCTTACTTACCCGACAGGGAAATATGGAGACTGCTGTAATACCGACAA	3562
Qy	3241	ggccgacacatattctctctacacccacatggaatgaagcggacgtctcctgtggggaacg	3300
Db	3563	GCCCGACACATATTCTCTTACACACACCATATGATGAAGCGGAGGCTCTGGGGACAG	3622
Qy	3301	attgccatcatctcccatgggaagctgtgcctgtgtgggctctccctgtttctgaagaac	3360
Db	3623	ATTGCCATCATCTCCCAATGGGAAGCTGCTGTGTGGGCTCTCCCTGTTCTGAAGAAC	3682
Qy	3361	cagctgggaagcagctactacccgacctgtgtcgaagaagaatgttgaatatccctccagt	3420
Db	3683	CAGCTGGGAACAGGCTACTACTCTGACTTGTGTCAAGAAAGATGTGCAATCTCCTCAGT	3742
Qy	3421	tcctgcagaaacagtagtagcacctgtgtcatactcgtgaaaaggagacagtgtttctcag	3480
Db	3743	TCTCTGACAAAACATGTACTACACTGTGTCTACTCTGAAAAGAGAGACAGTGTTCAG	3802
Qy	3481	agcaattctagtgtctgcgcgggcagccgacctgaagaatgtgaacgctgaacctgagctc	3540
Db	3803	ACCACTTGTGATGCTGGCCTGGGAGCGACATGAGATGACACGCTTACCATGGAATGTC	3602
Qy	3541	tctgtcatctcaaacccatcatcagaagaacatgtgtctgaagcccgcttgytggaaagata	3600
Db	3863	TCTGCTATCTCCAACCTCATCAGAGCAATGTCTGGAAGCCGGGCTGTGTAAGACATA	3922
Qy	3601	gggcatgtgcgcgacctatgtgtgcctaatgaagcgtcgtcaagaaaggagcccttgttgaa	3660
Db	3923	GGGCAATGAGCTACCTATGTGCTGCCATATGAAGCTGCTAAAGAGAGACCTTTGTGGAA	3982
Qy	3661	ccctctcatgtgatgtgacccgctctcagaccttggagattcagttatgatcatctca	3720
Db	3983	CTCTTTCAATGAGATTGATGACCGGCTCTGACCTGGGCAATTCTAGTTATGGCATCTCA	4042
Qy	3721	gagacgaccttggaaagaataatctcctaaggtgtggccgaagagatgtgggtgtgagtctgag	3780
Db	4043	GAGAGACCTCGGAAGAAATTTCTTAAAGTGGCCGAAGAGTGGGGTGGATGCTGAG	4102
Qy	3781	accatgagtgtacctgtcccgcaagaacgaaacggcggcctctcggggacaagcagagc	3840
Db	4103	ACCTGAGATGAGTACTCTGCCACGAAAGCAAGAACAGCGGGGCTTGGGGGCAACGACGAGC	4162
Qy	3841	tgctctgcgcgcttcaactgaagaatgagtctgtctgataccaatgatatctcgacatagacca	3900
Db	4163	TGCTCTTGGCCCTTCACTGAAGATGATGCTGTGATTCCAAATGATTTCTGACTATGACCA	4222

Oy	3901	gaatccagagacagactgctcagttggaatgaga tggcaaaaggtccataccaggtgaa	3960
Db	4223	gaattccagagacagactgctcagttggaatgaga tggcaaaaggtccataccaggtgaa	4282
Oy	3961	ggtctggaacttacaagcaacglttltgagcccttltgtgaagaagactgtaattgcc	4020
Db	4283	ggctggaaactttacacgcaacglttltgagcccttltgtgaagaagactgtaattgcc	4342
Oy	4021	agacgagctcgaaagatttltgtcgaatgtctgtcgaatgtctgtcgaatgtctgtcgaat	4080
Db	4343	agacgagctcgaaagatttltgtcgaatgtctgtcgaatgtctgtcgaatgtctgtcgaat	4402
Oy	4081	gacctgtgtcgaagctgtacgtgtgtccaccttltgcaagtaeccagctgtgaaattcag	4140
Db	4403	gcccttgtgttcacccctggaatgtgtccaccttltgcaagtaeccagctgtgaaattcag	4462
Oy	4141	cccttgatgtacaacgacagatlacatattgtcaagaatgtatgtcctgtgaagacagga	4200
Db	4463	cccttgatgtacaaacgacagatlacatattgtcaagaatgtatgtcctgtgaagacagga	4522
Oy	4201	acccttgaaactcttaaacgcccctacccaagacctgtgcttgggaacccgtgtatgaa	4260
Db	4523	acccttgaaactctttaaagcccttacccaaaagacctgtgcttgggaacccgtgtatgaa	4582
Oy	4261	ggaaacccaatccccagaacgcccctcccaagcaggggaagaaatgtggaacactgtccca	4320
Db	4583	ggaaacccaatccccagaacgcccctcccaagcaggggaagaaatgtggaacactgtccca	4642
Oy	4321	gtlccccaagacatcatatgagactcttccagaatlggaacttgacaatgagaaccttca	4380
Db	4643	gtttccccaagacatcatatgagactcttccagaatlggaacttgacaatgagaaccttca	4702
Oy	4381	cctgtcatgccagtttagcagcggcaaaatcaagaatatgtctccgtgtgtgtccccaagg	4440
Db	4703	cctgtcatgccagtttagcagcggcaaaatcaagaatatgtctccgtgtgtgtccccaagg	4762
Oy	4441	gcaagggggctgtccctccccaagaagaacaacaactgtcagatatacttccagacctg	4500
Db	4763	gcaggggggctgtccctccccaagaagaacaacaactgtcagatatacttccagacctg	4822
Oy	4501	acaaggaagaacatltcagatatacttctgtgaagaagtatgtcagatatacttccaaaagc	4560
Db	4823	acaggaagaacatlttccagatatacttctgtgaagaagtatgtcagatatacttccaaaagc	4882
Oy	4561	ttaagaagaagaatctgtgtgaatgtgatttagtatagtggagcttccctgtgtcagtt	4620
Db	4883	tttaagaagaagaatctgtgtgaatgtgatttagtatagtggagcttccctgtgtcagtt	4942
Oy	4621	aattactcaagcacttctccagatcaagaagttlaatgatgtccataccaacaatgaa	4680
Db	4943	aattactcaagcacttctccagatcaagaagttlaatgatgtccataccaacaatgaa	5002
Oy	4681	caactcaagctgtgcaagaagaagtttccagatccagatlttccaagcttggaaagatt	4740
Db	5003	caactcaagctgtgcaagaagaagtttccagatccagatlttccaagcttggaaagatt	5062
Oy	4741	atcacagagctgtgacacagaaataatgtcaaggtgtgttccaataacaagaagctgtgcat	4800
Db	5063	atcacagagctgtgacacagaaataatgtcaaggtgtgttccaataacaagaagctgtgcat	5122
Oy	4801	gcaatcagctcttccctgaatgtcatacaaatgtccattctccgggccaacctgtgaaag	4860
Db	5123	gcattatagcttcttccctgaatgtcatacaaatgtccattctccgggccaacctgtgaaag	5182
Oy	4861	ggaggaacacctcagcatlatggaatttactgtcttcaatcatccctgtgattccaag	4920
Db	5183	ggaggaacacctcagcatlatggaatttactgtcttcaatcatccctgtgattccaag	5242
Oy	4921	cagcagcttccagagtggtctctgatgacacatcagttgagtctctgtgtgtccatcgt	4980
Db	5243	caacacacttccagagtggtctctgatgacacatcagttgagtctctgtgtgtccatcgt	5302

QY	4981	gtaacatttgcaatgctccctgctccagcaagcttggatccctgctccaggaacg	504
Db	5303	gtcatctttgcacatctcttggctccacagcgttgcgtattcctgawccagagcgg	5362
QY	5041	gtccagcaagcaaaacacctgcagttcatcaagtgagtgagccttcaactcagctc	5100
Db	5363	gttcagcaagcaaaacacctgcagttcatcaagtgagtgagccttcaactcagctc	5100
QY	5101	tctaattttgtctgggatatgtgaattaaagtgtccctgcgcacactgtgtatcatc	5160
Db	5423	tctaattttgtctgggatatgtgaattaaagtgtccctgcgcacactgtgtatcatc	5160
QY	5161	ttcaatcgtctccagcaagaagttccatagtgttccctccacaactcgtcctgtacccct	5220
Db	5483	ttcaatcgtctccagcaagaagttccatagtgttccctccacaactcgtcctgtacccct	5220
QY	5221	ctaactttgtctgggtatgggtgtcatcaacacctcatgtacccagcctcctgtgttc	5280
Db	5543	ctaactttgtctgggtatgggtgtcatcaacacctcatgtacccagcctcctgtgttc	5280
QY	5281	aagatcccccagcaagcctatagtgtgtccaccagcgttaacaccttcaatgtgcaat	5340
Db	5603	aagatcccccagcaagcctatagtgtgtgtccaccagcgttaacaccttcaatgtgcaat	5340
QY	5341	ggcagcctgtggccacctttgtgcttgagcgtgttccagcaataagctgaataatacat	5400
Db	5663	ggcagcctgtggccacctttgtgcttgagcgtgttccagcaataagctgaataatacat	5400
QY	5401	gatacctccgaagtcgcgtgttcttgatcttccacatcttgccttgagcagggctctc	5460
Db	5723	gatacctccgaagtcgcgtgttcttgatcttccacatcttgccttgagcagggctctc	5460
QY	5461	gacatcgttggaaaacccagcaatgctgatgtcccttgaaagglttgaggagaatcgtctt	5520
Db	5783	gacatcgttggaaaacccagcaatgctgatgtcccttgaaagglttgaggagaatcgtctt	5520
QY	5521	gtgtacccattatcttggagcttgggttggtggagcaaaccttgcacatgacgttgaaagg	5580
Db	5843	gtgtacccattatcttggagcttgggttggtggagcaaaccttgcacatgacgttgaaagg	5580
QY	5581	gtgtgtgtcttccctcattactgttcttgatccagttacagattcttcatcagccagact	5640
Db	5903	gtgtgtgtcttccctcattactgttcttgatccagttacagattcttcatcagccagact	5640
QY	5641	gttaatgtcaaaagctatctctcttgaatgtgtaagatgtgtagcgggaaagacag	5700
Db	5963	gttaatgtcaaaagctatctctcttgaatgtgtaagatgtgtagcgggaaagacag	5700
QY	5701	agaattcttgatgttgtaggccaagatgacatcttgaatcaatgaagatltgacaaata	5760
Db	6023	agaattcttgatgttgtaggccaagatgacatcttgaatcaatgaagatltgacaaata	5760
QY	5761	latagaaggaagcggagcctgtcgttltgacaagatlttcggtggagattccctcctgtgtgag	5820
Db	6083	latagaaggaagcggagcctgtcgttltgacaagatlttcggtggagattccctcctgtgtgag	5820
QY	5821	tgcttgggtcctcctggagatgttaaigtggagcttggaataatcaacttcaagatgttaca	5880
Db	6143	tgcttgggtcctcctggagatgttaaigtggagcttggaataatcaacttcaagatgttaca	5880
QY	5881	gggaataccaactgttaccagaggaagatgcttcccttcaacaaaahaglatcttacaac	5940
Db	6203	gggaataccaactgttaccagaggaagatgcttcccttcaacaaaahaglatcttacaac	5940
QY	5941	atccataaagatacatcaagaacatgggcctacgtccctcagtttgatgcatcacaagcgtg	6000
Db	6263	atccataaagatacatcaagaacatgggcctacgtccctcagtttgatgcatcacaagcgtg	6000
QY	6001	ttgacttggagagaacaacgttgagatcttcttgcccttlttgagagatgccagagaagaa	6060
Db	6323	ttgacttggagagaacaacgttgagatcttcttgcccttlttgagagatgccagagaagaa	6060
QY	6061	gttggcgaagttgttgagtgtgggcgcatcggaaactggcctcgttgaaatgtgagaanaa	6120

Db	6383	GTGGCAAGGTGGTGTGCTGGCGAATTCGGAAATCGGCGCTCGTGAAGTATGGAGAAAA	6442
Qy	6121	tatgctggttaactatagttggaaggcaacaacgcgaagctctctacagccatgcttgatc	6180
Db	6443	TATGCTGTGTAACTATATGATGTGAGGCAACAAACGCAACCTCTCTACACCACTATGGCTTGAATC	6502
Qy	6181	ggcgggcctccctctggtggtttctcgtatgaaacccacacaggaatggtatcccaagcccg	6240
Db	6503	GGCGGGCGCTCTGTGGTGTCTTGATGATGAACCCACACAGCATGTGATCCCAAGCCCG	6562
Qy	6241	cggttctctgtggaattgtgtccctaagtgltgttcaaggaggggagatcaagtagtcttaca	6300
Db	6563	CGGTTCTTGGAATGTGTGCCCTTAAGTGTGTTCMAAGAGGGGAGATCACTAGTGTATACA	6622
Qy	6301	tccatagatgtgaagaatgtgaagctctttgacactagatgtgcaatcagtgtcaatgta	6360
Db	6623	TTCATATAGTATGGAAATATGTGAAGCTCTTTTGCACTAAGATGGCAATCATGGTCAATGGA	6682
Qy	6361	aggttcaagtgctctgtgcagtggtccagacatctaaanaataaggttttgagaatggtataca	6420
Db	6683	AGGTTCAAGTGCTCTGTGGCGAGTGCAGCATCTCTAAAAAATAGGTTTGGAGATGTATACA	6742
Qy	6421	atagttgttaagaaatagcaaggttccaaacccggccctgtgaagccgttcgaagatttcttga	6480
Db	6743	ATAGTTGTATGAATATACAGAGGTCCCAACCCGACCTTAAGCCGTGTCCAGGATTTCTTTGGA	6802
Qy	6481	cttgacatcttccctgtgaaagtgttcttaaaagagaacaacacgggaataatgtctacaatacagctt	6540
Db	6803	CTTGCACTTCTCTGAGAGTGTCTAAAAAGAGAAACACCGGAATCATGTACTAATACCAAGCTT	6862
Qy	6541	caactctgaattatctctctgtgccagagatatcagatctcttcccaagagcaaaaagcga	6600
Db	6863	CAATCTTCATATATCTTCTGTGGCCAGATATTTCAAGATCTCTCCAGAGCAAAAAAGCA	6922
Qy	6601	ctccacaatagaagactactctgtttctcaagacaacaactgtgaccagatattgtgaactt	6660
Db	6923	CTCCACATGTAGAAGACTACTCTGTTTCTGACAGACACACTTGACCAAGTATTTGTGAACTTT	6982
Qy	6661	ggcaagagaccaaaagtgtatgtatgacacacttaaaagacctctcatctcacaaaaacagaca	6720
Db	6983	GCCAAAGACCAAAAGTATGATATGACCACTTTAAAAAGACCTCTCATTAACAAAAACAGACA	7042
Qy	6721	gtatgtgacgtttgcagttctcacaactttctcagaagatgagaagaagtgaagaagcat	6780
Db	7043	GTAGTGTGACGTTGCAAGTTTCTCATACCTTTTCTTACAGAGATGAGAAAGTGAAGAAAGCTAT	7102
Qy	6781	gtatgaagaatccgttctacacgg	6804
Db	7103	GTATGAAAGAACTCTGTCTCATACG	7126
RESULT 6			
LOCUS	AX060898	10474 bp	DNA
DEFINITION	Sequence 7 from Patent W00078971.		
ACCESSION	AX060898		
VERSION	AX060898.1	GI:12406275	
KEYWORDS	human.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 10474)		
AUTHORS	Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.		
TITLE	Atp binding cassette transporter protein abc1 polypeptides		
JOURNAL	Patent: WO 0078971-A 7 28-Dec-2000;		
FEATURES	CV THERAPEUTICS, INC. (US)		
source	Location/Qualifiers		
	1..10474		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
BASE COUNT	2906 a	2305 c	2416 g 2843 t 4 others

QY	2101	gfgfcaaccctcgaagttaggaacccgctgccttacagtgatcccaagcgtggtgttgc	2160
Db	2423	ggggcattccgaaatttagaamaacctctccctccacagatgattccagctgggtttgtc	2482
QY	2161	ttccctgcggtgtttgctgtgtgtagaactccgcagtgcttccctgattagcaactctc	2220
Db	2483	tttcgtgtccggttttgctgtgtgtacaaattcctgcagtccttccgtatttagcaactcttc	2542
QY	2221	ttccagagccaacttgcagcagcagcctgttgggggcatcatctacttcaagcgttaccctgc	2280
Db	2543	ttccagagccaacttgcagcagcagcctgttgggggcatcatctacttcaagcgttaccctgc	2602
QY	2281	taacgtccggttltgtgagatgagctgagactaagtggtgttcaactaagaactctgcagc	2340
Db	2603	taacgtccggttltgtgagatgagctgagactaagtggtgttcaactaagaactctgcagc	2662
QY	2341	ctgcgtctccgtgtgccttlttggttgggttgggtgtgagtgacttggcctltttgagaagag	2400
Db	2663	ctgcgtgtccggttgggtgttgggtgttgggtgtgagtgacttggcctltttgagaagag	2722
QY	2401	ggcatttgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag	2460
Db	2723	ggcatttgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag	2782
QY	2461	ctccacacacttcgatccatcagatgagtgagtgagtgagtgagtgagtgagtgagtgagtgag	2520
Db	2783	ctccacacacttcgatccatcagatgagtgagtgagtgagtgagtgagtgagtgagtgagtgag	2842
QY	2521	taeatltgagctgtcctltccaagccagtlacggaatltccagccctgtatlttccctgc	2580
Db	2843	taeatltgagctgtcctltccaagccagtlacggaatltccagccctgtatlttccctgc	2902
QY	2581	accaagctccactgtgttgcgcgaggaagtgtatgagaagaagcaccctgttccaaacag	2640
Db	2903	accaagctccactgtgttgcgcgaggaagtgtatgagaagaagcaccctgttccaaacag	2962
QY	2641	aagaaatgtlcaagaatctgcatlgtgagtgaggaacccaactlttaagctgtgcgttcc	2700
Db	2963	aagaaatgtlcaagaatctgcatlgtgagtgaggaacccaactlttaagctgtgcgttcc	3022
QY	2701	alttagaaccctgtgaaaaagctctacagatgtgagtgagtgagtgagtgagtgagtgagtgag	2760
Db	3023	alttagaaccctgtgaaaaagctctacagatgtgagtgagtgagtgagtgagtgagtgagtgag	3082
QY	2761	ctgaatttltatgtgagggcagatcaccctctccctgcgggcacaaatggagcggggaagag	2820
Db	3083	ctgaatttltatgtgagggcagatcaccctctccctgcgggcacaaatggagcggggaagag	3142
QY	2821	accacaatgtcaatcctgacccggtgtgttccccccagacctggtgggacacgcgtacatctgt	2880
Db	3143	accacaatgtcaatcctgacccggtgtgttccccccagacctggtgggacacgcgtacatctgt	3202
QY	2881	ggaaaaaagacttgcctcttgaatgtgagcacaccacccgagcaaacctgtgggtgtgttccccag	2940
Db	3203	ggaaaaaagacttgcctcttgaatgtgagcacaccacccgagcaaacctgtgggtgtgttccccag	3262
QY	2941	cataagctgtgtgttgaacatgctgacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	3000
Db	3263	cataagctgtgtgttgaacatgctgacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	3322
QY	3001	aaagagctctctgtagaagcaagtgaagcggagatgtgaagcaagatgtgcctgtgaltgtgt	3060
Db	3323	aaagagctctctgtagaagcaagtgaagcggagatgtgaagcaagatgtgcctgtgaltgtgtgt	3382
QY	3061	tttgcaatcaagcaagctgtgaagaacaaagaacgaagcgtgtgaagtgtgaatgtgaagaag	3120
Db	3383	tttgcaatcaagcaagctgtgaagaacaaagaacgaagcgtgtgaagtgtgaatgtgaagaag	3442
QY	3121	ctatctgtgtgccttgccttgttgcgggagatcaaggttgcattcttcgtgtgaaccaca	3180
Db	3443	ctatctgtgtgccttgccttgttgcgggagatcaaggttgcattcttcgtgtgaaccaca	3502

QY	3181	gctggtgtgtagaccttaaccgcaaggagaaatacggagagctgtgtcttgaaataccgaa	3244
Db	3503	gctggtgtgtagaccttactcccgacggggaaataggagctgtgtcttgaaataccgaa	3562
QY	3241	ggcgagaccattatctctctcaacacaaatggatgaagcggaagtccttgaggagcag	3300
Db	3563	ggcgagaccattattctctctcaacacaaatggatgaagcggaagtccttgaggagcag	3622
QY	3301	atggcatcatcctccatcgggaagctgtgctgtgtggccctccctgtcttctgaagac	3360
Db	3623	atggcatcatcctccatcgggaagctgtgctgtgtggccctccctgtcttctgaagac	3682
QY	3361	cagcttgggaacagcgtactacccttgacacttggtaagaagaatgtgaaacccctcagt	3420
Db	3683	cagcttgggaacagcgtactacccttgacacttggtaagaagaatgtgaaacccctcagt	3742
QY	3421	tccttcagagaacagtagtagcactgttcaactctgaagaagaaggaagcgttcttcag	3480
Db	3743	tccttcagagaacagtagtagcactgttcaactctgaagaagaagaaggaagcgttcttcag	3802
QY	3481	agcagcttcctgatactgtcgtcttggcagagacatagaagatgaaacgctgtgaacatc	3540
Db	3803	agcagcttcctgatactgtcgtcttggcagagacatagaagatgaaacgctgtgaacatc	3862
QY	3541	ttctgtatctccaacctcatagaagcaatgttctgaaagcccgctgtgtggaagcata	3600
Db	3863	ttctgtatctccaacctcatagaagcaatgttctgaaagcccgctgtgtggaagcata	3922
QY	3601	ggagcatgagcctggaactatgtctctcaatagaagctgtcaagaaggaagaccccttgaa	3660
Db	3923	ggagcatgagcctggaactatgtctctcaatagaagctgtcaagaaggaagaccccttgaa	3982
QY	3661	cccttcatgagatgtgatgacccgctctcagaccttggcattctagtatgacatca	3720
Db	3983	cccttcatgagatgtgatgacccgctctcagaccttggcattctagtatgacatca	4042
QY	3721	ggagcagaccctgggaagaataatcctccaagtgagccgaagagatgtgggtgatgtcag	3780
Db	4043	ggagcagaccctgggaagaataatgttctctaagctggccgaagaaatgtgggtgatgtcag	4102
QY	3781	acctcaagatgtactcttgcagcaagaacgaacagcgagccttcogggagcaagcaagc	3840
Db	4103	acctcaagatgtactcttgcagcaagaacgaacagcgagccttcogggagcaagcaagc	4162
QY	3841	tgctctgcccgttcactggaagatgtatgtctgcatccaatgtatctcgacaagaacca	3900
Db	4163	tgctctgcccgttcactggaagatgtatgtctgcatccaatgtatctcgacaagaacca	4222
QY	3901	gaatcacaagagacagactgtctcaatgtggatgtgatgtgaagaaggtctctaccaggttaa	3960
Db	4223	gaatcacaagagacagactgtctcaatgtggatgtgatgtgaagaaggtctctaccaggttaa	4282
QY	3961	ggcttggaaacttacacagcaacagttgttgcccttlttggaaagagactgtctaattgc	4020
Db	4283	ggcttggaaacttacacagcaacagttgttgcccttlttggaaagagactgtctaattgc	4342
QY	4021	agaacggagtcggaaggaatttttgtctgaattgtcttcgcaagctgtgtttgtctgcat	4080
Db	4343	agaacggagtcggaaggaatttttgtctgaattgtcttcgcaagctgtgtttgtctgcat	4402
QY	4081	ggccttgtgttcagcctgtacgtgcgcaaccccttggcaagtaaccacagcctgaaactcag	4140
Db	4403	ggccttgtgttcagcctgtacgtgcgcaaccccttggcaagtaaccacagcctgaaactcag	4462
QY	4141	cccttgatgtacaacggaacgatacattgtccagcaatgatgtccttgaggaacgga	4200
Db	4463	cccttgatgtacaacggaacgatacattgtccagcaatgatgtccttgaggaacgga	4522
QY	4201	accttggaaacttaaacgcccacacaaagcccttgcttcoggaacccgctgtatgtgaa	4260
Db	4523	accttggaaactttaaanaaccccttcaccaanaagaccttgcttcoggaacccgctgtatgtgaa	4582
QY	4261	ggaacccaatccagacacgccccttgcagaggaagggaaggatgtgacaactgtgccc	4320

4583 GGAAGCCATCCAGACACGCCCTGCCAGGAGGAGAAAGATGGACCTGCCCA 4642
4321 gtccccaacacatcatgaagctctccagaa tgggaactgagacaatcagaacctca 4380
4643 GTTCCCAACCATCATGTGAACTCTTCCGAAATGGGAATGACATGACAAACCTTCA 4702
4381 cctgcatacgtatgtagcagcgacaaatcaagaagatgctgctgtgtgtcccaagg 4440
4703 CCGCATGCCAGTGTAGCAGCACAATAATCAAGAAGATGCTGCTGTGTGCCAGAGG 4762
4441 gcaaggagctgctcctccacaagaacaaacacacgagatatactcttaagacctg 4500
4763 GCGAGGGGCTGCTCTCCACAAGAAACAAACACTGCGATATACCTTGAAGNCTG 4822
4501 acagagaagaacatctcgatatactgctgaagacglatgtagatcaatagccaagc 4560
4823 ACGAGAAACATTTGGATTATCTGTGAAAGCATGTGCAAGTATAGCAGAAAGC 4882
4561 ttaagaacaagaatctgggtgaatgaatgaatgaatgaatgaatgaatgaatgaat 4620
4883 TTAAGAAACAGATCTGGGTGATGATGATGATGATGATGATGATGATGATGATGAT 4942
4621 aataccaagacactcctccagatcaagaagatgaatgaatgaatgaatgaatgaat 4680
4943 AATACTCAAGACTTCTCCGAGTCAAGAACTTAATGATGATGATGATGATGATGATGAT 5002
4681 caccataagctggcacaagacagctctgagatcgaatcttcaacaagcttgggaatt 4740
5003 CACCTTAAGCTGGSCAAGGACAGTCTGAGATGATGATGATGATGATGATGATGATGAT 5062
4741 atgacagagctgagacccagaataatgctcaaggtggtgtgtgtgtgtgtgtgtgtgt 4800
5063 ATACAGGAGTGGACACCAAAATATGTCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5122
4801 gcaatcagctcttccctgaatgctcaacaatgacatctccgggccaacctgcaaaag 4860
5123 GCATACAGCTCTTCTCGAATGTCATCAACAATGCCATTCGCGGCAACGTCAGAAAG 5182
4861 ggaagaagaacctagacatataatgaatgaatgaatgaatgaatgaatgaatgaatga 4920
5183 GGAAGAAACCTTGAATGAAATTAACGTTTCAATCATCTCCCTGAATCTCACCAAG 5242
4921 cagaagctcagaaggtggtctgtagacacacacacacacacacacacacacacacac 4980
5243 CAGCAGCTCTCAGAGGTGCTGTGATGACACATCACTGATGATGATGATGATGATGATGAT 5302
4981 gtaactcttgcaatgctcctgctcccaagcagcttggctgctgctgctgctgctgctg 5040
5303 GTCATCTTGTCAATGTCCTTGTCTGCCAGCAGCTTGTGTGTGTGTGTGTGTGTGTGT 5362
5041 gtcagcaagaacaaac 5100
5363 GTTCGCAAAACCAAAACCCCTGCAAGTTCATGAGTGAAGCCTGTGATCTAGTGTGCTC 5422
5101 tctaattctgctggaatgctgaatgaatgaatgaatgaatgaatgaatgaatgaatga 5160
5423 TCTAATTTTGT 5482
5161 ttaactgcttcccaagcaagctcctatgctcctcaacaatctgctgtgtgtagccct 5220
5483 TTCAATCTGTCTCCAGCAAGAGTCTATGTGTCTCCACCAATGTGCTGTGTGTGTGTGT 5542
5221 ctacttctgctgtaggtgtgctcaacacacacacacacacacacacacacacacacac 5280
5543 CTACTTTTGT 5602
5281 aagatcccaagcagacatctatgctgctcaacacacacacacacacacacacacacac 5340
5603 AAGATCCCAAGCAGCAGCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5662
5341 ggaagcgtggtgac 5400

5663 GCGAGCGTGCCACACTTTGT 5722
5401 gatccctgaagctccgt 5460
5723 GATATCCGAAAGTCCGTTGT 5782
5461 gacatgtgtaaaac 5520
5783 GACATGTGTAAGAAACCAAGCAATGCTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 5842
5521 gtgtacacatatacttggagcttggagcgaacacacacacacacacacacacacacacac 5580
5843 GTGTACCATATTATCTGT 5902
5581 gt 5640
5903 GT 5962
5641 gtaatgcaagcctac 5700
5963 GTAATGCAAAACATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6022
5701 agaatcttgatgltgagcgcagaatgaatcctagaatcagaaggttgaagata 5760
6023 AGAATTTGTGATGT 6082
5761 tataagaagaagcgaagac 5820
6083 TATAGAAGAAACGGAACACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6142
5821 tgccttggcctcctgagatgaatgagcctggaatcacaatcacaatcacaatcacaatc 5880
6143 TGCTTTGGGCTCTGT 6202
5881 ggaagataac 5940
6203 GGAGATACCACTGT 6262
5941 atccatgaagatcacaagaac 6000
6263 ATCCATGAAGTATCATCAGAACATGAGGCTACGCTCCTGATTGATGCCATCAGAGCTG 6322
6001 ttgactgagagaaac 6060
6323 TTGACTGGGAGAAACACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6382
6061 gttgcaaggt 6120
6383 GTTGGCAAGGT 6442
6121 tatgctgtaactatagtgaggaacacacacacacacacacacacacacacacacacacac 6180
6443 TATGCTGTGATATGATGTGAGGCAACCAACGATCTCTACAGCATGCTTGTGATC 6502
6181 ggcgggctcctgt 6240
6503 GCGGGGCTCTCTGT 6562
6241 cgttcttggaatgt 6300
6563 CGGTTTGTGAAATGT 6622
6301 tctcatagataggaagaatgtagctcttgcactagaatgtagcaatcaatgtagcaatg 6360
6623 TCTCATAGATAGGAAGAATGTGAAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6682
6361 aggttgaagtgctgt 6420
6683 AGGTTCAAGGTGCTTGT 6742
6421 atagttgtaagaaatgagaggttccaaacacacacacacacacacacacacacacacac 6480
6743 ATAGTTGTAGGAATAGCAGGATGCAACCCGAGCTGAAACCTGTGCTGAGATTTTGTGGA 6802

QY	6481	cttgcaccttcctggaaagtcttcctcaaaaggaaacaccgggaacactgctacaatccagctt	6540
Db	6803	cttggcatcttccctggaaagtcttcttAAAAGGAAACACCGGAACTGCTACAATTCACAGCTT	6862
QY	6541	ccatcttcattatctctctcgtgcagaagatatcagcatcctctccagagcctcaaaaagcga	6600
Db	6863	ccatcttccatcttcttcttcttgcgcaggaattatcagcatcctctctccagagcctcaaaaagcga	6922
QY	6601	ctccacatagaagaactactctgtcttctcagacaacacttgacaagctatttggaaacttt	6660
Db	6923	ctccacatagaagaagaactactctgttcttctcagacaacacttgacaacacttatttggaaacttt	6982
QY	6661	gcccaaggaccaagatgatgatgacacttaaaagacctctcattaccagaaaaaaccagaca	6720
Db	6983	gcccaaggaccaagatgatgatgacacttaaaagacctctcattaccagaaaaaaccagaca	7042
QY	6721	gtagtggaaagtctgcagtttctccacatcttcttctcagagatggagaagctgaagaagaactat	6780
Db	7043	gtagtggaaagtctgcagtttctccacatcttcttctcagagatggagaagctgaagaagaactat	7102
QY	6781	gtagtgaagaatctgcttcatcagc	6804
Db	7103	gtagtgaagaatctgcttcatcagc	7126

	RESULT	7			
	AX060900				
LOCUS	AX060900	10474 bp	DNA	linear	PAT 22-JAN-2001
DEFINITION	Sequence from Patent WO078971.				
ACCESSION	AX060900				
VERSION	AX060900.1	GI:12406276			
KEYWORDS					
SOURCE	human.				

FEATURES	source
REFERENCE	1 (bases 1 to 10474)
AUTHORS	Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
TITLE	ATP binding cassette, transport protein
JOURNAL	CV THERAPEUTICS, INC. (US) Patent: WO 0078971-A 9 28-DEC-2000;
FEATURES	Location/Qualifiers
source	1..10474
BASE COUNT	/organism="Homo sapiens"
ORIGIN	/db_xref="taxon:9606"
	2907 a 2304 c 2415 g 284 t 4 others

QY	301	atgtgtgcgcgccttctcagatgctcgcgcgcgccttcttatacagccgaagaagcacc	360
Db	623	ATTGTGGCTCGCGCTTCTCTCAGATGCTCGAGGCTTTTATATACGCCAAGAAAGACACC	682
QY	361	agcatgaaggaatgcgcaaaagtctctagaacattacaagatgatacaagaatccagctca	420
Db	683	AGCATGAAGGACATGCGCAAAAGTTCTGAGAAACATTACAGCATGAAGAAATCCAGCTCA	742
QY	421	aacttgaagcttcaagatttcctctgttgacaaatgaaacctctcctcgtgttctatatcac	480
Db	743	AACTTGAAGCTTCAAGATTTCTCTGTGTGACAAATGAACCTTCTGTGGTTCCTATATATAC	802
QY	481	aaacctctctcccaaaagtctactgttgacaagaatgtctgaagctatgtlcaatccac	540
Db	803	AACCTCTCTCTCCCAAAAGTACTGTGGACAAGATGCTGAGGGCTATGTCAATTCTCCAC	862
QY	541	aaggtatatttggcaagctacagctatcatlttgacaagctcgtgaaatgataatcaatca	600
Db	863	AAGGATATTTTGGCAAGCGCTACCACTTACATTTGCAAGTCTGTGCATATGATCAAAATCA	922
QY	601	gaagagatgatccaacttgtgtgacacaagaagttcttgaagcttgtgcttaccacaagag	660
Db	923	GAAAGAGATGATTCAACTTGGTGACCAAGAAATTTCAGCTTTGTGTGCTTACCAAAAGAG	982
QY	661	aaactgtgtcgaagcagagcgaatctcgttccaacatgaaacatccctgaagccaatctgt	720
Db	983	AAACTGGCTGCAGCAGACGCGAGTACTTGTTCCACATGATGACATCCTGAAGCCATTCCTG	1042
QY	721	agaacactaaactctacatctccctctccgagacaagagagctgtgtcgaagccaataaca	780
Db	1043	AGAACACTTAACTCTACATCTCCCTTCCCGAGAGAGAGCTGTGCATGAACCCCAAAATCA	1102
QY	781	tgtgcgtcagtagtcttggagctctgtgccagaagctgtcaagcatgaaagctcgtgaatgc	840
Db	1103	TGTGCTGATATCTTGTGGAGCTCTGTGCCAGAGACTGTTCAGCATGAGAAGCTGGAGTAC	1162
QY	841	atgcgacagaagtgatgttctctgaaccaatgtgaacagctlcaagctcctcccaaccaatc	900
Db	1163	ATGCGACAGGAGGATGATGTTCTGTACCAATGTGAACAGCTCCAGCTCCGCCCAAAATC	1222
QY	901	taccagagctgtgtctgttatgtctctggggacatcccgaaaggaggaggagcttgaatacag	960
Db	1223	TACCAAGCTGTGTCTCTGATTTGTCTGCGGAGCATCCCGAAGGAGGGGGCTGTGAAGTCAAG	1282
QY	961	tctctcaactcgttatgtagaacacaataaagccctcttcttgagagcaatgtgcactgtag	1020
Db	1283	TCTCTCAACTGATGTAGAGGACAACTACAAAGCCCTCTTGTGAGGCATATGGACACTGAG	1342
QY	1021	gaagtgcttgaacctctcttgaacaactctaacacacctcttatgtgaatgatttgaatgaag	1080
Db	1343	GAGATGCTGAACCTTCTGTATGACAACCTTACAACTCTCTTACTGTGAATGATTTGATGTAAG	1402
QY	1081	aatttgaagcttagtccctctcttcccgatlatcttgaaagctcgtgaagcgcgtcgtctgt	1140
Db	1403	AATTTGAGGTACTAGTCTCTTCTTCCCGATTTATCTGGAAGAGCTGTAAACCCCTGCTGTT	1462
QY	1141	gggagaatctctgtatacacttgacactccaagccaaaggcagtgatagtgtgaagtgaac	1200
Db	1463	GGGAGAATCTCTGTATATACACTGTGACACTCCAGCCACCAAGGACAGCTATGGCTGAGGTGAC	1522
QY	1201	aagagcttccaggaacatcgtgtgtcttcatatgtcttgaaagagatgttggaagaaactaagc	1260
Db	1523	AAGAGCTTCCAGGAACCTGGCTGTGTTCCTATGATCTGGAAGGCATGTGGAGGAACACTAGC	1382
QY	1261	cccaagaatcttgagactlcaltgagaacaacgccaagaatatgagactgtctcgaatgtctgtg	1320
Db	1583	CCCAAGATCTGGACCTTCAATGAGAACACCAAGAAATGAGACTTGTGCGGATCTGTGG	1642
QY	1321	gacagcagggacaatgacaacttttgggaacagcagcttgatgtgcttagatattgacaagcc	1380
Db	1643	GACAGCAGGGACATATACCACTTTTGTGGAAACAGAGTTGGATGTGCTTATGATTTGACAGCC	1702

Dh 3863 TCTGATCTCCAACTCATGAGGAGAGCATGTGTCTGAGCGCCGCTGTGGAACATA 3922
Qy 3601 gggatgagctgacctatgtgtcctatagaagctgtctaaaggagagccctgttgaa 3660
Db 3923 GGGGATGAGCTGACCTATGTGCTCCCATATGAACCTGCTAAAGGAGGAGCCTTTGTGAA 3982
Qy 3661 cctcttaagatgtatgtaacggctctcagacctgagccttcttaagttatgcatctca 3720
Db 3983 CTCTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCAATTTCTATGTATGCAATCTCA 4042
Qy 3721 gagaagacctgagaagaataatctcctaaggttgccgaagaagatggagtgatgtcag 3780
Db 4043 GAGAGGAGCCCTGGAAGAAATTTCTCAAGTGCGCCAGAGAGAGTGGGTGGATGCTGAG 4102
Qy 3781 acctcaatgtacctgtgccaagcaagaagaagcgggccctcgaggagaagaagc 3840
Db 4103 ACCTCAATGTGTACTTGTCCAGCAAGAGCAAGGCGGCGCTTGGGGCAAGAGAGC 4162
Qy 3841 tgtcttgcccgcttcaactgaagatgatgtcgtgatccaaatgatctcagatagacca 3900
Db 4163 TGTCTGCGCCGTTCACTGAGATGATGCTGCTGATCCAAATATTTCTGATAGACCA 4222
Qy 3901 gaatacgaagaagacagactgtctcagatggagatggaaaggtctcaccagatgaa 3960
Db 4223 GAATCCAGAGAGACAGACTTGTCTCAGTGGGATGATGGCAAAAGGCTCTACAGTGAA 4282
Qy 3961 gactggaacttacaacagcaacagtttgcccttcttggaagaagactgctaatgccc 4020
Db 4283 GGGTGAAGACTTACACGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACGTAAATGGCC 4342
Qy 4021 agacgagatcgagaagaatltttgtcagatgtctgtcgaagctgtgttctgcatc 4080
Db 4343 AGAGGAGTGGGAAGGATTTTGGCTCAGATGTCTGCGACAGCTGGTTGTGCTCANT 4402
Qy 4081 ggccttgctcagcctgagctgtgccaaccccttggaagatgacccagcctgtgaactcag 4140
Db 4403 GCCCTTGTGTTCAGCTGTGATGCTGACCCCTTGTGGAAGAGACGTAAATGGCC 4462
Qy 4141 cccttgatgtacaacagacagatcatgtctcagcaatgatgtctcctagagacagga 4200
Db 4463 CCTGATGTACAAAGCAAGAGTACATTTGTGCAATGATGCTCTGAGGACAGGGA 4522
Qy 4201 acccttgaaactttaaagccctcaccaaagacccctgacctgagagcccgctgtatgaa 4260
Db 4523 ACCCTGGAATCTTAAACGGCCCTCACCAAAAGACCCCTGCTGGGACCCGCTGTATGAA 4582
Qy 4261 ggaaccccaatcccaagacagccctgccaagcgaggaggaagaatggaacactgcccc 4320
Db 4583 GGAACCCCAATCCCAACAGACGCGCTCCAGCGAGGAGGAGAGAGTGGACCACTGCCCA 4642
Qy 4321 gtcccccaagcatcatgtgactcttcacgaatbggaactgtgacaatgcacacctca 4380
Db 4643 GTTCCCAAGACCTCATGTGACCTCTTCCAGAAATGGGAATGGCAATGACAAACCTTCA 4702
Qy 4381 cctgtcatgtcagatgtagcagcgacaacaatcgaagaatgtctcgtgtgtgtcccaagg 4440
Db 4703 CCGCATGTGCAGATGTGAGCGACGCAAAATCAAGAAATCTGCTGTGTGCTCCCAAGG 4762
Qy 4441 gcaaggggagctgacctcctccacaagaanaaacaacactgcagatatccttaaggactg 4500
Db 4763 GCAAGGGGGGCTGCTCTCTCCACAAGAAACAAACACAGATATCTCTTAGGACCTG 4822
Qy 4501 acagagaagaacattcggattatctgtggaagacgtatgtgcatacatagccaagaagc 4560
Db 4823 ACAGGAGAAATTTTGGATTATCTGGTGAAGACCTATGTCAATCATATACCAAAAGC 4882
Qy 4561 ttaagaagaagaatctggatgtgaatagtttaagttatgagtggtcttccctgtgtcagt 4620
Db 4883 TTAAGAAGAACAGATCTGGGTGAATGAGTTAGTATGGGGCTTTTCCCTGGGTGTCACT 4942
Qy 4621 aatctctcaagccttccctcagatcaagaagtttaatgagcaacaacaatgaagaa 4680
Db 4943 AATACTCAAGCACTTCTCTCCGAGTCAAGAAATTAATGATGCATCAACCAATGAAGAA 5002

Qy 4681 caactaaagctgccaagagacagctctcagatcatctcctaacagcttggaaagatt 4740
Db 5003 CACCTAAAGCTGGCCAAAGAGAGTTCTGCAAGTGCATTTCTCAACAGCTTGGAAAGATT 5062
Qy 4741 atgacagagctggaacccaagaataatgtcaagttgtgttcaataaacaaggtgtgat 4800
Db 5063 ATGACAGGAGCTGACACCAAGAAATATGTCAAGGTGTGTTCATTAACAAAGGGCTGCAT 5122
Qy 4801 gcaatcagctcttccctgaatgtcaacaatgcatcttccgggccaactctgaagaag 4860
Db 5123 GCAATCAGCTCTTCTCTGATGTCAATCAAAATGCATTTCTCCGGCCAACTGCANAG 5182
Qy 4861 ggaagaacccctagccaatataggaatctactgtcttcaatcatalccctgaatccaag 4920
Db 5183 GGAGAGAACCCCTAGCCATTAATGAAATTAATGCTTCAATCATCCCTGAATCTCACAG 5242
Qy 4921 cagcagctctcagaaggtgtgtctgtatgacccaatgaatgagatgtcctgtgtcatctgt 4980
Db 5243 CAGCAGCTCTCAGAGGTGGCTGTGATGACCAATCAGTGAATGATCTTGTGTCAATCTGT 5302
Qy 4981 gtcactcttgcaatgtctctcgtcccaagcagcttgcgtatctcctgatacagaagcgg 5040
Db 5303 GTCATCTTGAATGTCTGTGTGTCCACAGCCTTGTGTATCTGTATCTCAGAGCGG 5362
Qy 5041 gtcagcaagaagcaaacacctgcagttcatcagttgagatggaactgtcatctactgtctc 5100
Db 5363 GTCAACAAAGCAAAACACCTGCATCATCAGTGAATGAGGAGCCGTGTATCTGTGCTC 5422
Qy 5101 tctaatttctgtggaatgtgcaatlaagctgttccctgcacaactggtcatatc 5160
Db 5423 TCTATTTTGTCTGGATATGTGCAATTAATGCTTGTCTCCACACTGTGTATTAATC 5482
Qy 5161 ttcactgtctccagcagaagtcctatgtctcctccacaactgtgctgtgtagccct 5220
Db 5483 TTCATCTCTTCCAGCAAAATCCTATGTGTCTCCACCAATGTGCTGTAGCCCTT 5542
Qy 5221 ctacttctgtatgtgtgtgtcaatacactctcaatgtgaacagctcttgtgttc 5280
Db 5543 CTACTTTTGTGTATGGTGTGTATCAACCTCTCATATGACCAAGCTCTTGTGTTC 5602
Qy 5281 aagatcccaagcaacagcctatgtgtgtcaccagcgtgaacccctcattatgcatat 5340
Db 5603 AAGATCCCAAGCAAGCCTATGTGTGTACAGCGGGAACCTTCATTTGGATTAA 5662
Qy 5341 ggcagcgtggccaccttgtgtgtgagctgttaccgaataaagctgaataataat 5400
Db 5663 GGCAGCGTGGCCACCTTGTGTGTGAGCTGTCAACCAATAAGCTGAATAATATCAAT 5722
Qy 5401 gataccttgaagctcgtgtcttcatctccacatlttggccttggagcgaagcctatc 5460
Db 5723 GATATCCTGAAGTCCGATGTGTGTATCTTCCACATTTTGGCTGGGAGCAGGCTATC 5782
Qy 5461 gacatgtgtgaaaacacaggaatgtcgtgtagtgcctgtgaagaagtttgggaagatcgctt 5520
Db 5783 GACATGTGAAAAACCAAGCAATGTGATGCCCTGTGAAAGGTTTGGGGAATTCGCTT 5842
Qy 5521 gtgtcaccatatcttggagctgtgtggaagaaaccttgcacatgagcggtggaag 5580
Db 5843 GTGTACCATTAATTTGGAGCTTGTGTGAGCAAAACCTCTTCCCATAGCGGTGGAAGG 5902
Qy 5903 GTGTGTCTTCCATTAATGATGTGTATGATCAGTACAGATTCTTCAACAGCCCAAGCT 5962
Qy 5961 gtaaatgcaagctatctccttgaatgagatgaagaatgtgagcggtggaagaagc 5700
Db 5963 GTAATGCAAGGCTATCTCTGAATGATGAAGATGAAGATGTGAGCGGGAAGAAAG 6022
Qy 5701 agaattcttgaatgtggaagccagaatgacatcttgaataatcaagaagttgaagaata 5760
Db 6023 AGAATTTGTATGTGTGAGGCGCAAGATGACATCTTGAATAATCAAGAGTTGACGAAGATA 6082

QY 5761 tataagaaggaagcggagcctgctgttgcagagatttgcgtgggattctctctgtgtgag 5820
 |||||
 Db 6083 TATAGAGGAAAGCGGAAAGCCCTGCTTGTACAGAGATTTGCGGGGATTCCTCGGTAG 6142
 |||||
 QY 5821 tgccttgggagccttgaggttaagggcgtgaaatacatcaacttcaagaatgtaaca 5880
 |||||
 Db 6143 TCTTTGGGCTCTGGAGATTATGAGGGCTGGAAATATCATCACTTTCAAGATGTAA 6202
 |||||
 QY 5881 ggaataacactgttaccagagagatgcttctcttaacaaataglatcttacaac 5940
 |||||
 Db 6203 GGAGATACACATGTTACAGAGAGATGCTTCTTAAACAAAATAGTATCTTATCAAC 6262
 |||||
 QY 5941 accaatgaatcatcagagaacatgggtctactgctcctcagtttgcacatcaagagctg 6000
 |||||
 Db 6263 ATCCATGAAGTACATCAGAACATGGGCTACTCCCTCAGTTGATGACATCAGAGCTG 6322
 |||||
 QY 6001 ttgacttgagagagacacgttgaagttcttgccttctgaagaggtccacagagagaa 6060
 |||||
 Db 6323 TTGACGGGAGAGAACAGCTGAGTTCTTCCCTTTTGAGAGAGTCCACAGAAAGA 6382
 |||||
 QY 6061 gttgcaaggttgttgaatggcgatctggaaactgggctcgtgaagtatgagaaaaa 6120
 |||||
 Db 6383 GTTGGCAAGTGTGTGAGTGGGCGATTCGAAACTGGGCTGTGAGATGTGAGAAAAA 6442
 |||||
 QY 6121 tatgctgtaactatagttgagagcaacaagcagctctctacagccatggctttgac 6180
 |||||
 Db 6443 TATGCTGTAATATAGTGGAGCAACAAACCAAGCTCTTACAGCCATGGCTTTGATC 6502
 |||||
 QY 6181 ggcggccctctgtgtgttcttgaagaaaccacacacagagatgaltccaaagccgg 6240
 |||||
 Db 6503 GGGGGGCTCTCGTGGTGTCTTGTGATGAACCCACACAGCATGATGCCAAACCCGG 6562
 |||||
 QY 6241 cggctcttgaagatgtgtcctaaagtgttgcagagagagagatcagtaatgtctaa 6300
 |||||
 Db 6563 CGGTTTGTGGAATGTGCCCTTAAGTGTGCAAGGAGGAGATCACTAGTGTCTTAA 6622
 |||||
 QY 6301 tccatagatagagaaatgtgaagcttctgaactagatggaatcagtaatgtaag 6360
 |||||
 Db 6623 TCTCATAGTATGGAATATGTAGAGCTTTTGACACTAGATGCAATCATGTGCAATGA 6682
 |||||
 QY 6361 aggttcaagtccttgcagagtgctcagacatctaaataaagtttggagatggttataca 6420
 |||||
 Db 6683 AGGTTCAGGCTCTGGAGTGTCCAGCATCTPAAAAAATAGTTTGAATGTGTATACA 6742
 |||||
 QY 6421 atagttgtgaagaaatgaaggttccaaacccggagctgaagcgttgcagagttcttga 6480
 |||||
 Db 6743 ATAGTTGTAGAAATACAGAGGTCCAAACCGGACCTGAAGCTGTCCAGATTTCTTGA 6802
 |||||
 QY 6481 ctgcaatttccgtgaaggtgtctaaagaagaacacccggaacatgctacatcacagctt 6540
 |||||
 Db 6803 CTTCATTTCTCTGGAAGTGTCTTAAAGAGAAACACCGGAGATGCTACATATCCAGCTT 6862
 |||||
 QY 6541 ceatctcatlactctctcgtgcagagatatcagcalccctccacagagcaaaagcga 6600
 |||||
 Db 6863 CCATCTTCAATTATCTTCTGCGCCAGGATATTCAGCATCTCTCCCAAGCAAAAAGCGCA 6922
 |||||
 QY 6601 ctccaataaagaactactgttcttgcagagaacacttgaacaaatatttgyaactt 6660
 |||||
 Db 6923 CTCACATTAAGAACTACTGTGTTTCTCAGCAACACTTGGACCAAGTATTGGAACCTT 6982
 |||||
 QY 6661 gcaagaagcaaaagtatgatagcacacttaaaagacctcatatcaacaaacacagaca 6720
 |||||
 Db 6983 GCCAAGAGCAAAAGTATGATGACCACTTAAAGACCTCTCATTTACCAAAAACAGACAC 7042
 |||||
 QY 6721 gtagtgaagttgcagttctcacaatcttctacagagatgagaagtgaagaagctat 6780
 |||||
 Db 7043 GTACTGACCTTGCAGTTCTACATCTTTTCTACAGATGAGAAAGTGAAGAAAGCTAT 7102
 |||||
 QY 6781 gtagaagaatcctgtcatcacg 6804
 |||||
 Db 7103 GTATGAAGAAATCTGTTCAATACG 7126

RESULT 8
 AX092594 7860 bp DNA linear PAT 21-MAR-2001
 LOCUS Sequence 6 from Patent WO0115676.
 DEFINITION
 ACCESSION AX092594
 VERSION AX092594.1 GI:13444651
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 7860)
 AUTHORS Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M.
 TITLE Compositions and methods for modulating hdl cholesterol and triglyceride levels
 JOURNAL Patent: WO 0115676-A 6 08-MAR-2001;
 University of British Columbia (CA) ; Xenon Genetics Inc. (CA)
 FEATURES
 source 1..7860
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 2014 a 1860 c 2008 g 1978 t
 ORIGIN
 Query Match 99.9%; Score 6796; DB 6; Length 7860;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 6799; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 atggtcttggcctcagctgaagttgctgtgtggaagaacctcaacttcagaagaaga 60
 |||||
 Db 75 ATGGCTGTGGCCCTACACTGAGTGTGCTGTGGAAGAACCTTCACATTCAGAAAGA 134
 |||||
 QY 61 caaatgtaagctgttacttgaagttggcctgacctatattctccatcgtatc 120
 |||||
 Db 135 CAACATGTACGCTGTACTGGAAGTGGCTGGCTCTATTATCTTCATCTGATCTGATC 194
 |||||
 QY 121 tctgtcggcggagctacccaccatgaaacaatgaaatgcaatcttccaaataagcc 180
 |||||
 Db 195 TCTGTGGGTGAGGTACCCACACCGATGACACATGATGCCATTTTCCAAATTAAGCC 254
 |||||
 QY 181 atgcccctgcagaacaacttcccttgggttcaagggaattatctgtaatgccaacaacccc 240
 |||||
 Db 255 ATGCCCTGCGAGAACCTTCCTGGGTTCAGGGGATTACTGTAAAGCCCAACACCCC 314
 |||||
 QY 241 tgttcgcttaccgacctcctgggagagctcccgagttgttggaaactttaacaatcc 300
 |||||
 Db 315 TGTTCCTGTACCCGACCTCTGGGAGGCTCCCGAGTTGTGGAACCTTTAACAAATCC 374
 |||||
 QY 301 attgtgctcgctgttctcagatgtctggaggtcttcttatacagccagaagaacac 360
 |||||
 Db 375 ATTGTGGCTCGCGCTGTCTGACATGCTCGAGAGCTTTTATACAGCCCAAAAGACACC 434
 |||||
 QY 361 agcatgaagagacatgcgcaaaagttcttgagaacattacagcagatcaagaatcaagctca 420
 |||||
 Db 435 ACCATGAAGAGCATCGCAAAAGTTCTGGAACATTTACGACATCAAAATATCCAGCTCA 494
 |||||
 QY 421 aacttgaagcttcaagattctctgttggacaatgaaaccttctctggtttctcatalcac 480
 |||||
 Db 495 AACCTTGAACCTTCAAGATTCTCTGTGTGACATGAACACTTCTCTGGTCTCTGATCAC 554
 |||||
 QY 481 aaactctctcccaaaagtctactgttgaacaagatgtcgaaggtcgtatgtcatctcac 540
 |||||
 Db 555 AACCTCTCTCTCCCAAAAGCTACTGTGACAAAGAGCTGAGGCTGATGTCAATCTCCAC 614
 |||||
 QY 541 aaggtatttttgcagaagcttaccagatgttgaacaaagttctgtgaatgtgcaatgca 600
 |||||
 Db 615 AAGGTATTTTTCAGAGGCTACCAAGTTTACATTTGCAAGTCTGTGCAATGATCAAAATCA 674
 |||||
 QY 601 gaagagatcatcaacttgttgaacaagaagtttctgaagcttgttggcttaccacaagag 660
 |||||
 Db 675 GAAGATATGATTCACCTGTGTCAGCAAGAGTTTGTGAGCTTTGTGGCTTACCAAGGAG 734

QY 661 aaactgctgcagcagacgagtaacttgltccaaatgagacatccctgaagccaactctg 720
|||||
Db 735 AAACCTGGCGACAGCAGGAGTACTTCCTTCCAACTGGACATGACATCTGTGAAGCAATCTGT 794
QY 721 agaacactaacctcactccctccctccgagcaagagctgctggaagcccaaaaaa 780
|||||
Db 795 AGAACCTAAACTCTACATCTCCCTTCCGAGCAAGAGCTGCTGMAAGCCCAAAAACA 854
QY 781 ctgtgcatagctcttgagacactgcccagagctggttcagcatgagaagctgagtgac 840
855 TTGCTGCAATAGTCTTGCGACTCTGGCCCGAGAGCTGTTACGATGAGAAAGCTGAGTAC 914
QY 841 atgcagcagagagatgagtcttgaccaaagtgaacagctccactcccccacac 900
|||||
Db 915 ATGCGACAGAGAGTATGTTTCTTGACCAATGGAACAGCTCCACCTCCCAAAATC 974
QY 901 taccagctgtgtctgtaagtctgcyggaactcccgagagagagggctgaaatcaag 960
|||||
Db 975 TACAGAGCTGTGTCTGCTATGTGTGCGGAGATCCCGAGAGGGGGGCTGAAGATCAAG 1034
QY 961 tctctaaactgtatgagagcaaacactaacaaagccctcttgagagcaatgagcag 1020
|||||
Db 1035 TCTCTAACTGGATGAGGACAAACAAGCCCTCTTGGAGGCAATGGCACTAG 1094
QY 1021 gaagatgctgaaacctctatgacaactctaacactccctactgcaatgattgaag 1080
|||||
Db 1095 GAAGATGCTGAACCTTCTATGACAACCTCTACACTCCTTACTGCAATGATTGATGAAG 1154
QY 1081 aattggagctagctcctctctcccgatlaactggaagagctctgaagccgctgctg 1140
|||||
Db 1155 AATTGGAGTGAATGCTCTCTTCCGCAATATCTGMAAGCTCTGAAGCCGCTGCTGCTT 1214
QY 1141 gggaaatcctgtatacaacctgacactccagcacaagcagagtgatgctgaagtgaac 1200
|||||
Db 1215 GGGAGATCCTGTATACACCTGACACTCCAGSCACAGGAGATGCTGAGTGTGAAC 1274
QY 1201 aagacctccagaaactgctgtgltccaatgactctggaagagctgtggagaaactcagc 1260
|||||
Db 1275 AAGACCTTCCAGGAACCTGCTGTCTCCATGATCTGGAAGGATGCGAGAGCACTGACG 1334
QY 1261 cccaagatctgacactctatgagaacagccaaagaatgagactgtccgagtgctgtg 1320
|||||
Db 1335 CCCAGATGTGACCTTCAATGAGAACACCAAGAAATGAGACTTGTCCGGATGCTGTG 1394
QY 1321 gacagcaagagacaatgacacactcttggaagacagcagctgagtgcttagatggaagcc 1380
|||||
Db 1395 GACAGAGGAGCAATGACCACTTTGGGAGACAGCTTGATGATGACAGACCC 1454
QY 1381 caagacatgctgtgttttttgccaaagacccagagagatgtccagttcaagtgttct 1440
|||||
Db 1455 CAAGACATGCTGGCTTTTGGCCAAAGCACCCAGAGATGTCACATGCCAATGATGCTTCT 1514
QY 1441 gttacacactgagagaaagcttcaacagagactaacaggcaatccgagacatatctgc 1500
|||||
Db 1515 GGTACACTGAGAGAAAGCTTTCACAGAGACTAACCAAGCAATCCGAGCAATATCTGCG 1574
QY 1501 ttcatgagtggtgtcaacctgacaagctagaaacccatagaaacagaagctgtgctc 1560
|||||
Db 1575 TTCAATGGAGTGTGTAACCTGMAAAGCTAGAACCAATAGCAACAGAGCTGGGCTGATC 1634
QY 1561 aacaagatcagagactctgcatgagagagaaagtctggtgctgtatgtttcaatgga 1620
|||||
Db 1635 AACAGATCCATGAGACTCTGATGATGAGAGAAATTCGGGTGATTTGTATTCAGTGA 1694
QY 1621 attactcagcagcagatgagctgcccacatgltcaagtcaaatccgaatgagact 1680
|||||
Db 1695 ATTACTCCAGGAGAGATTGAGCTGCCCATCATGTCAGATGACAGATCCGAATGAGACTT 1754
QY 1681 gacaaatgtgagagagaaataaataaagatggtgtaactgagagccctgtcctcgact 1740
|||||
Db 1755 GACAAATGTGAGAGAGCAAAATTAATCAAGAGATGATGAGAGCCCTGCTCGAGACT 1814
QY 1741 gacctctgagagacatgctgctgctgctgctgctgctgctgctgctgctgctgctg 1800
|||||
Db 1815 GACCCCTTTGAGGACATGCGGTACGTGGGGGGGCTTCCCTACTTGCAGAGATGTGTC 1874
QY 1801 gacagcaatcatcagagtgctgagagagccagagaagaactggtgtctatgca 1860
|||||
Db 1875 GAGCAGCAATCATCAGAGTGTCTACGGGCAACGAGAAAGAAACTGTGTCTATATGCA 1934
QY 1861 caatgcccataccctgttcaagtatgacacactctctcgaggtgatgagccgltcaatg 1920
|||||
Db 1935 CAGATGCCCTATCCCTGTACGTGATGATGATCTTTCTGCGGGTGAATGACCCGGTCAATG 1994
QY 1921 cccctcttaagcagctgagctgagttactgagtgagtgctgtgtaataagagcatctg 1980
|||||
Db 1995 CCCCTTTCATGAGCTGCTGGCTGATTTACTCAAGTGTGTGATTCATCAAGGAGCATGTG 2054
QY 1981 tatgagaagagagcagcagctgaaagagacatgcatgactgagccctgacaacaagcata 2040
|||||
Db 2055 TATGAGAAGAGGAGCAGCTGMAAAGACCATGGGATCATGGGGCTGACAAACAGCATC 2114
QY 2041 ctctggttagctgtgttcattagtagcctatccctctctctgtgagcctgtgctgcta 2100
|||||
Db 2115 CTCTGTTTACGTGTTCATTAAGTACCTATTCCTCTTCTTGTGAGCCGTGGCTGTGA 2174
QY 2101 gtgttcaactgaaagttaagaaacctgctcccttaacagtgatccagcagtggtgtgtc 2160
|||||
Db 2175 GTGCTATTCCTGAAGTTAGGAACCTGCTCCCTACAGTATCCAGCGTGTGTGTC 2234
QY 2161 ttctgtccgtgtgtgtgtgtgtgacaatccgtcagtgctctctgattagacactctc 2220
|||||
Db 2235 TTCTGTCCGTTTGTGTGTGTGAGCAATCTCAGAGCTTCTGTGATGACACACTCTTC 2294
QY 2221 tccagagcaaacctgagcagcagcctgtgagggacalcaactcaactcagctgtaccc 2280
|||||
Db 2295 TCCAGAGCAACCTGGAGAGACCTGTGGGGGATCATCTACTTCAAGCTGTACTGCCC 2354
QY 2281 taagtcctgt 2340
|||||
Db 2355 TACCTCTGT 2414
QY 2341 ctgtgtctctgt 2400
|||||
Db 2415 CTGCTGTCTCTGT 2474
QY 2401 ggcattgagtgagtgagtgagcaaacctgttctgaagctctgtgagagaaatgagctcaat 2460
|||||
Db 2475 GGCATTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTG 2534
QY 2461 ctcaacacactcagatctccatgagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2520
|||||
Db 2535 CTCACCACTTGT 2594
QY 2521 tacattgaagctgtctcttccagccagtaagcaatccagagccctgtgattctctc 2580
|||||
Db 2595 TACATTGAGCTGTCTTCCAGGCCAGTACGAAATCCAGGCCCTGTGTATTTCTCTTGC 2654
QY 2581 accaagtcctactggt 2640
|||||
Db 2655 ACCAAGCTCTACTGT 2714
QY 2641 aagagaatgtcagaatctgtcagtgagagagaaacccacacttgaagtgtgctgtcc 2700
|||||
Db 2715 AAGAGAAATATCAAAATCTGATGAGAGAGAAACCCACCCACTTGAAGCTGGGCGTGTCC 2774
QY 2701 attcaagacctgtttaaagctctacagagatgagatgaagtgtgtgtgtgtgtgtgtgtgt 2760
|||||
Db 2775 ATTCAAGACTGTGTAAGTCTACCGAGATGGGATGAAGTGTGTGTGTGTGTGTGTGTGT 2834
QY 2761 ctgaatttataagagcagatcacctctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2820
|||||
Db 2835 CTGAATTTTATGAGGGCAGATCACCTCTCTGCGCCCAATGAGAGCGGGGAAGAG 2894
QY 2821 accacatgtcaatctctgacccgt 2880
|||||

Db 2895 ACCACCATGTCATCTCTACCGGGGTTTCCCGACCTGGGACCGCCTACATCTG 2954
QY 2881 ggaagaacatctcgtctgagatgagacacatccggcgaacccctgggggtctctccag 2940
Db 2955 GGAAGAAAGCATTCGCTGTGAGATGAGACCATCCGGCAGAACCTGGGGGTCTGTCGCCAG 3014
QY 2941 catacgtcgtcttgagatgctgacgtctgagaacacatctggttctatgcccgtctg 3000
Db 3015 CATTAACGTCGTGTTGATGCTGACTGTCGAAGAACATCTGGTTTATGCCCCGCTTG 3074
QY 3001 aaaggcctctcgtgaaagacgctgagggcgagatgagacagatgcccctgagtgtgt 3060
Db 3075 AAAGGCGCTCTCGAAGACAGCTGAAGCGGAGATGAGACAGATGCGCCTGGATTTGGT 3134
QY 3061 ttgcatcaagcaagctgaaagcaaaacaaagccagctgtcaagctgaaatgcaagaag 3120
Db 3135 TTGGCATCAAGCAAGCTGAAGAAAGCCAGCTGTGAGTGAATGAGAGAAAG 3194
QY 3121 ctatctgtgacctgtgacctgtgtggggatctaaagttgtcatcttgatgaaacaca 3180
Db 3195 CTATCTGTGGCTTGTGGCTTTGTGGGGATCTAAAGTTGTATTCTGGATGAACCCACA 3254
QY 3181 gctgtgtgaccttaactcccgaggaatatagagctgtctgtaaataccgaaca 3240
Db 3255 GCTGTGTGACCTTACTCTCCGCGAGGGGAATATGGAGCTGCTGTAATATCGGACAA 3314
QY 3241 ggcgcacatattctctctacacacacatgtaagcgagcgtccctggggagag 3300
Db 3315 GGGCGACCATATTCTCTCTACACACCACATGATGAAGCGAGCTGCGGGGACAGG 3374
QY 3301 attgcatcatctccatgaggaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3360
Db 3375 ATTGCATATCTCCATGGGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3434
QY 3361 cagctgtgagacagctactacactgacactgtgtcaagaagaagctgtgaaatccctcag 3420
Db 3435 CAGCTGGGAACAGCTACTACTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3494
QY 3421 tccctgagaagaagtagtagcaactgtgtcaactgaaagaagaagcaagtttctcag 3480
Db 3495 TCTGTGAGAAACAGTAGTAGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3554
QY 3481 agaaattctgagctgtgacctgtggcgacacatgagatgagacagctgtgcaatcgttc 3540
Db 3555 AGAAGTCTGATGCTGTGCTGTGGCAGCAGACATGAGAGTGAACGCTGACATCATGTC 3614
QY 3541 tctgtcatctccaactcaatcaaggaagcagtgtgtcaagcccgctgtgtgaaacata 3600
Db 3615 TCTGTATCTCCAACTCATCAAGAGCATGTGTGTGAAGCCGGCTGTGGAAGACATA 3674
QY 3601 gggcagatgagctacatactgtgtgacatatgaaagctgtcaaggaaggaagcctttgtgaa 3660
Db 3675 GGGCATGAGCTGACATGT 3734
QY 3661 ctcttcatagatgtagtgcggcctcagacactgtgacattctctgatagtcatctca 3720
Db 3735 CTCTTTCATAGATGTATGACCGGCTCTCAAGCTGGGCAATTCTGTATGTGCACTCA 3794
QY 3721 gagaagacccctggaagaataatctcctcaaggtgtgccaagagagtggtgtgtgtgt 3780
Db 3795 GAGACGACCTCGAAGAAATATTCTCAAGGTGTGCGAAGAGAGTGGGTGTGTGTGTG 3854
QY 3781 acctcaagatgtagtacctgtgcagagaagaagaagcgagccttgagggaacagagagc 3840
Db 3855 ACCCAATGATGATCTTGTGCGAAGAGAGCAAGAGGGGGCTTTGGGAGACAGCAGAGC 3914
QY 3841 tttcttgcgacctcactgagaatgtagtgcgtgataccaatgattctgataagacca 3900
Db 3915 TGTCTTGGCCGTTTCATGAGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3974
QY 3901 gaatccagagagacagactgtctcagtgagatgtagtgaagaggtctctcagtgagaa 3960
Db 3975 GAATCCAGAGAGAGACTTGTCTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4034

QY 3961 ggcctggaacttaacagcaacagattgtgtgacctttgtgtgaagagactgtaattgcc 4020
Db 4035 GGCTGGAACTTACACAGCAACAGTTTGTGCCCCCTTTGTGGAAAGAGACTGCAATTTGCC 4094
QY 4021 agacgagctcgaaagagatttttctgcatgattgtcttgcaagctgtgtgtgtgtgtgt 4080
Db 4095 AGACGAGTGGAAAGGATTTTGTGTCAGATTGTCTTGCACAGTGTGTGTGTGTGTGTGT 4154
QY 4081 ggcctgtgtcagcctgtatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4140
Db 4155 GCGCTGT 4214
QY 4141 cccctgagatgtaacagcaagatcacattgtgcaagaatgattcctctgagacagagga 4200
Db 4215 CCCTGT 4274
QY 4201 accctggaactcttaaacgacctcaccacaagacctgtgtgtgtgtgtgtgtgtgtgt 4260
Db 4275 ACCGTGGAACCTTAAAGCCCTTACCAAGACCCCTGTGTGTGTGTGTGTGTGTGTGTGT 4334
QY 4261 ggaacccaatcccaagacagccctgtccagcgagggaggaagagatgtgtgtgtgtgtgt 4320
Db 4335 GGAACCCCAATCCACAGACACCCCTGCGAGGAGGAGAGAGTGTGTGTGTGTGTGTGTGT 4394
QY 4321 gtcccccagaccatcatggaacctcttcagaatgtgtgtgtgtgtgtgtgtgtgtgtgt 4380
Db 4395 GTTCCCGACACATCATGTGACCTTTTCCAGAAATGTGGAACCTGTGTGTGTGTGTGTGT 4454
QY 4381 cctgtatgcagctgtgacagagcaaaatcaagaagatgtgtgtgtgtgtgtgtgtgtgtgt 4440
Db 4455 CCTGTATCCAGT 4514
QY 4441 gcaagggggt 4500
Db 4515 GCAGGGGGGTGCTCTCCACCAAGAAACAAACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 4574
QY 4501 acaggaagaacatcttgatgattctgtgtgaagacgtatgtgtgtgtgtgtgtgtgtgtgt 4560
Db 4575 ACAGGAACAAACATTTGGATTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4634
QY 4561 ttaagaaacagatctgt 4620
Db 4635 TTAAGAAACAAAGT 4694
QY 4621 aatatcaagaactcctccagatgaagaagttaatgtagtgcatacaaaatgaagaa 4680
Db 4695 AATACTCAAGCACTTCTCCAGAGTCAAGAGTTAATGTGTCATCAAAATGCAAGAA 4754
QY 4681 caactaaagctgtgccaagagacgtctgtcagatcgatttctcaaacagctgtgtgtgt 4740
Db 4755 CACCTTAAGCTGGCCAGAGACGTTCTGCAGATGATTTTCAACAGCTGTGTGTGTGTGT 4814
QY 4741 atgacagactgtgacacagaataatgtcaagtggtgtgtgtgtgtgtgtgtgtgtgtgt 4800
Db 4815 ATGACAGAGCTGTGACACAGAAATATGTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGT 4874
QY 4801 gcaatcagctcttctgt 4860
Db 4875 GCAATCAGCTCTTCTGT 4934
QY 4861 ggaagaaacctagccattatgaaatlaactgtcttcaatcaatccctgtaatccaag 4920
Db 4935 GGAGAGAACCTTAGCCATTATGAAATTACTGCTTCAATCAATCCCTGAATCTCACCAAG 4994
QY 4921 cagcagctctcagagtggt 4980
Db 4995 CAGCAGCTTCTGAGAGT 5054
QY 4981 gtcatcttgaatgtctgt 5040
Db 5055 GTCATCTTGTGCAATGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5114

Query Match 99.8%; Score 6788; DB 6; Length 7260;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6794; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 atgagcttgctgagcctcagctgaggttctgctgtggaagaacctcactcttcagaagaaga 60
DB 321 ATGGCTTGTGGCCCTCAGACTGAGGTTGCTGTGGAAGAACCTCACACTTTCAGAGAAGA 380
QY 61 caaatatgctgagctgttacttgaagtgagctgagctctattactctccgactgac 120
DB 381 CAAGAATGTCAGCTGTACTGTGAATGGCTGGCTCTATTATTACTTCTGATCTGATC 440
QY 121 tctgttcgctgagctacccaacctatgaacaatgaatgcaatttcacaataaagcc 180
DB 441 TCTGTTGGCTGAGCTACCCACCTATGACAACTGAATGCCATTTCCTCAATAAAGCC 500
QY 181 atgacctctgaggaacaacctctctgggttcaagggtatctgtaatgccaacaacccc 240
DB 501 ATGCCCTTGCAAGAACACTTCTGGGTTCAGGGGATTAATCTGAATGCCAACACCC 560
QY 241 tcttcctgtacccagacctcctggaggctcccgagttgttggaaaccttaacaatcc 300
DB 561 TGTTCCTGATACCCAGCTCTGGGAGGCTCCGGAGTTGTTGGAAACTTTAACAATGCC 620
QY 301 attgtgctgcgctgttctcagaagctcggaagcttcttatacagccagaagaacc 360
DB 621 ATTGTGGCTGCGCTGTTCAAGATGCTGGAGGCTTCTTTATACGCCAAGAACACACC 680
QY 361 agatgaagaagatgagcaagttctggaacattacagcagatcaagaataatccagctca 420
DB 681 AGCATGAAGAACATGGCAAAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA 740
QY 421 aactgaagcttcaagaatttccctgglygacaatgaaaccttctcctggttccatatacc 480
DB 741 AACTTGAAGCTTCAAGATTTCCTGGTGACATGAACACTTCTGCGTCTGATATCAC 800
QY 481 aaacctctctcccaagactactctgagcaagatgctgagagctgagatgtaattctcac 540
DB 801 AACCTCTCTCTCCCAAGTCTACTGTGACAGATGCTGAGGGCTGATGTCTTCTCCAC 860
QY 541 aaggtatttttgaaggtaccaggttacttgaacaagctgtgcaatgagatcaaatca 600
DB 861 AAGGTATTTTGAAGGCTACAGGTTACATTGACAAAGCTGTGCAATGAGATCAAAATCA 920
QY 601 gaagagatgattcaactgtgtgaccaaagaatttctgagcttctgtgacctaccacaagag 660
DB 921 GAAGAGATGATCACTGTGTGACCAAGAAAGTTCTGAGCTTGTGGCTTACCAAGGAG 980
QY 661 aaactgctctcagcagagagagactctgttccaacaatgacatccctgaagccaactctg 720
DB 981 AAATGTGCTCAGACAGGACAGTACTTCTGTCCACATGAGACATCTGAAAGCAATCTCG 1040
QY 721 agaacaataaactatcatctccctcccgagcaagagctgctgaaagccacaataaaca 780
DB 1041 AGAACACTAAACCTACATCTCCCTTCCGAGCAAGAGACTGGCCGAAGCAACCAAAAAA 1100
QY 781 ttgtctgatagtcttggagactctggcccagagctgttcaagatgagaagctggagttac 840
DB 1101 TTGCTGATAGCTGTGGGACTGTGGCCCAAGAGCTGTTCAGCATGGAAGCTGTGAGTGC 1160
QY 841 atgagcagagagatgattcttctgaaccaatgtaacagctccagctccctccaccaatc 900
DB 1161 ATGGGACAGGAGGTGATGTTCTTGACCAATGTGAACAGCTCCAGCTCTCCACCCAAATC 1220
QY 901 taccagagctgctgtctgctatgtctcgggacatcccgaggagggggctgtaagatcaag 960
DB 1221 TACCAAGCTGTCTCTGCTATTTGCTGGGGCATCCGAGGAGGAGGGGCTGAAGATCAAG 1280
QY 961 tcttcaacatgtagttagggacaacaactataaagccctcttggaggaatgacctgag 1020
DB 1281 TCTCTCAACTGATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1340

QY 1021 gaagatgctgaagaaccttctatgacaactcttacaactcttactgcaatgatttgaag 1080
DB 1341 GAAGATGTGAAACCTTGTATGACACTTACACTCTTACTGCAATGATTTGATGAAG 1400
QY 1081 aatttgagctagctcctctctccgacatlatctgaaagctctgaaagccgctgtcgtt 1140
DB 1401 AATTTGGAGCTAGTCCCTTTCGCCGATTTATGGAAGCTGTGAAGCGCGTCTGTT 1460
QY 1141 ggaagatctgtlatacaactgaaacctccagccaagagcagatgagttgagggagaa 1200
DB 1461 GGAAGATCTCTGTATACCTGACCTCCACCAAGGAGGCTATGCTGAGGTGAAC 1520
QY 1201 aagacctccaggaacttgctgtgttccatgatatctggaagcagatgtggaagtaac 1260
DB 1521 AAGACCTTCCAGGAACCTGGCTGTGTCATGATCTGGAAGGCAATGGGAGAACTCAG 1580
QY 1261 cccaagatctggaaccttcaatggaagacccaagaatgaaacttgcgagatgctgtt 1320
DB 1581 CCCAAGATCTGAGACCTTCATGAGAACAGCCAAAGAAATGACCTTGTCCGATCTTTG 1640
QY 1321 gacagcaggaacaatgaccacttggaggagaagatgtagtggcttagattggaagcc 1380
DB 1641 GACAGCAGGACAAATGACCTTTGGGAGACAGCATTTGGATGGCTTAGATTGACAGCC 1700
QY 1381 caagacatgctgctgttlttggccaagcaccagaagatgtctcagatccagtaatgttct 1440
DB 1701 CAAGACATGTGTGGCTTTTGGCCAAAGCACCGAGATGTCAGTCCAGTAATGTTCT 1760
QY 1441 ggttacacctggaagaagcttcaagagactaaccaagcaatccggagcaatatctcgc 1500
DB 1761 GTGTACACTGGAGAAACCTTTCACAGACGACCTAACCAAGGCAATCCGACCATATCTGC 1820
QY 1501 ttcatgagatgtgtcaactctgaaacaagcttagaaccttagaacaagaatctgagctatc 1560
DB 1821 TTCTATGAGTGTCACTCACTGAACCAAGCTAGAACCCATAGCAACGAGATGTGGCTATC 1880
QY 1561 aacaagttcatgagctgtctgtatgagagaagttctgagctgtatgtgttcaatgga 1620
DB 1881 AACAACTCATGAGCTGCTGATGAGAGAACTTCTGGGCTGGATTTGTTGTTCACTGGA 1940
QY 1621 attaccctcaggaagattagctgagcccaatcaatgcaatgaataatccgaatgacat 1680
DB 1941 ATTACTCCAGGACGATGAGCTGCTGCCCATCTATGTCMAATGACAAATCCGAATGACATT 2000
QY 1681 gacaatgtgagagagacaataaataaagaatgagttgagctgagacctgtctcagact 1740
DB 2001 GACAAATGTGAGAGGACAAATAAATCAAGATGGGTACTGGGACCTGTGCTCGAGCT 2060
QY 1741 gaaccttgaagacaatgctgtctgtgaggggctctgcctacttgcaagatgtgtg 1800
DB 2061 GACCCCTTTGAGGACATGCGGTACGTTGGGGGGCTTGCTGCTACTTGAGGATGTGGTG 2120
QY 1801 gaggaggaatcaatcagaggtgtgacgaggaacccagaagaataactggtgtctatgaa 1860
DB 2121 GAGCAGGCAATCATCAGAGTGTGACGGGACCGGACCGAATAAATACTGTCTATATGCA 2180
QY 1861 cagatgcccataccctgtttagttagtgaatcttctgcgggtgagtagagccgttcaatg 1920
DB 2181 CAGATGCCCTATCCCTGTACGTTGATGACATCTTCTCGGGTGTATGAGCCGGTCAATG 2240
QY 1921 cccctcttcaatgagctgagctgtgatttactcagtgctgtgatactcaaggaactgtg 1980
DB 2241 CCCCTTTTCATGACGCTGGGCTGTGATTTACTAGTGGCTGTATCTCAAGGGCATCTGTG 2300
QY 1981 tatgagaagagagcagctggaagaagaccatgctgagataltgagccttgacaacagcata 2040
DB 2301 TATGAGAAAGAGAGGAGGCTGAAGAAGACCATCGGATCATGGGCTTGACAACAGCATC 2360
QY 2041 ctctgtttagctgtgttcaatgtagtcaatctcctctctctgtgtgagcgtgtcgtcta 2100
DB 2361 CTCTGTTTACTGTTCATTAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2420
QY 2101 gtgtatccctgaagattaggaataactctgacctacagtagatccagcgtgtgtgttc 2160

[illegible]

Db	3501	GGGGGTGGAGACCCCTTACTCTCCCGAGGGGGAATATGGGACCTGCTGCTGAATAACCGACAA	3550
QY	3241	ggccgacacatlatctctctacaacacacatgatalgaagcgtaacgtccctggggagacag	3300
Db	3561	GGGCGGACCATATTTCTCTCTACACACCATGATGATGAAGACGGACGATCTCTGGGACAGG	3620
QY	3301	attgcacatctctccatgggaacgtctgtgtgtgggtctctccgttctctgaagac	3360
Db	3621	ATTGCCATCATCTCCCATGGAGAACTGCTGTGTGGGCTCTCCCTGTGTTCTGAAGAAC	3680
QY	3361	caagctgggaacagagctactaaccttacctgtgtacaagaagaatgtgtgaacacccctcaat	3420
Db	3681	CAGCTGGGAACGGGCTACTACTGACTGACTTGTGTCAAGAAAGATGGAAATCCCTCTAGT	3740
QY	3421	tccctcgagaacaagtatgacatctgtgtcaactcgtgaaaaaagagagacagtgttctcag	3480
Db	3741	TCCCTCAGAAACAGTAGTAGACACTGTGTCTATACCTTAAAAAGAGAGACAGTGTTCACG	3800
QY	3481	agcagttctcgatgtcgcgctgggagagagacatgaagatgaacgtctacatcagatgc	3540
Db	3801	AGCAGTTCTGATGCTGGCCTTGCGGACGACCATGAAGTAGAACCTTCACATGATGATC	3860
QY	3541	tctgtatctccaacctcaatcaagaagacatgtgtctgaagcccgctgtgtgaagaata	3600
Db	3861	TCTGCTATCTCCAACTCATGAGAACATGTGTGAAGCCCGCTGTGTGAAGACATA	3920
QY	3601	gggagctggcgagacctatgtgtgtccatatgaagctgctcaagagagagaccttgtgtga	3660
Db	3921	GGGCAATGAGCTGACCCCTATGTGTCTGCCATATGAAGCTGCTAAAGAGGAGCCCTTGTGTAA	3980
QY	3661	ccctctcaatgatctatgaacgagctctcagacgttggacattctagtatacgcattca	3720
Db	3981	CTCTTTCATGATGATTGATGAACCGGCTCTCAGACCTTGCGATTTCAGTTATGGCATCTCA	4040
QY	3721	gagagagacctggagaataatctctcaaggtgtgcccgaagagatgtgggtgtgatgtgtag	3780
Db	4041	GAGAGACCCCTGGAGAAATATTCCTCAAGTGCGCCGAAAGACAGGGGCTGATGCTGAG	4100
QY	3781	acctcagaatgtacctgtccagcaagaacgaacgaacgacgagcctctggggagacaagcagc	3840
Db	4101	ACCTCAGATGCTACTCTTGCCACGACAAACAGACGGCGGCTTGGGGGACACAGCAGNC	4160
QY	3841	tgctctgcgccgtcactagaatgtagtgcctgtatccaatlyatctgcataagacca	3900
Db	4161	TGCTTCTGCCCGTTCACATGAAGATGATGCTGCTGATCCAAATGATTCGACATGACCCA	4220
QY	3901	gaatccagaagaagaagctgtcctcaatggatgtgtgtgcaaaaggtctctaccaggtgaag	3960
Db	4221	GATTCAGAGAGACAGACTTGCTCACTGAGATGAGATGGCAAAAGGCTCTTACACAGCTAAA	4280
QY	3961	ggcttgaaacttacaacagcaacagttctgtgagccttcttggaaagagactctaattgcc	4020
Db	4281	GGCTGGAACCTTACACAGCAACAGTTGTGTGGCCCTTTGTGGAAGACAGCTAATTTGCC	4340
QY	4021	agaacgaggtctggaaagatatttctgtcaagatctgtcttcgacagtgtgttctgtcat	4080
Db	4341	AGACGGAGTGGGAAAGGATTTTGTCTGAGATTGTCTTGCCACAGCTGTGTGTCTGATT	4400
QY	4081	ggccttgatctcagcgcgtatgtgtccacaccttggcaagtaaccacagcctggaaactcag	4140
Db	4401	GCCCTTGTTGTTCAAGCGTGAATCGTGCACCTTTTGGCAAGTACCCACACTTGGAACTTCAG	4460
QY	4141	ccctgtatgtacaagaaacagtaacacattgtcagaacatgtatgtcctctgagaacagga	4200
Db	4461	CCCTGGATGTACAAACAAAGTACACATTTGTCAACAATGTATGCTCTCTGAGACAGGGGA	4520
QY	4201	aaccttgaaacttcaaacgcccctcaacaaagacccctgtctcggagacgcgttatgtga	4260
Db	4521	ACCTGGAACTCTTAAACGCCCTCTACCAAAAGACCTGTGCTTGGGACCCCGCTTATGAGA	4580
QY	4261	ggaacaccaaaccacagacgcctctgcaaggaagggagggagaggtgaaacacatgtgccca	4320
Db	4581	GGAAACCAATCCCAACACAGCCCTCTCCAGCAGGAGGGAGGAAGTGTGACCACTGGCCCA	4640

QY 4321 gtcccccaacatcattggaactctccagaaatgggaactggcaatgacagaacctca 4380
|||||
Db 4641 gttccccacacatcattggaactctccagaaatgggaactggcaatgacagaacctca 4700
|||||
QY 4381 cctgacatcgaatgtgagcagcagaataatcagaagaatgctcctgtgtgtcccccag 4440
|||||
Db 4701 cctgacatcgaatgtgagcagcagaataatcagaagaatgctcctgtgtgtcccccag 4760
|||||
QY 4441 gcaaggaggctgctcctcccaagaagaacacacacacacacacacacacacacacac 4500
|||||
Db 4761 gcagggggctgctcctcccaagaagaacacacacacacacacacacacacacacac 4820
|||||
QY 4501 acaggaagaac 4560
|||||
Db 4821 acaggaagaac 4880
|||||
QY 4561 ttaagaagaac 4620
|||||
Db 4881 ttaagaagaac 4940
|||||
QY 4621 aatctcaac 4680
|||||
Db 4941 aatctcaac 5000
|||||
QY 4681 caactaaagctggcagaagaacacacacacacacacacacacacacacacacacacac 4740
|||||
Db 5001 caactaaagctggcagaagaacacacacacacacacacacacacacacacacacacac 5060
|||||
QY 4741 atgacaggaactggcagaagaacacacacacacacacacacacacacacacacacacac 4800
|||||
Db 5061 atgacaggaactggcagaagaacacacacacacacacacacacacacacacacacacac 5120
|||||
QY 4801 gcaatcaac 4860
|||||
Db 5121 gcaatcaac 5180
|||||
QY 4861 ggaagagaac 4920
|||||
Db 5181 ggaagagaac 5240
|||||
QY 4921 cagcagac 4980
|||||
Db 5241 cagcagac 5300
|||||
QY 4981 gtaactcttgcaatgtcctcctcctcctcctcctcctcctcctcctcctcctcctc 5040
|||||
Db 5301 gtaactcttgcaatgtcctcctcctcctcctcctcctcctcctcctcctcctcctc 5360
|||||
QY 5041 gtaactcttgcaatgtcctcctcctcctcctcctcctcctcctcctcctcctcctc 5100
|||||
Db 5361 gtaactcttgcaatgtcctcctcctcctcctcctcctcctcctcctcctcctcctc 5420
|||||
QY 5101 tctaattcttctggaatgtggaatgtggaatgtggaatgtggaatgtggaatgtggaat 5160
|||||
Db 5421 tctaattcttctggaatgtggaatgtggaatgtggaatgtggaatgtggaatgtggaat 5480
|||||
QY 5161 ttaactcttgcaatgtcctcctcctcctcctcctcctcctcctcctcctcctcctc 5220
|||||
Db 5481 ttaactcttgcaatgtcctcctcctcctcctcctcctcctcctcctcctcctcctc 5540
|||||
QY 5221 ctactcttgcaatgtcctcctcctcctcctcctcctcctcctcctcctcctcctc 5280
|||||
Db 5541 ctactcttgcaatgtcctcctcctcctcctcctcctcctcctcctcctcctcctc 5600
|||||
QY 5281 aagatcccaac 5340
|||||
Db 5601 aagatcccaac 5660
|||||
QY 5341 ggcagcgtggcagcgtggcagcgtggcagcgtggcagcgtggcagcgtggcagcgtgg 5400
|||||
Db 5661 ggcagcgtggcagcgtggcagcgtggcagcgtggcagcgtggcagcgtggcagcgtgg 5720
|||||

QY 5401 gatactcgaagctcgtgttcttgaatcttccacacatttggcctgggagcagggctc 5460
|||||
Db 5721 gatactcgaagctcgtgttcttgaatcttccacacatttggcctgggagcagggctc 5780
|||||
QY 5461 gacatgtgaaac 5520
|||||
Db 5781 gacatgtgaaac 5840
|||||
QY 5521 gtlcaccatcttcttggagctgtgtggagcgaacacacacacacacacacacacacacac 5580
|||||
Db 5841 gtlcaccatcttcttggagctgtgtggagcgaacacacacacacacacacacacacacac 5900
|||||
QY 5581 gtfgtgttcttccatcttcttcttcttcttcttcttcttcttcttcttcttcttctt 5640
|||||
Db 5901 gtfgtgttcttccatcttcttcttcttcttcttcttcttcttcttcttcttcttctt 5960
|||||
QY 5641 gtaaatgcaagctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5700
|||||
Db 5961 gtaaatgcaagctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 6020
|||||
QY 5701 agaattcttgatgt 5760
|||||
Db 6021 agaattcttgatgt 6080
|||||
QY 5761 tatagaagaac 5820
|||||
Db 6081 tatagaagaac 6140
|||||
QY 5821 tgccttggcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5880
|||||
Db 6141 tgccttggcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 6200
|||||
QY 5881 ggaagatcac 5940
|||||
Db 6201 ggaagatcac 6260
|||||
QY 5941 atccatgaaatcac 6000
|||||
Db 6261 atccatgaaatcac 6320
|||||
QY 6001 tgaactgggagagaac 6060
|||||
Db 6321 tgaactgggagagaac 6380
|||||
QY 6061 gttggcgaagctgt 6120
|||||
Db 6381 gttggcgaagctgt 6440
|||||
QY 6121 tatgtctgaactatagttggaagcaac 6180
|||||
Db 6441 tatgtctgaactatagttggaagcaac 6500
|||||
QY 6181 ggcgggcccctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 6240
|||||
Db 6501 ggcgggcccctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 6560
|||||
QY 6241 cggcttcttggaatgt 6300
|||||
Db 6561 cggcttcttggaatgt 6620
|||||
QY 6301 tctcatagatggaagaatgtgaagctccttgcacatggaatgtgaatgtgaatgtgaat 6360
|||||
Db 6621 tctcatagatggaagaatgtgaagctccttgcacatggaatgtgaatgtgaatgtgaat 6680
|||||
QY 6361 aggttcaagctgtcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 6420
|||||
Db 6681 aggttcaagctgtcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 6740
|||||
QY 6421 atagttgtgaatggaatggaatggaatggaatggaatggaatggaatggaatggaatggaat 6480
|||||
Db 6741 atagttgtgaatggaatggaatggaatggaatggaatggaatggaatggaatggaat 6800
|||||
QY 6481 ctgcatttctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 6540
|||||

Db 6801 CTTGATTTCTGGAAGGTTCCAAAAGAGAAACCCGGAACATGCTACATACCATCTT 6860
QY 6541 ccatttcattatctctctgagagatatctcagcatctctccagagcaaaagcga 6600
Db 6861 CCATCTTCATATCTTCTCTGGCCAGATATTCAGCATCTCTCCAGACAAAAGCGA 6920
QY 6601 ctccacatagaagactactctgttctcagaacaacacttgacaagtatttgaactt 6660
Db 6921 CTCACATAGAGACTACTCTGTTTTCAGACAAACCTTGACCAAGATTTGGAACCTT 6980
QY 6661 gccaaagaccaaagtatgatgaccacttaaaagacctccattacacaaacccagaca 6720
Db 6981 GCCAAGAGCAAAAGTATGATGACCACTTAAAGACCTTCATATACAAAACCCAGACA 7040
QY 6721 gtatgagacgttgacgtctcacaactcttctcagaatgagaagtgaagaagacat 6780
Db 7041 GTAGTGAGCGTTGCAGTTCTCACATCTTTCTACAGATGAGAAAGTGAAGAGCTAT 7100
QY 6781 gtatgagaatccgttcataagc 6804
Db 7101 GTATGAGAAATCTGTTCAATACG 7124

RESULT 10
AX127830 9741 bp DNA linear PAT 15-MAY-2001
LOCUS AX127830
DEFINITION Sequence 69 from Patent WO0130848.
ACCESSION AX127830
VERSION AX127830.1 GI:14134477
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 9741)
Denelle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,J., Lemoine,C., Duverger,N., Jaje,M., Searfoss,G.H.,
Remaley,A., Brewer,H.B. and Dean,M.
Nucleic acids of the human abci gene and their therapeutic and
diagnostic application
Patent: WO 0130848-A 69 03-MAY-2001;
JOURNAL Avenir Pharma S.A. (FR)
FEATURES
source Location/Qualifiers
1..9741
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2650 a 2180 c 2290 g 2620 t 1 others
ORIGIN

Query Match 99.7%; Score 6784.8; DB 6; Length 9741;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6792; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 atggctgtgtgcttaagctgagtgctgctgctggtggaagaacacttcagaagaaga 60
Db 185 ATGGCTGTGTGGCTCAGCTGAGAGGTTGCTGTGGAAACCACTTCAGAGAAAGA 244
QY 61 caaacaatgcagctgttactggaagtgcgctgacctatcttctcctgactgac 120
Db 245 CAAACATGTCAGCTGCTGTGGAAGGCGCTGGCTCTTTATCTCTCTGATC 304
QY 121 tctgttcgctgagctaccacccatgaacaatgaatgacatttcacaataagcc 180
Db 305 TCTGTTCGGCTAGCTACCCACCTATGAACAACATGATGCAATTTCCAAATAAAGCC 364
QY 181 atggccttcgaggaacacttccttggttgaggagattatctgtaaatgacaacccc 240
Db 365 ATGGCTTCGCAAGAACCTCTCTGGGTTCAAGGGAATTAATCTGAATGCCAAACCC 424
QY 241 tcttcctgtaaccactctgaggaggtcccgagatgttggaaacttaacaatcc 300
|||||

Db 425 TGTTTCGTTACCCGACTCTCTGGGAGGCTCCCGAGTGTGTGAACCTTAACAATCC 484
QY 301 attgagctcgctgttctcagaatgctcggaagctcttcttataagcagaagaaccc 360
Db 485 ATTTGGCTCGCTGTCTTCACATGCTCGAGGCTCTTTTATATACGACAGAAACACC 544
QY 361 agcatgaaggaatgcgaagtcttgagaacattacagagatcaagaatccagctca 420
Db 545 AGCATGAAGACATGCGCAAAAGTTCTGAACATTACAGAGATCAAGAAATTCAGCTCA 604
QY 421 aactgaagcttcaagattctctgttgacaatgaacactctctggttctatatac 480
Db 605 AACTGAACCTTCAAGATTCTCTGGTGACATGAACCTTCTCGGGTCTCTGATCAC 664
QY 481 aacctctctcccaagctactcttgacaagatgctggaagctgagctatctccac 540
Db 665 AACCTCTCTCCCAAGTACTCTGTGACAAAGATGCTGAGGGCTGATCTATCTCCAC 724
QY 541 aagtaattttgcaagctacagtlacattgacaagtctggaatgatacaaatca 600
Db 725 AAGTATTTTTCGAAGCTACAGTTACATTTGACAACTCTGTGCAATGATCAAAATCA 784
QY 601 gaagatgatattcaactgtgtgacaagaagttcttgagcttctggtctacaagaag 660
Db 785 GAAGATGATTTCAACTTGTGTGACCAAGATTTCTGAGCTTTGTGGCTACCAAGGAG 844
QY 661 aaactgctgcagcagcagagctactctgtccacaatgacatctcgaagccaatcgt 720
Db 845 AAACGTGCTGACGACGACGAGTACTCTGTTCCAAATGACATCTGAAACCAATCCTG 904
QY 721 agaacaactaacctaacctccctccctccagcagaagcgtggtgaaagccaaaca 780
Db 905 AGAACAATTAACCTTACATCTCTCCCTCCGAGCAAGAGGCTGSCGAAACCAAAAACA 964
QY 781 ttgctgcaatgcttggaactctgcccagaagcgtgttcaagcatgaaagctgagac 840
Db 965 TTGCTGCAATGCTTGAGACTCTGGCCAGGAGCGTTTACACATGAGAGCTGAGAGTAC 1024
QY 841 atggcagagaggggagatgttctcgaacaaatgtaacagctccagctcccaaccaatc 900
Db 1025 ATGCGACAGAGGCTGATGTTCTGACCAATGTGAACGCTCCACCTCCACCAATC 1084
QY 901 taccagctgtctcgtatgtctgtctgcggacatcccgaggagggtcgaaatcaag 960
Db 1085 TACACAGCTGTGCTCTGATGTCTGCGGAGATCCCAAGGAGGCGGCTGAAGATTAAG 1144
QY 961 tctctcaactgtgtatgagacaacaactacaagaagccctcttggaggcaatgagact 1020
Db 1145 TCTCTCAACTGTGTATGAGGACAACTACAAACCTCTTTGGAGGCAATGACATGAG 1204
QY 1021 gaagatgtgaacactcttaatagaacacttaacactcttaactgaatgattgaaag 1080
Db 1205 GAAGATGTGAACCTTCTGTATGACAACCTCTTAATCTTAATGATTTGATGAAG 1264
QY 1081 aattggaagctagctctcttcccgatatacttgaaagctcgaagccgctgtcgt 1140
Db 1265 AATTGGAGTCTACTCTCTTTCCGATTAATCTGAAACCTCTGGAAGCGCTGCTGTT 1324
QY 1141 gggaagatccctgtatacaactgcgaactcccgacaaggaagtcagtgtgagagac 1200
Db 1325 GGGAGATCTCTGTATACACTGTGACCTGACGCAAGAGGAGGTCATGAGGTGAGTAAAC 1384
QY 1201 aagaccttccaggaactgctgtgttccatgatactggaaggaatgttggaggaactcagc 1260
Db 1385 AAGACCTTCGCAAGACTGTGCTGTTCATGATCTGGAAGGCAATGAGGAACCTCAGC 1444
QY 1261 cccaagatctggaactctcaatggaagaacccaagaatggaactgtccgagtgtgtg 1320
Db 1445 CCCAAGATCTGAGACTTCATGGAAGAACGCAAGAAATGAGACCTTGGCCGATGCTGTTG 1504
QY 1321 gacagcaggaacaatgacaacttltggaaacagcaatgttgaatgaaatggagaccc 1380
Db 1505 GACAGCAGGACATGACCACTTTTGGGAACAGCAGTTGATGCTTACATTTGACAGCC 1564
|||||

QY 5761 tatagaagaagcggaagcctctgtctacagagatttgctgaggatctctctgtgtgag 5820
|||||
Db 5945 tttatagaagaagcggaagcctctgtctacagagatttgctgaggatctctctgtgtgag 6004
QY 5821 tctcttgagcctcttgagagatttgagggctggaataatcacaacttcaagaatgataca 5880
|||||
Db 6005 tctcttgagcctcttgagagatttgagggctggaataatcacaacttcaagaatgataca 6064
QY 5881 ggaagatcaccactgttaccagagagagatgcttctcttaacaaaataagatattatcaaac 5940
|||||
Db 6065 ggaagatcaccactgttaccagagagagatgcttctcttaacaaaataagatattatcaaac 6124
QY 5941 atccatgaatgatacacaagaacttgagcctctgagcctctgagcctatgagcacaagaagctg 6000
|||||
Db 6125 atccatgaatgatacacaagaacttgagcctctgagcctctgagcctatgagcacaagaagctg 6184
QY 6001 ttgacttgagagagagagagagatgagatcttctgaccttttgagagagagatcccaagaaga 6060
|||||
Db 6185 ttgacttgagagagagagagagatgagatcttctgaccttttgagagagagatcccaagaaga 6244
QY 6061 gtttgcaagagttgtgtgagtgagtgagcgtatctcggaacttgagcctctgagagatgagagaaa 6120
|||||
Db 6245 gtttgcaagagttgtgtgagtgagtgagcgtatctcggaacttgagcctctgagagatgagagaaa 6304
QY 6121 tatgtctgtaactataagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 6180
|||||
Db 6305 tatgtctgtaactataagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 6364
QY 6181 ggggggccccctgt 6240
|||||
Db 6365 ggggggccccctgt 6424
QY 6241 cgggtctgtggaatgtgtgccccctgaagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6300
|||||
Db 6425 cgggtctgtggaatgtgtgccccctgaagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6484
QY 6301 tctcagaatgag 6360
|||||
Db 6485 tctcagaatgag 6544
QY 6361 aggttcaagtgccccctgt 6420
|||||
Db 6545 aggttcaagtgccccctgt 6604
QY 6421 atagttgtacgaatgag 6480
|||||
Db 6605 atagttgtacgaatgag 6664
QY 6481 ctgtgacattctctgtgag 6540
|||||
Db 6665 ctgtgacattctctgtgag 6724
QY 6541 ccatcttcaattatctctctgtgag 6600
|||||
Db 6725 ccatcttcaattatctctctgtgag 6784
QY 6601 ctccacaatagaagaactactctgttctcagaagaacacttgagcagaagatattgtgaacttt 6660
|||||
Db 6785 ctccacaatagaagaactactctgttctcagaagaacacttgagcagaagatattgtgaacttt 6844
QY 6661 gccaagaag 6720
|||||
Db 6845 gccaagaag 6904
QY 6721 gtagtgagagcttgagcttctcacaacttctcacaagaatgagagagagagagagagagagag 6780
|||||
Db 6905 gtagtgagagcttgagcttctcacaacttctcacaagaatgagagagagagagagagagagag 6964
QY 6781 gtagtgagagcttgagcttctcacaacttctcacaagaatgagagagagagagagagagagag 6804
|||||
Db 6965 gtagtgagagcttgagcttctcacaacttctcacaagaatgagagagagagagagagagagag 6988

RESULT 11
AX139817
LOCUS AX139817 9741 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 69 from Patent EP1096012.
ACCESSION AX139817
VERSION AX139817
KEYWORDS GI:14275399
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 9741)
AUTHORS Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,
Remaley, A., Brewer, H.B. and Dean, M.
Nucleic acids of the human abci gene and their therapeutic and
diagnostic application
Patent: EP 1096012-A 69 02-MAY-2001;
Aventis Pharma S.A. (FR)
FEATURES
Location/Qualifiers
source 1..9741
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2650 a 2180 c 2290 g 2620 t 1 others
ORIGIN
Query Match 99.7%; Score 6784.8; DB 6; Length 9741;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6792; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 atggtcttgagcctcagctgagtgagtgctgt 60
|||||
Db 185 atggtcttgagcctcagctgagtgagtgctgt 244
QY 61 caaatatgacagctgttactgtgaagtgagcctgagcctctatcttctctgactgactg 120
|||||
Db 245 caaatatgacagctgttactgtgaagtgagcctgagcctctatcttctctgactgactg 304
QY 121 tctgtcgttgagcttaccac 180
|||||
Db 305 tctgtcgttgagcttaccac 364
QY 181 atgccccttgagagagac 240
|||||
Db 365 atgccccttgagagagac 424
QY 241 tgttccgttaccac 300
|||||
Db 425 tgttccgttaccac 484
QY 301 attgtgctgcagctgttctcagaatgctgagagcttcttatacagccagaagaagacac 360
|||||
Db 485 attgtgctgcagctgttctcagaatgctgagagcttcttatacagccagaagaagacac 544
QY 361 agcatgaagagacatgagcaaatgttctgagaacattatgagagagagagagagagagagagagag 420
|||||
Db 545 agcatgaagagacatgagcaaatgttctgagaacattatgagagagagagagagagagagagagag 604
QY 421 aacttgaagcttcaagattctctgtgtgacaatgaaacacacacacacacacacacacacacacacac 480
|||||
Db 605 aacttgaagcttcaagattctctgtgtgacaatgaaacacacacacacacacacacacacacacacac 664
QY 481 aacccctctctccaaagtctctactgtgagaagaatgagcagagagagagagagagagagagagag 540
|||||
Db 665 aacccctctctccaaagtctctactgtgagaagaatgagcagagagagagagagagagagagagag 724
QY 541 aaggtattttgcaagagctacagcttatacttgagaatgtctgtgagatgagatgagatgagatgag 600
|||||
Db 725 aaggtattttttgcaagagctacagcttatacttgagaatgtctgtgagatgagatgagatgagatgag 784
QY 601 gaagagatgattcaacttggtgagcagaagaagttctctgagcttctgtgaccttaccacaaaggag 660

Db 785 GAAAGATGATTCACCTGGTGACCAAGAGTTCTGAGCTTTGTGGCTTACCAAGGAG 844
QY 661 aaactgctgcagcagcagagactcgttccaaacatgacacccgaagccatcctg 720
Db 845 AAATGCGCTGAGAGAGAGAGTACTGTTTCCAAATGACATGCAATCCGAAGCCAAATCC 904
QY 721 agaacataactacatctccctccccaagagagctgctgaagccacacaa 780
Db 905 AGAAGACTAAACTCTACATCTCCCTCCGAGCAAGAGCTGGCCCAAGCCCAAAAAA 964
QY 781 ttgctgatagtcttggagactctgcccagagctgttcaagcatgaagctgagtgac 840
Db 965 TTGCTGATAGTCTTGGGACTGTGGCCAGAGACTGTTCAGATGAGAACTGAGATGAC 1024
QY 841 atgcgaaagagatgtagtcttccgaacatgtaaacagctccagctccaccacac 900
Db 1025 ATGGAGACGAGAGGTGAGTGTTCGACCAATGTGACAGCTCCAGCTCCACCCAAATC 1084
QY 901 taccagctgtctcgtatgtctgcggcaccgccagagagaggggctgaagatcaag 960
Db 1085 TACAGGCTGTGCTGATATGCTGCGGCAATCCGAGGAGAGGGGCTGAAGATCAAG 1144
QY 961 tctctcaactgtaagagcaaacatacaagccctcttggagagcaatggagctgag 1020
Db 1145 TCTCTCAACTGATGAGGACAACTACAAAGCCCTTTGGAGCAATGCACTGAG 1204
QY 1021 gaagatgctgaacactctctatgacacactacacactctactcgaatgattgtaga 1080
Db 1205 GAAGATGCTAAACCTTCTATGACAACTCTACAACTCTTACTGCAATATTGATGAAG 1264
QY 1081 aatttggagctagctcctctcccgacatctctgaagagctctgaagcgctgctgt 1140
Db 1265 AATTGGAGTCTGCTCTCTTCCGCAATATGAGAAAGCTGTGAAGCGCTGCTGCTT 1324
QY 1141 gggaaatctgtatatacactgacactcgaagcaagcaagagctgaagtgagtgaa 1200
Db 1325 GGGAAATCTGTATACACTGACCTGACCTCCAGCAAGCAGGTCAATGCTGATGAAAC 1384
QY 1201 aagacttccaggaactgctgtgtcctatgactctgaagagatgtaggaagcaactc 1260
Db 1385 AAGACTTCCAGGAACCTGGCTGTGTTCCATGATCTGGAAGGCTGTGGAGGAACCTCAGC 1444
QY 1261 cccaagatctgacactctatgagaaacagccaagaatgagactgtgtccgga 1320
Db 1445 CCCAAGATCTGACCTTCAATGAGAACGCCAAGAAATGAGCTGTGCGATGCGTGG 1504
QY 1321 gacagagaggaacatgacacacttgggaaacagcagtgtagtcttagattggaagc 1380
Db 1505 GACAGAGGAGCAATGACCACTTTGGGAACAGCAAGTTGATGGCTTACATTTGAGACGC 1564
QY 1381 caagacatctgtgcttcttctgccaagcaccagagatgctcagctccagtaagttct 1440
Db 1565 CAAGACATGCTGGCTTTTGGGCAAGCACCCAGAGAGTGTCCAGTCCAGTAAATGCTCT 1624
QY 1441 ggtgacactgtagaagcttccaagagactaaaccaggaatcccgacatctcgc 1500
Db 1625 GTGTACACTGGAGAGAACTTTCAACGAGACTTAACCAAGCAATCCGAGCATATCTGCGC 1684
QY 1501 ttcatggagtggttaaaccttgaaacagctaaagccatagcaacgaagctgtgctcacc 1560
Db 1685 TTCTATGAGTGTGCTAACCTGAACAAAGCTAAGAACCAAGAGTGGTGGCTCATC 1744
QY 1561 aacaagctcatlgagctgtctgtagagagaaagcttctggtctgtatgtgttcaactga 1620
Db 1745 AACAGATCATGAGAGCTGTGATGAGAGAGAGTCTGTGGCTGTATGTGTCTGCTGGA 1804
QY 1621 attactcagcagcagctgagctgtcccatcaatgtcaagtaagaatccgaatgacat 1680
Db 1805 ATTACTCAGCGAGATGAGCTGCCCATCATGTCAAGTACAAAGATCCGAATGAGACTT 1864
QY 1681 gacatgtggagagacaataaataagaatgtagtactgtgagccgtgtccctgagct 1740
Db 1865 GACAAATGTGAGAGAGCAAAATAAATCAAGAGATGGTACTGGACCTGTCTGAGCT 1924
QY 1741 gaccccttgaagacatgcgtgactgtgggggcttcgactacttgcagatgtagtg 1800
Db 1925 GACCCCTTTGAGAGATGCGGTACTCTGCGGGGCTTCCGCTACTTCCAGATGTGTG 1964
QY 1801 gacgagcaatcaatgaaggtgtctgagggcaacggaagaaactgtgtctatagcaa 1860
Db 1985 GAGCAGGCAATCATAGGTGTGTGACGGCACCCGAGAGAAAGAAATGAGTCTATATCA 2044
QY 1861 cagatgcccataccctgttactatgatacacttctcgggggtgtagagccgctcaatg 1920
Db 2045 CAGATGCCCTATCCCTGTAGCTTATGATCAATCTTCTGCGGGTATGAGCCGGTCAATG 2104
QY 1921 cccctcttaatgacgtgagcctggaattactcaatgagctgtgatacatcaagagatcgt 1980
Db 2105 CCCCTTCAATGACCTGCTGATTTATCAAGAGCTGTGATCATCAAGGATGCTG 2164
QY 1981 tatgagagagagagcaggtgaagagacatgagatcatagggcctggaacacata 2040
Db 2165 TATGAGAGAGAGGACGGCTGAAGAGACATGCGATCATGAGGCTGTGACAAAGCATC 2224
QY 2041 ctctgtttagctgttcaatlagcctcaatcctcctcttctgtagagcgtgctgcta 2100
Db 2225 CTCTGTGTTAGCTGTTCATTAGTACCTCATTCCTCTTCTTGGAGCGCTGCTGCTA 2284
QY 2101 gtgtcatctcgaagttagaagaaactgtcctcaagtgatccagcgtgtgtgtc 2160
Db 2285 GTGGTCATCTGAAGTTAGGAACCTGCTGCTCAAGTATCCACAGTGTGTGTGTC 2344
QY 2161 ttccgtgcgt 2220
Db 2345 TTCCGTGCTCGGT 2404
QY 2221 tccagagcaacactgagcagcagcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2280
Db 2405 TCCAGAGGCAACCTGGGAGCAGCTGTGGGGGATCATATCACTTCAAGCTGTACCTGCC 2464
QY 2281 taagtctgt 2340
Db 2465 TACGCTGCTGT 2524
QY 2341 ctgctgtctcctgt 2400
Db 2525 CTGCTGTCTCTGT 2584
QY 2401 ggcatttgagtgagtgagtgagcaactgttgaagagctcgtgtgtgtgtgtgtgtgt 2460
Db 2585 GGCATTGGAGTGCAGTGGGACCACTCTTGAAGAGTCTGTGAGGAGAAATGCTTCAAT 2644
QY 2461 ctcaacacttgcactcctcaatgagtgttggaaacacttctctatgaggtgtagactgtg 2520
Db 2645 CTCACCACTTGGCTCTCATGATGCTGTGTGACACTTCTCTATGGGGATGAGACTGTG 2704
QY 2521 tacattgagctgtcttccagggcagtaagaaatcccaagccctgtgtatcttctcgtg 2580
Db 2705 TACATTTAGGCTGTCTTCCAGGCACTAGGAATTCAGAGGCTGTGTGTGTGTGTGTGT 2764
QY 2581 accaagctcactgt 2640
Db 2765 ACCAAGTCTTACTGT 2824
QY 2641 aagagatgtcagaataatctcatggaaggaagaaacccaacttgaagctgtggcgtgtcc 2700
Db 2825 AAGGAATATCAGAAATCTCATGAGAGAGAAACCAACCTTGAAGCTGGGCGTGTCC 2884
QY 2701 attcagaacctgtttaaagtctaacgagatggaatgaagtgagctgtcgtgtgtgtgtgt 2760
Db 2885 ATTCAAGAACTGTGAAAGTCTAACGAGATGGATGAAGTGTGTGTGTGTGTGTGTGTGT 2944
QY 2761 ctgaatttttatgtagggcagatcaactcctctcgtgtgtgtgtgtgtgtgtgtgtgtgt 2820
Db 2945 CTGAATTTTATGAGGGCCAGATCACTCTCTGCGGCACAAATGAGAGCGGGAAGAGC 3004

QY	2821	accacatgcaatcctcgaccgggtgtgtcccccgcgacctcgggacccgcctaatcctc	2880
Db	3005	ACCCACATGTCAMCTCGACCCGGGGTGTTCCTCCCGACCTCGGGACCGCTCCATATCTCG	3064
QY	2881	ggaagaacatcgccttcgtgatgagcacacacccgcagaaacctcgtgggtctgtccccag	2940
Db	3065	GGAAAGACATTCCCTTGAGATGAGCACCATCCGGCAGAACCTGGGGTCTGTCCCGAG	3124
QY	2941	cataacgtgctgttttgacacgtgcgtgtgtcgaagaacatctgttctatgcccgttg	3000
Db	3125	CATACCGTCGTGTGTGACATGCTGACTGTGCAAGAACACATCTGGTGTATGCCGGTTGG	3184
QY	3001	aaaggctcttcgagaagcaagtgaaggcgagatgagacagatggtcccttgatgttgt	3060
Db	3185	AAAGGGCTCTCTGGAAGCGACGTGAAGGGCGAGATGTGACACATGGCCCTGTGATTTGGT	3244
QY	3081	ttgcacatcaagcaagctgcgaagaacaaacaaagccagctgtcaagtggaatgcagaagaag	3120
Db	3245	TTGCGATCAGCAAGCTGGAAGCAAAACAGCCACTGTCAAGGTGCAATGCAGAGAAAG	3304
QY	3121	ctatctgtgacctgtgacctgtgtccggggagatcctaagttgtcatctcgtatgaaccaca	3180
Db	3305	CTATCTGTGGCCTTGCGCCTTGTGTGGGGAGCTAAAGTGTGCTATCTGGATGAACCCACA	3364
QY	3181	gctggtgtgaaaccttaactccgcgaagggaataatgtagcgtcgtctgtaataaccgaca	3240
Db	3365	GCTGTGTGGACCTTACTCTCCCGAGGGCAATGTGGAGACTCTGTGTAATACCGACA	3424
QY	3241	ggccgcaccatattctctctaaacacacaatgaatgaagcgagcttccttggggagag	3300
Db	3425	GGCCGCACCATTATTCTCTCTACACACACATGGATGAAGCGAGCTCCTGGGGGACAG	3488
QY	3301	attgcacatctcccaatgggaagctgtgctgtgtgtgacctccctgtttctgaagaac	3360
Db	3485	ATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGGGCTCCTCCTGTTTCTGAAGAAC	3544
QY	3361	cagctgggaacaaagctactactacgtacctgtgtcaagaagaatgtgtaaacctccctcagt	3420
Db	3545	CAGCTGGGAACAGGCTACTACTCTGACCTTGGTGAAGAAATGTGAAATCTCCCTCAGT	3604
QY	3421	tccctgcagaacagtagtagcactgtgtcaacctgaagaagaagagatgttctcag	3480
Db	3605	TCCCTGACAAACAGTAGTAGCAGCTGTGTACTACTGAAAAGSAGSAGAGTGTTCAG	3664
QY	3481	agcagttctgtatgtcgtgcgtgtggcagcgaacatgtagatgacagctgtgacatcgatgc	3540
Db	3665	AGCAGTTCGTGATGCTGGGCTGGGACGAGCACTAGAGTAGACAGCTGCACATCGATGTC	3724
QY	3541	tctgtctatctccaaacctcatagaagaacatgtgtctgaagcccggtgtgtgaaagacata	3600
Db	3725	TCTGTATCTCCAACTCATATAGGAACATGTGTCTTAACCCCGCTGTGGGAAGACATA	3784
QY	3601	gggcaatgacgtacactatgtatgtcacaatgaagctgtclaaggaaggagccttgtgaa	3660
Db	3785	GGGCAATGAGCTGACTATGTCTCTGCATATGAACCTCTTAAGSAGGAGGCTTTGTGGAA	3844
QY	3661	ctcttctcatgagatgtatgacccggtcctcagaacctgtggcatlcttagttaatgcatctca	3720
Db	3845	CTCTTTCATGAGATGTGATGACCGGCTCTAGACCTGTGGCATTTCTAGTTATGACATCTCA	3904
QY	3721	ggagacacccctgggaagaataatctcctaagtggtgcgaagaagaaggttgggtgtgagtgtag	3780
Db	3905	GGAGACACCCCTGGAAAGAAATATTCTCTCAAGTGTGGCCCAAAAGATGGGTGTGATGCTGAG	3964
QY	3781	acctcagatgtgacctgtgcagcaagaacgaacaaacagcgcggtccttcggggacaagcagagc	3844
Db	3965	ACCTCGATGATGTACTTGTGCGAAGCAAGCAAGAAACAGGCGGGCCTTCGGGGACAAGCAGAGC	4024
QY	3841	tgctctgcgcgttcaactgaaatgatatgtctgtcatccaaatgatcttgacatagaccca	3904
Db	4025	TGTCTTCCGCCCTTCACTGAAGATGATGCTGCTGATCCAAATGATTTCTGCATAGACCCA	4084

QY	3901	gaalccagagagacagacttgctccag	tggatgagatgagtcgaagggtctctccaggtgaa	3960
Db	4085	GAATTCGAGAGAGACGCTTGGCTCACTGGAGTGCATGCGAAAGGGCTCTACAGGTGAA		4144
QY	3961	ggtcggaaacttaacagcaacagttctgagccctcttgtagaagagactgctaattgcc		4020
Db	4145	GGCTGGAAACTTACACGACAAAGTTTGtGGCCTTTGTGGAAGAGACTCTAATTGCC		4204
QY	4021	agacgagatcgnaaaggatttttgcctcagattgtcttcagattgtcttcagctggtttgtcgtcat		4080
Db	4205	AGACGAGATCGGAAAGGATTTTGTCTCAGATTGTCTTGCCAGCTGTGTTGTCTGCATT		4264
QY	4081	ggcccttggttcagccggtacgtcgtgcaaccccttggcaagtaaccacgcctggaacttcag		4140
Db	4265	GCCCTTGTTCCACCTCGATGTGGTCCACCCCTTTGGCMACTACCAGCTGGAACTTTCAG		4324
QY	4141	ccttgatgtaacaacggaacagtaacacattgtctcaagcaatgatatgctccttgaggaacgga		4200
Db	4325	CCCTGGATGTCAACGGAAGTACACTATTGTGACAAATGATGCTCTCGAAGACACGGGA		4384
QY	4201	accttggaactctttaaagccctccaccaaggccctggtcttcggagaccggtgtaatgaa		4260
Db	4385	ACCCCGGAACCTTTTAAAGCCCTTCACCAAGACCTGCTTGGAACCCGCTGTATGGA		4444
QY	4261	ggaaccccaatccccagacagccctccagcgcaaggagaaagatgagaccatgcccaca		4320
Db	4445	GGAAACCCAATCCACAGACAGCCCTCGCAGGACGGGAGGAAGATGGACCACTGTGCCCA		4504
QY	4321	gttcccagaccatcatatgacactcttcacgaatggyaactgtgacaatgcgaacccctta		4380
Db	4505	GTTCCTCCAGACATCATGAGACTTTCCTCCAGAAATGGACATCGCAATCAACACCTTTCA		4564
QY	4381	cctgtaatccagatgtagcagcagcaaaacaagaagatgctccctggtgtgccccaggg		4440
Db	4565	CCTGATGCCAGTGTAGCAGCGACGCAAAATCAAAACATGCTGCTGTGTGCCCCAGGG		4624
QY	4441	gcaaggggggtgctcctccacaagaanaaacaacatgtcagatataccttcagagacctg		4500
Db	4625	GCAGGGGGGCTGCTCCTCCACAAAGAAAACAACACTGCAGATATCCTTCAGACCTG		4684
QY	4501	acaagaaanaaactttcggattatcgtgtgaagaatgattgcagatatagcacaagc		4560
Db	4685	ACAGGAAGAAACATTTTGCGATTATCTGTGTAAACGTATGTGCAGATCATGCCAAAAGC		4744
QY	4561	ttaaagaacaagaatctgggtgaatgagttlaagtatgcygagcttttcctcggtgtcagt		4620
Db	4745	TTAAAGAACAAGATCTGGGTGAATGATTTAGTATGCGGCTTTTCCCTGGGCTGCAGT		4804
QY	4621	aatactcaagcaactctctccgagtcgaagaatgataatgatacgccataaanaaataagaag		4680
Db	4805	AATACTCAAGCATCTTCTCCAGTCAAGAAATTAAATGATGCCAACCAAAATAATGAGAA		4864
QY	4681	caacttaaaactgycacaagaacagttctgcagatctgatalctctcaacagcttggagaatt		4740
Db	4865	CACCTAAAGCTGGCCAAAGACAGTTTGCAGATTCGATTTCTCAACAGCTTGGAGAGATT		4924
QY	4741	atgacagagactgagacacagaataatgtaaggttggttcaataaacaaggctcgcat		4800
Db	4925	ATGACAGGACTGTGACACACAGAAATAATGTAAGGTGTGTTCAATTAACAAAGGGCTGGCAT		4984
QY	4801	gcaatcaagcttcttcgtgaatgtaatacaaaatgcaatctccggycacaactgtcaaaag		4860
Db	4985	GCAATCAGCTCTTTCCTTAATGTATCATCAACAATGSCATTCTCGGGCCAACTGCAAAAG		5044
QY	4861	ggaagagaacctagccaattatgtaatactgcttcaatcaatcccttgaaattccacag		4920
Db	5045	GGAGGAACACCTTAGCCATTATGGAATTATGCTTTCAATATCCCTGGAATTCACCAAG		5104
QY	4921	cagaagctctcagaggtggctctgataacaaactcaatgaaatgctctgtgtaacatcgt		4980
Db	5105	CACGCACTCTTCAGAGGTGCTCCATGTACACATCACTAGTGAATGCTTGTGTGCATCTGT		5164
QY	4981	gtatcattttgcaatgtcctctgctgccagcaagcttgtcgatattcctgtaaccagagcgg		5040

Db	5165	GTCACTTTGGCAAGTCCCTTCGTCGCCAGCCAGCTTTGTGTGATTCCTGTATCCAGACGGG	5224
OY	5041	gtcagcaagcaaaaacacccctcggagttcataagtgaggtgaagcctctcaacagctc	5100
Db	5225	GTCAACCAAGCAAAACCTCGACATTCTATAGTGGAGTGAAGCTGTCTCATCTACGGCTC	5288
OY	5101	tcctaatctgtctcgtggaatacgtgaacttaacgtttgctccctgcgcacactgtgcaatc	5160
Db	5285	TCTAATTTTGTCTGGATATGTGCAATTACGTTGTGCCGCGCCACACTGTGCTATTCATC	5344
OY	5161	ttcaatcgtctcccaagcaagagttcctatagtttctctcccaactctgcctgtctgaacct	5220
Db	5345	TTCACTCTCTCCACGCAAGATCCTATGTGTCTCTCCACCAATCTGCTGTGTACCCCTT	5404
OY	5221	ctactttgtcgtatacgttggtgaatcaacacctctatgtaccgaacctccttgttctc	5280
Db	5405	CTACTTTTGGCTATGGGTGGTCAATCACACCTCTCATGTACCCAGCCCTCTTTGTGTTC	5466
OY	5281	aagatccccaagcacagcctatgttgggtctcaacagcgtgaacctctcaatgtgcaataa	5340
Db	5465	AAGATCCCCACACACAGCCCTATGTGTGTCTCCACAGCGTGAACCTCTTATGTGGATTAA	5524
OY	5341	ggcagcctggcgcacctttgtgtcggagcgtgttaccgcaataaagctgaataatacaat	5400
Db	5535	GGCACCGGGCCACTTTGTGTGCTGGACCTGTTCACGCAATPAAGCTGATATATTCAT	5584
OY	5401	gataccctcgaagtcgcgtgttcttgatcttcaccaatctttgtccctgagcaagagctcac	5460
Db	5585	GATATCCCGAAGTCGCGTGTCTTGATCTTCCACATTTTGTGCTGGAGACAGGCTCATC	5644
OY	5461	gacatggtgtaaaaaacagcaaatggtcgtatgtccctggaagaagtttggggagaaatcgctt	5520
Db	5645	GACATGGTGAATAAACCGAGGAATGGCTGATGCCCTGGAAAGGTGTGGAGATATGCTTT	5704
OY	5521	gtgtcaaccatatctcttggagcttgggtggagacgaacctcttcgcaatggccgttgaag	5580
Db	5705	GTGTCAACCATTAATTGTGGACCTTGCTGGAGCAGAAACCTCTTGCCATGGCCCTGGAAAGG	5766
OY	5581	gtgtgtgtctctccatctactgtctcgtatccagtaacagatcttccatcaagccagacct	5640
Db	5765	GTGGTGTCTTCCTCATTAACCTATGTTGTGATCCATACAGATTTCTTATCAGGCCCGACCT	5824
OY	5641	gtaaatgcaaaagcattctccctcgtgaatgaatgaagatgtaagatgttgaaggggaaagac	5700
Db	5825	GTAATGTCAAAAGCTATCTCCTCTGTAATGATGAAGATGAAGATGTGAGCGGGAAGACAG	5884
OY	5701	agaatctctgtatgttggagggccgaatgtaacatctagaataaagaagtttgcagaata	5760
Db	5885	AGAAATCTTGATGTGTGAGGAGCCAGAAATGATCTTGTGAATACAGAGATTGTGACAAATTA	5944
OY	5761	tataagaaggaagcgaagcctgtcgttttgaacagaatttgggtggcatctccctcgtgtag	5820
Db	5945	TATGAAAGGAAGCGGAAGCCGTGCTGTGACAGGATTTGGTGCGCATTCCTCCGTGTAG	6004
OY	5821	tgcttgggctccctcgggaagttaatggggctcggaaatcaacaaacttcaagaatgttcaaa	5880
Db	6005	TGCTTTGGGCGTCCGTGGAGATTAAATGGGGCTGGAAATCAATCAACTTTCAAGATGTTAAC	6064
OY	5881	ggagatatccactgtttacagagaagatgcttttccctaaacaaatagtatcttcaaac	5940
Db	6065	GGAGATTCACACTGTTTACCAAGAGAGATGCTTTCCTTAAACGAAATATGATCTTATCAAC	6124
OY	5941	atccataaagatacacaagacatgggctctacgtccctcaagtttgaatgcatacagaagct	6000
Db	6125	ATCCATTAATTAATCATCAGAACTAGGGCTACGTGCCCTCAGATTGATGCCATCATCAAGCTG	6184
OY	6001	ttgactgtggagagacaacgcttgaagctctcttgcccttttgaagagagatcccaagaaagaa	6060
Db	6185	TTTGACTGGGAGAAACACGTGGAGTCTTGTGCCCTTTTGAAGAGAGTCCCGAGAAACAA	6244
OY	6061	gttggcaaggttggtagtggggagatctcgaaacatgggctctgttaagtataggagaaaa	6120

D6	6245	GTGGGCAAGGTTGTGTAAGGAGGCGATTGGGAAACTGGGCTCTGTGAAGTATGCAAGAAAA	6304
QY	6121	tatgctgtgtaactatgtaggaagcaacaacgcaagctcttcaagccatgpgcttttgac	6180
D6	6305	TATGCTGTGTAAGTATGCTGAGGCAACAACCAAGCTCTTACAGCCATGCGCTTTGATC	6364
QY	6181	gacgagcctctctgtgtgttcttctgtgaatgaaccacacacgaagcatatgaaccacccg	6240
D6	6365	GCGGGGCTCTCTGTGTGTTTCTGATGTAACCCACACAGCAGCATGATGCCAAAGCCGG	6424
QY	6241	cgtgtctctgtggaattgtgtccctaagtgltgtccaagggggggaataagtaagtgcttaa	6300
D6	6425	CGGTTCTTGGAAATTTGCTCCCTAAAGTGTGTCAAGGAGGGGGAATATGATGAGCTTTACA	6484
QY	6301	tctcatagtaatgaagaatgttaagctctcttgcacttaagatgtagcaatcaatgltcaatga	6360
D6	6485	TCTCATATGATGGGAACAATAGTAAAGCTCTTTTGTGCATAGATGGCAATCATGTGCATGGA	6544
QY	6361	aggltcaagtgctctgtgcagtgltccagcatcctaaanaatagtglttgagatggttatcaa	6420
D6	6545	AGGTTTCAGGAGCCTTGTGGCAGTGTCCAGCATCTAAAAAATAGTTTGGAGATGGTTATACA	6604
QY	6421	atagtgtagcaatagcaaggttccaaacccggaacctgaagcctgtccagagattctttga	6480
D6	6605	ATGAGTTGTACGAATAGCAAGGTCACACCGGACCTGTGAAGCCTGTCCAGGATTTCTTTGGG	6664
QY	6481	cttgcaatttccttgaagtglttctaaagaagaaacacccggaacatgctcacataaccagctt	6540
D6	6665	CTTGCAATTTCTGTGAAGTGTTCCTCAAAAGAGAAACCCGGAAACATGTACAAATACAGCTT	6724
QY	6541	ccatcttcattatctctctctctgccaagatatcatgaactctctcccaagacaaaagcga	6600
D6	6725	CCATCTTCATATTCCTCTCTGGCCAGGATATTACACATCTCTCCAGACCAAAAAGCGCA	6784
QY	6601	ctccacaataagaacactacctgttctctcaagaacaactgtccaaagatatttgaacctt	6660
D6	6785	CTCCACATAGAAACATACACTCTTCTCTCAGAACACACTTAGCAAGATATTGTGAACTTT	6844
QY	6661	gccaaaggaaccaagtgaatgaatgaccacttaagaagacctctcaataacaaacacagaca	6720
D6	6845	GCCAAAGACCAAAAGTCATGATGACCACTTAAAGACCTCTCATTTACCAAAAACCAAGACA	6904
QY	6721	gtatgtgaagctgcagttcttccatccttcttctcaagagatggaagatggaagaagctat	6780
D6	6905	GTACTGGACCTTGCAATCTCTCACAATCTTTTCTACAGATGAGAAAGTGAAGAAACTAT	6964
QY	6781	gtatgaagaatcctgttcatacgg	6804
D6	6965	GTAATGAAGAATCCTGTTCATACGG	6988
RESULT 12			
AX351038			
LOCUS	AX351038	9741 bp	DNA
DEFINITION	Sequence 10 from Patent WO0183746.		linear
ACCESSION	AX351038		
VERSION	AX351038.1	GI:18616393	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (sites)		
JOURNAL	Rosler-Montus, M. P., Prades, C., Lemme, C., Naudin, L., Deneffe, P., Breuer, B., Nueviger, N., Remaley, A. and Santamaria-Foto, S. Regulatory nucleic acid sequences of the abci gene Patent: WO 0183746-A 10 08-NOV-2001; Aventis Pharma S.A. (FR)		
FEATURES	Location/Qualifiers		
source	1..9741		
BASE COUNT	2650 a	2180 c	2290 g
		2620 t	1 others

ORIGIN

Query Match	99.7%;	Score 6784.8;	DB 6;	Length 9741;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 6792; Conservative	0;	Mismatches 12;	Indels 0;	Gaps 0;

QY	1	atgctgtgttgcgcctcaagctgaagttggtctgtctgtgttgagaagaccctacttcaagaagaga	60
Db	185	ATGGCTTGTGTGGCCCTCAGCTGAGTTGGCTGCTGTGTGGAAGAACCTTCCAGTAAGAGA	244
QY	61	caaacatgctcaagctgttacttgaagtgagcttgacctattattcttccttgatctgatac	120
Db	245	CAAAACATGTACAGTGTGCTGCTGGAATGGCTCGCTCTATTTATCTTCGTATCTGATC	304
QY	121	tctgttcgcgttagcgtaccaccacctatgaacaacttgatgcatttccaaataaagcc	180
Db	305	TCGTGTCGGCTGAGCTACCCACCTATGTACACACTGAAATGCAATTTTCCAAATAAAGCC	364
QY	241	tgtttccgtttaccgcgctctcgttgggaaggtcccggaagttgtttgaaactttaacaatcc	300
Db	425	TGTTTCCGTATACCCGACTCTTG66GAGGCTCCCGAGTGTGGAAACTTTTAACAATTC	484
QY	301	attgtgctgcgcgtgtctcgaatgctctgagagcttcttatalacagccagaagaacac	360
Db	485	ATTGTGGCTCGCCTGTTCAGATGCTGAGAGCTTCTTTATACAGCCAAAGAACACC	544
QY	361	agcatgaaggacatgagcaaaagtctctgagaacattacagcagatcaagaataacagttca	420
Db	545	AGCATGAGGACATGGCGAAAGTTCTGAAACATTTACAGCAATCAAAATTCACAGCTCA	604
QY	421	aaactgaagcttaagattctctgtgtgagcaatgaaactctctcgtgttctcattatcac	480
Db	605	AACCTGAAGCTTCAAAATTTCCGTGTGGAGCAATGAACCTTCTGTGGTCTCTGTATCAC	664
QY	481	aaacctctctccaaagtctactgttgaaacaagtctgaagggtcgtatgatactctccac	540
Db	665	AACCTCTCTCTCCCAAGCTCTACTGTGTGACAAGATGCTGAGGGCTGATGTATCTCTCAC	724
QY	541	aaggtattcttgaaggtctaccagttacacttgaacaagctgtgaaatgagctcaaaatca	600
Db	725	AAGGTATTTTTCGAAGGCTTACCGATTTCATTGACAAAGTCTGTGCATGTGATCAAAATCA	784
QY	601	gaagaagatgaatcnaacttgtgtgacccaagaagttcttgagcttgtgacctcaaaagag	660
Db	785	GAAAGATGATTCACACTTGCTGACCAAGAAAGTTTCTGACTTTGTGGCTTCCACAAAGGAG	844
QY	661	aaactggtctgacgagagagagagacttggttccaacatgaaatcttgaagcaatctgt	720
Db	845	AAACTGGCTCTCAGAGAGCGCAGTATTCCTTCACATGTGAATCTTGAAGCAATTCCTG	904
QY	721	agaacataaacctcacaatctccctctcccgagcaagagctgtgctgaagccacaanaaca	780
Db	905	AGAACACTTAACCTCTACATCTCCCTTCCGAGAGAAAGACTGTGGCGAAGCCACAAAACA	964
QY	781	tgtgtcatagttcttggagctctgtgcccaagagctgttcaagcatgaagaagcttgaagtac	840
Db	965	TGTGTGATATGTCTTTGGAGACTTGTGGCCGAGAGACTGTTTCAGATGAGAAGCTGGAGTAC	1024
QY	841	atlgagacaaggagtgtatgtttctgacaacaatlgaaagaagctcaagttctccacccaatc	900
Db	1025	ATGCGACAGAGGGTGAATTTCTTGACCAATGTGAACGTCTCCAGCTCTCCACCCAAATTC	1084
QY	901	taccagagctgtctcgtatgtctctgcgagcaatcccgaaagagggggggtctgaagaataag	960
Db	1085	TACCAAGGCTGTCTGCTATTGTCTCGGGGCATCCGAGAGGGGGGCTGAAGATTCAG	1144
QY	961	tctctcaactgtgtatgagaacaactacaagaagccctcttggaggaatgagcaatgag	1020

[illegible]

QY	3181	ggaggatgaggaccccttaactcccggaagggaataibggagctgtgtctgtgaataacgcagaa	324
Db	3365	GGTGGTGTGGACCCCTTACTCCCGAGGGGAATATGGAGAGCTGCTGCTGAATAACGAGAA	3424
QY	3241	ggccgacacatattctctcaacacacatggaatgaaacggaagctctctggggacag	3300
Db	3425	GGCCGACACATTATTCTCTCTACACACCATGATGTAAGCGAGACTCTCTGGGGACAG	3488
QY	3301	attgccatcatctcccatlgggaagctgtgtgtgtgtgtcctccctgtttctgaagac	3360
Db	3485	ATTGGCAATCATCTCCCAATGGGAAGCTGCTGTGTGGCTCCCTCTTTCGTGAAGAC	3544
QY	3361	caagctgggaacaggctactactacccttgttaagaagaatgltgnaatccctccagt	3420
Db	3545	CAGCTGGGAACAGGCTACTACTACTCTTGTTGTAAGAAAGATGTGAATCTCTCCCTCAGT	3604
QY	3421	tccctgcaagaacagtagtagactgtgtcaacctgtaaaagagagacagttttctcag	3480
Db	3605	TCCCTCAAGAAACAGTAGAGACTGTGTACTACTGTAATAAGAGAGACAGTGTTCCTCAG	3664
QY	3481	agcagttctgttgtctgtgcctgggagcagaccatgaaagtgtacaagctgtacatgtc	3540
Db	3665	ACCACTTCTGATGTGGCTCGTGGAGGACCAATGAAGACAGACACCTGACATCATATCTC	3724
QY	3541	tctgtatctccaaccccatcaagaagacatgtgtcgaagcccgctgtgtgaagaata	3600
Db	3725	TCTGTATCTCCAAACCTCATCAGAAACATGTCTTGAAAGCCCGCTGTGTGAACACTA	3784
QY	3601	gggcattgagctgtaccataatgtgtgtgcatatgaagctgtctaagaaaggagcccttgtga	3660
Db	3785	GGGCATGTAGCTGACCTTATGTGCTGCCATATGAAGCTGTATGAAGAGAGACCTTGTGTGA	3844
QY	3661	ctcttcaatgagcttgaatgacgcgcctcaagacccctggagattcaagtatgagctcca	3720
Db	3845	CTCTTCAATGAGATTGATGACCGGCTCTCAGACTTGGCATTTCTAGTTATGGCACTCA	3904
QY	3721	gagacgacctgtgaagaatatctcctcaagtgtagcgaagaagatgvggggtgtgattgtag	3780
Db	3905	GAGACGACCCCTGGAAAGAAATTTCTCAAGATGGCGGAGAGACAGGGGATGTGATGTAG	3964
QY	3781	accccaatgttactcttgcagcaagaagaagaacagcgcgctcttgggagaaagcagagc	3840
Db	3965	ACCTCAATGTGTACTCTTGCCAGCAACACGAAGAGCGGAGCTTGTGGGAGCAACGAGC	4024
QY	3841	tgcttcgcgccttcaactgaagaatgagtgtctgtgtatccaaatgattctgcataagacca	3900
Db	4025	TGCTTGGCCCGTTCACTGTGAAGATGATGCTGCTGATCCAAATGATTTGACATGTAGCCA	4084
QY	3901	gaatccagagagacagaactgtgtcagtaggatatgtatgtgcagaaggtctctaccagtgaaa	3960
Db	4085	GAATCCAGAGAGACAGACTTGTGCTCAATGTGGATGGATGGCAAGGGTCTCTACAGGTGAAA	4144
QY	3961	ggctggaacttacaagcaaacaggtttctggccctttgtgaaagaaactgtatattgac	4020
Db	4145	GGCTGGAACCTTACACAGCAACAGTTTGTGTGGCCCTTTGTGAAGAGACTCTTAATTGCC	4204
QY	4021	agaacgagctcgaaaggaatttttctcagattgtcttcgaagctgtgttattgttcgatt	4080
Db	4205	AGAGAGAGTGGGAAAGATTTTGTCTCAGATTGTCTTGCCACAGCTGTGTGTGCAATT	4264
QY	4081	ggccttgtgtcagcctgtgactgtgtgcaaccccttbgcaagtaacccaagcttgaaacttcag	4140
Db	4265	GCCCTTGTGTTCAGCCTGATCGTGCACCCCTTTGGCAAGTACCCAGCCTGGAACCTTCAG	4324
QY	4141	ccctgtgattacaagaagaacagtatacaattgttcagcaaatgtatcctctgaaagaaagga	4200
Db	4325	CCCTGTGATGTACAAACAAAGTATACATTTTGCACAAATGATGTGCTTGAGGACAGCGA	4384
QY	4201	accctggaactcttaagagccttcaacaaagccctgtgcttcggagcccgctgtatgaa	4260
Db	4385	ACCTGTGAACCTTTTAAACCCCTCTCACAAAGACCTGTGCTTGAGACCCGCTGTATGGAA	4444
QY	4261	ggaacccaattcccaaacagcccttgcacagagagagagagagatgtgaacactgtccca	4320

4445 GGAATCCCAATCCAGACGACCCCTGCGAGCAGGAGGAGAGGTGACCACTGCCCA 4504
4321 gtccccgacatcatagacacctccagataggaacttgaaatgcaaaccttica 4380
4505 GTTCCCGAGACATCATGAGACCTCTCCAGAAATGGAACCTGACAAATGCAAGACCTTCA 4564
4381 cctgcatacagatagtagcagcgaacaaatcaagaatgtctgctgtgtgtcccaagg 4440
4565 CCTGCATGCCAGTGTAGCAGCAGCAAAATCAAGAAATGCTGCTGTGTGCTCCCAAGG 4524
4441 gcaagggggctgctcctcccaagaacaaacactgcagatatccctcagagactg 4500
4625 GCAGGGGGGCTCCTCTCCCAAGAAACAAACACTGCAATATCTTCCAGAGACTG 4684
4501 acagaagaagaacattcgataltcgtgtgaagacgtatgtcagatcatagccaagc 4560
4685 ACAGGAAGAAACATTTGGATTATCTGTGAAGAGCATATGTCAGATCATAGCCAAAAGC 4744
4561 ttaagaagaagaatctgggtgaatagtttagttgtagtgaggcttccctgtgtgaat 4620
4745 TTTAAACAAACATCTGGGTGAATAGTTAGTATGGCGCTTTTCCCTGGGTGACT 4804
4621 aactcaagcaactccctccgagtcagaagttaaatgacatgcaataaagaaga 4680
4805 AATACTCAAGCACTTCTCCGAGTCAAGAGATTATGATGCGACCAACAAATGAGAAA 4864
4681 caactaaagctggcgaagagacagtlctgcagatcattctcaacagcttggagaattc 4740
4865 CACCTTAACCTGGCCAAAGACAGTTCTGCAGATCATTTCTCAACAGCTTGGGAAGATT 4924
4741 atgaagagagctggacacagaataatgtcaagtggtgttcaataaagaagcttgcat 4800
4925 ATACAGGACTGAGACCCGAAATATGTCAGAGTGTGTTCATTAACAAAGGGCTGAT 4984
4801 gcaatagctcttccctgaatgtcaacaaatgcatctcccgagcaaacctgcaaaag 4860
4985 GCATACAGCTTTTCTGATGATCATCAACATGTCATTTCTCCGGCCCAACCTGCAAAAG 5044
4861 ggaagagaacctagcattatagaaatcttcaatcaatccctgaatcacaag 4920
5045 GGAGAGAACCTTATGCAATATGCAATCTGCTTCAATCAATCCCTGAATCTCAACAG 5104
4921 caacagactcagaagtggtctgtagacacatagtagtgcctgtgtcactgct 4980
5105 CACAGCTCTCAAGGTGGCTCGATGACCAATCAATGATGATGCTGTGTGCTCACTGCT 5164
4981 gtaactcttgcaatgtccttctccagcaagcttctgcatctccatccagagagc 5040
5165 GTCATCTTTGCAATGTCCTTGTCCAGCAGCTTTGTGTATCTCTGATCCAGAGCGG 5224
5041 gtaagcaagaacaacactgcagtcacatcagtggaatggaagctgtcactcagctc 5100
5225 GTGAGCAAAACAAACCTGCACTGATCAACAGTGAAGTGAACCTGATCAATCAACGCTC 5284
5101 tctaatttgcgtggatagtgcaattagctgttcccgcaacactgtgcatc 5160
5285 TCTAATTTTCTGGGATATGTCATTAACGTTGTCTCCGCAACACTGCTATTATCATC 5344
5161 tcaactgtctccagagaagtcctatgtctcctccacaactctgctgtgtagccct 5220
5345 TTATCTGCTTCCAGCAGAAAGTCTATGTGTCTCTCCACCAATCTGCTGTAGCCCTT 5404
5221 ctactcttgctgtatgggttgatcaatcaactctcaatgtaccagcctctgtgttc 5280
5405 CTACTTTTGTGTATGGGTGTGCAATCAACCTCATATACCAACCTCTTTGTGTTC 5464
5281 aagaatcccaagcaagcctatgtgtgtcacaacagctgaacactctcaatgtgcaat 5340
5465 AAGATCCCGACAGCCTTATGTGTGCTCACAGCGTGAACCTCTTCAATTTGGCAATTA 5524
5341 ggcagcgtggcacaacttctgtcgtgagctgttcaaccgaataagctgaataataatca 5400
5525 GGCAGCTGCGCCACCTTTGTCTGAGCTGTTCACGACAAATAGCTAATATATCAAT 5584
5401 gataccctgaagtcggtgttcttgatctccacatcttgcctggagagagagctcac 5460
5585 GATATCTGGAAGTCCGTCTTGTATCTTCCACATTTTGTCTGGACACAGGGCTCATC 5544
5461 gacatgtgaaacaaacagcaatgctgatatcccttgaaaggttggggaaatcgctt 5520
5645 GACATGTGAAAAACACAGCAATGCTGATGCCGAAAGTTTGGGAGAAATCCGCTT 5704
5521 gtgcacatlatcttggacttggtggacgaacactctgcacatgagccgtggaaagg 5580
5705 GTGTACCACTTATCTTGGGACTGTGTGGAGCAAACTCTTGGCATGGCGTGGAAAGG 5764
5581 gtgtgtcttccatcaactacgttctgacacagtagatcttcatcagcccaagct 5640
5765 GTGGGTCTTCTCTATTAAGTCTTGTATCCAGTACAGATCTTCAACAGGCCAGACT 5824
5641 gtaatgcaaaactatctcctctgaatgaatgaatgtagatgtgaagcggaagaag 5700
5825 GTAAATGCAAAAGCTATCTCTCTGAAATGATGAAGTGAAGATGTGAGCGGAAGACAG 5884
5701 agaattcttgatgtgtggagccagaatgacatctagaatcaagaggttgagcaagata 5760
5885 AGAATCTTGTATGTGTGGAGCCAGATGACATCTTAGAAATCAAGAGATTGACGAGATA 5944
5761 tatagaagaagcgaagcctgtctgtacagatcttgcgtggacatccctcgtgtga 5820
5945 TATAGAGGAAGCGAGAGCTCTGTGACAGATTTTCGTGGCANTTCCCTCGTGAAG 6004
5821 tgccttggagctctggagttlaatlggggctggaataatcaacttcaaatgttaca 5880
6005 TGCTTTGGGCTCTCGGAGATTAAATGGGCTGGAATATCATCACTTCAAGATTTAA 6064
5881 ggaagataccaactgttaaccaagagagatgcttcccttaacaaatagatcttcaaac 5940
6065 GGAGATCCACCTTTTCCAGAGAGATGCTTCTTAACAGAAATGATATTTATCAAC 6124
5941 atccatgaagtaacatcagacatgggctactgcctcagtttgatgcatcacagagctg 6000
6125 ATCATGAAATGATCATGAAACATGGGCTACTGCTCATGTTGATGCCATCAGAGCTG 6184
6001 ttgactggagagaacagltgagttcttgccttctgagaagagttcccaagaaagaa 6060
6185 TTGACTGGGAGAGAACACGTGATCTTTGCCCTTTGAGGGAGTCCACAGAAAGAA 6244
6061 gttggcaaggttggtgagtggtgagcttggaaacgggctcgtgtgaatgaggaagaa 6120
6245 GTTGGCAAGGTGTGATGTGGCGGATTCGAAACTGGGCTCTGTAAGTATGAGCAAAAA 6304
6121 tatgtgtgaactatagtgaggaacaaacgaagctctctacagcaatggttgaatc 6180
6305 TATGCTGTATACATATATGTGAGGCAACAAACGACGTCTTACAGCCATGGCTTGTATC 6364
6181 ggcgggctcctgtgtgttctgtgaatgaacccacaagcaatgattcccaagccgg 6240
6365 GCGGGGCTCTGTGTGTTCTGTGATGAACCCACACAGGATGATGCCAAACCCCGG 6424
6241 cggttcttgaggaatgtgtcccaagtggttcaagaagggagagatcagtagtcttca 6300
6425 CGGTTCTTGTGAATTTGTGCTTAAGTGTGTCAAGAGAGGAGATCAGTACTGTTTACA 6484
6301 tctcatagtagtgaagaatgtgaagctcttgcactagaatgtgcaatcatggtcaatga 6360
6485 TCTCATGTATGGAAGATGTGAAGCTCTTTGACTAGATGCAATCATGTGTAATGGA 6544
6361 aggttcagtgctgtgcagtgccaagatctaaataagtttggagatggttatata 6420
6545 AGGTTCAAGGTGCTTGGCAGTGTCCAGCATCTAAAAAATGAGTTTGGAGATGTTATCA 6604
6421 atagtgtacgaatagaaggttcacacccgagacctgaagccgttccaagattcttga 6480
6605 ATAGTTGTACGAATAGCAGGGTCCAAACCGAGACTGAACCTGTCTCAGATTTCTTGTGA 6664

QY	6481	ctgtacattccctggaaagdtgttctaaagaagaaacccggagaaatgttacaatlaaccagctt	6540
Db	6665	ctttgcattttcctggaaagtgtttccaaagaagaaacaccggagacatgctctaaatAACGAGCTT	6724
QY	6541	ccattcttcattalcctctctcgtgcgaagatatacgaatcctctctccagagcaaaagcga	6600
Db	6725	ccattcttCAATTATTCCTCTCTGGCCAGAGATATTACAGATCTCTCCAGAGCAAAAAGCA	6784
QY	6601	ctcccaatagaagactacctctgtttctcagacaacacttgacaagatttgtgaacttt	6660
Db	6785	cttccCAATGAAGAGACACACCTGTGTTCTCAGACAAACCTTGACCAAGTATTGTGAACCTTT	6844
QY	6661	gccaaagaccaagttgatgatgacacacttaagaagacctctcattcacaaaaaccagaa	6720
Db	6845	GCCAAGACCAAAAGTATGATATATACCACTTAAAGAGCTTCTATTACACAAAACGAGACA	6904
QY	6721	gtatgtgacgtttgcagttctccacatctttctcagagatgagaagtgaagaagacgtat	6780
Db	6905	GTAGTGTGAGAGTGTGCAGTTCTTCACACTTTTCTTACAGAGATGAGAAGTGAAGAAAGCTAT	6964
QY	6781	gtatgaagaatctcgttctatacgg	6804
Db	6965	GTATGAGAGATCTCTGTTCATACGG	6988
RESULT	13		
LOCUS	AX127831	9854 bp	DNA
DEFINITION	Sequence 70 from Patent WO0130848.		linear
ACCESSION	AX127831		
VERSION	AX127831.1	GI:14134478	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 9854)		
AUTHORS	Denefle, P., Rosler-Montus, M.F., Arnold-Reguigne, I., Prades, C., Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H., Renaudy, A., Brewer, H.B. and Dean, M.		
TITLE	Nucleic acids of the human abcl gene and their therapeutic and diagnostic application		
JOURNAL	Patent: WO 0130848-A 70 03-MAY-2001;		
FEATURES	Aventis Pharma S.A. (FR)		
source	Location/Qualifiers		
	1..9854		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
BASE COUNT	2665 a 2219 c 2334 g 2635 t		1 others
ORIGIN			

[illegible]

Qy	241	tggttcggttaccgacatccctcgggaggtcccgagttgtttggaacttaacaatcc	300
Db	538	tggtttccgttaccgacatccctcgggaggtcccgagttgtttggaacttaacaatcc	597
Qy	301	atgtgtgcctgcctgtttccagatgtctcgaagctctcttatacagccagaagaacc	360
Db	598	attgtgtgcctgcctgtttccagatgtctcgaagctctcttatacagccagaagaacc	657
Qy	361	agcatgaagaagacatbcgcaaaagttctctggaacattacaagaagtcaagaatccactca	420
Db	658	agcatgaagaagacatbcgcaaaagttctctggaacattacaagaagtcaagaatccactca	717
Qy	421	aacttgaagcttcaagaattctcctgtgtggaacaatgaacctctctggttctatacga	480
Db	718	aacttgaagcttcaagaattctcctgtgtggaacaatgaacctctctggttctatacga	777
Qy	481	aaacctctctcccaagaattcaactgtgtgacaagaatctctgagggcgtatctatctccac	540
Db	778	aaacctctctcccaagaattcaactgtgtgacaagaatctctgagggcgtatctatctccac	837
Qy	541	aaggtatatttgcgaagctacagttcaatattgacaagctctgtgcgaatgatacaaatca	600
Db	838	aaggtatatttgcgaagctacagttcaatattgacaagctctgtgcgaatgatacaaatca	897
Qy	601	gaagagatgatccaactgtgtgacccaagaagttctgaagcttctgtgacctataccaagag	660
Db	898	gaagagatgatccaactgtgtgacccaagaagttctgaagcttctgtgacctataccaagag	957
Qy	661	aaactggtctgcagcagcagcagtagtactcgttctccaaatgacaatccatgaagccaatctcg	720
Db	958	aaactggtctgcagcagcagcagtagtactcgttctccaaatgacaatccatgaagccaatctcg	1011
Qy	721	agaacactaaactctacatctccctccctcccgagcaagagctgtgcttgaagccacaanaaca	780
Db	1018	agaacactaaactctacatctccctccctcccgagcaagagctgtgcttgaagccacaanaaca	1077
Qy	781	tgtcgctcaatctcttggagactctgcgccaagagctgtctcaagctgaagaagctcggaagtgaac	840
Db	1078	tgtcgctcaatctcttggagactctgcgccaagagctgtctcaagctgaagaagctcggaagtgaac	1137
Qy	841	atgcgacagcaggttgaatgttcttgaaccaatgtgaacagctccagctccctcccaaccaatc	900
Db	1138	atgcgacagcagcaggttgaatgttcttgaaccaatgtgaacagctccagctccctcccaaccaatc	1197
Qy	901	taccagagctgtctcgttatgtctctgtggacatcccgagagggggggtctgaagaatcgaag	960
Db	1198	taccagagctgtctcgttatgtctctgtggacatcccgagagggggggtctgaagaatcgaag	1257
Qy	961	tctctcaactgtgtagtgagacaacaataaagacctcttcttgaagcgaatgacactgag	1020
Db	1258	tctctcaactgtgtagtgagacaacaataaagacctcttcttgaagcgaatgacactgag	1312
Qy	1021	gaagatgttgaaacctctctatgaaactctcaaacctctactgtgcaatgatttgatgaag	1088
Db	1318	gaagatgttgaaacctctctatgaaactctcaaacctctactgtgcaatgatttgatgaag	1377
Qy	1081	aatttgaagcttaagctctctctcccgatatacttgaagaagctctgaagcgcgtgtcgtt	1140
Db	1378	aatttgaagcttaagctctctctcccgatatacttgaagaagctctgaagcgcgtgtcgtt	1437
Qy	1141	gggaagaatcctgtatatacactgaaactccaagccaagaagcagtgatgcttgaagtgaac	1200
Db	1438	gggaagaatcctgtatatacactgaaactccaagccaagaagcagtgatgcttgaagtgaac	1497
Qy	1201	aagacctctcagaagaactggtgtgtctcaatgtcttggaaagcatgttggaaggaactcagc	1260
Db	1498	aagacctctcagaagaactggtgtgtctcaatgtcttggaaagcatgttggaaggaactcagc	1557
Qy	1261	cccagaatcttgcgaactctcaatgcgggaacacgaagaatgagacctgtctccgagtctgtg	1320
Db	1558	cccagaatcttgcgaactctcaatgcgggaacacgaagaatgagacctgtctccgagtctgtg	1617
Qy	1321	gacagcagggacaatgacaccttcttgggaacagcagttgagatgcttagatttgacagcc	1380

```
|||||
Db 1618 GACAGAGGAGACAAATACCACTTTTGGGAAACGACATTTGGATGGCTTAATTGGAGAGCC 1677
|||||
Qy 1381 caagacatcgttgcgttcttcttgccaagcaaccagagatgctccagtcgaatggtctt 1440
|||||
Db 1678 CAAGACATCGTGGCGTTTGGCCAAAGCACCCAGAGAGATGTCAGTCCAGTAAATGGTTCT 1737
|||||
Qy 1441 gtttacacctgagaaagcttccaacgactaaccaagcatccggaccatctctgc 1500
|||||
Db 1738 GTGTACACCTGGAGAAACCTTTCAACGAGACTAACCCAGGCAATCCGGACATATCTCC 1797
|||||
Qy 1501 ttcatgagtggttcaacctgaaacagctagaaccatagcaacaagcttgcgtctac 1560
|||||
Db 1798 TTATGAGAGGTGTCAACCTGGAACAGCTAGAACCCATAGCAACAGAACTGGCTCATC 1857
|||||
Qy 1561 aacaatgccatgtagctgtctgtagaagaaagttctggctgtgtaattgttctactgta 1620
|||||
Db 1858 AACAGTCCATGGAGCGTGTGATGAGAGGAAGTTCTGGGCTGGTATGTGTCACTGGA 1917
|||||
Qy 1621 attactccagagcaattgagctgcccacatgctcaagtaagaatccgaatgagcatt 1680
|||||
Db 1918 ATTACTCCAGGACGATTGAGCTGCCCATCATGTCAAGTACAAAGATCCGAATGGACATT 1977
|||||
Qy 1681 gacaatgtgagagaggaacaataaatacaagatggtgtactgtgagccctgttccctgagct 1740
|||||
Db 1978 GACAAATGAGAGAGACAAATTAATAATCAAGATGGGTACTGGGACCCCTGGTCTCGAGCT 2037
|||||
Qy 1741 gaacctctttagagacatgcygtactgtctggggggtctgcctacttgcagaatgtgtgt 1800
|||||
Db 2038 GACCCCTTTAGAGACATGCGGTACGTCTGGGGGGCTTCCCTACTTGGAGATGTGTGTC 2097
|||||
Qy 1801 gagcaggaatcatcagagtggtgtcgaagggacccgagaagaactggtgtctatagcaa 1860
|||||
Db 2098 GAGAGGCAATCATCAAGGTGCTGAGCGGACCCGAGAAAGAACTGGTGTATATGACAA 2157
|||||
Qy 1861 cagatgcccatccctgtctcgtttagatgacatcttctcgggtgtatgaaacggttaagt 1920
|||||
Db 2158 CAGATGCCCATATCCCTTTACGTTGATGACATCTTTCTGGGGGATGAGACCGGTCAATG 2217
|||||
Qy 1921 cccctctcatgacgtgacctgagattactcagtgagctgtgcatcaagagacatcggt 1980
|||||
Db 2218 CCCCTTTCAATGACGCTGGCTGTGATTTACTCAGTGGCTGTGATCATCAAGGGCATCTGTG 2277
|||||
Qy 1981 taibaagaagagagcagagcgtcgaagaagacacatcgagatcagctggccctggacaacagata 2040
|||||
Db 2278 TATAGAAAGAGGACCGCTGAAAGAGACCATGGGATCTAGGGCTGGACAAACAGATC 2337
|||||
Qy 2041 cctcgtttagcgtgtcatatagtagcctcatctctctcttctgtgagcgctggcgtcta 2100
|||||
Db 2338 CTCTGGTTTAGCTGTTCAATAGTAGGCTCATTTCTCTTGTGAGCGCTGGCTGTCTA 2397
|||||
Qy 2101 gttgtcatcctgaagttaagaacacctgctgcctacaagtagatcccgctggtgtgtgtc 2160
|||||
Db 2398 GTGTGTCAATCCGAAGTTAGGAAACCTCTGCCCTACAGTATCCACCGTGGTGTGTGTC 2457
|||||
Qy 2161 ttctgtgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2220
|||||
Db 2458 TTCTGTGTCGTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2517
|||||
Qy 2221 tccagaagccaacctgtagcagcagcctgtgtgggggacatcctactacacgtctgtaacctg 2280
|||||
Db 2518 TCCAGAGCCAACTGGCAGCGCTGTGGGGGACATCATCTACGTCAGCTGATCCTGCC 2577
|||||
Qy 2281 taagctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2340
|||||
Db 2578 TACGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2637
|||||
Qy 2341 ctgctgtctcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2400
|||||
Db 2638 CTGCTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2697
|||||
Qy 2401 ggcatgtgagtgagtgaggagacaacctgtttagaagctcctgtgagaagaatgtgctcaat 2460
|||||
```

QY	3541	tcgcgtatctccaaacctcaagaagcattgcttgaagcccgctggttgaagacata	3600
Db	3838	TCGTGATCTCCAAACCTCATAGGAACATCTGTCAAGCCCGCTGTGGAAACATA	3897
QY	3601	gggcattgaagctaacctatgctgctccataagaagctgctaaagaagagccttttgaa	3600
Db	3898	GGGCATGAAGCTACCTATGTCTCTCCATTGAAGCTGTGAAGAGGAGACCTTTTGGAA	3957
QY	3661	ctcttcatgagattgatalgacacggctctcaagacctgggacttctgattatgcatccca	3720
Db	3958	CTCTTTCATGAGATTGATGAGACGGGCTCTGACACCTGGGACTTTCATGATTGAGCATCTCA	4017
QY	3721	ggagagaccocctggaaagaataatctcctaagtggtccgaagagatggtgggtgatagctgag	3780
Db	4018	GGAGAGACCCCTGGAGAAATTTCTTAAGTGGCCGAAGACAGTGGGTGATGCTCTGAG	4077
QY	3781	acctcagatggtaaccttgcagcagaacgagcgggaccttcggggagacaagaagc	3840
Db	4078	ACCTCAGATGGTACCTTGCCAGCAAGACGAAGACGGGGGCTTCGGGGACAGAGAGC	4137
QY	3841	tgcttcgcccgttcactggaagatgatatgctgctgatatcaaatgatatctgacatagaacca	3900
Db	4138	TGTCTTTCGCCGCTTCACTGGAAGATGAGCTGCTGATCTCAAAAGATTCGACATTAACCCA	4197
QY	3901	gaatccagaagagacaagacttgctcaatggtgagatgtagtgcgaagaaggctccatacgaattgaa	3960
Db	4198	GAATCCAGAGACAGACAGACTTCTCAGTGGGATGTGATGCGAAAGGCTCTACCAAGGTGAAA	4257
QY	3961	ggcttggaaactlacacagcaagatttgtgtgcccttttggaagaagactgtaattgccc	4020
Db	4258	GGCTTGGAAACTTACACAGCAACAGATTGTGTGGCCCTTTGTGGAAGAGACTGTAAATGGC	4317
QY	4021	agaaggaatgsgaaagatttttgcacagattgctcttgcaagctggttttgctgcaatt	4080
Db	4318	AGACGAGATCGGAAAGATTTTGTGCTCAAGATTGTTCCAGCTGTGTTGTCTGTGCAATT	4377
QY	4081	ggccttgtgttcacgcctgcatctgtgcaaccttgtgcaagtaaccagacgttgaacttcag	4140
Db	4378	GGCCTTGTGTTCACTGATGATGTGTCGACACCTTTGGGAATACCCAGGCTTGGAACTTCAG	4437
QY	4141	cccttgatgtacaacgaacagatcacattgttcgaacatgatatgctctctgaagacagga	4200
Db	4438	CCCTGGAGTGAACAAAGCAACAGTACACATTGTTCAGCAATGATGATCTCTGAGAGAACGGGA	4497
QY	4201	acctgggaactcttaaacgacctcaccaaaagccctggtcttggaacccgctgtatagaa	4260
Db	4498	ACCTGGAACTTTAAACGCCCTTCACCAAGACCTCGGCTTGGGACCCGCTGTATGGAA	4557
QY	4261	ggaaacccaatcccaagacagaccttgcagagcagggaggaagatlgagcaactgcccaca	4320
Db	4558	GGAAACCCAATCCAGACACGCGCTCTCCAGGCGAGGAGGAAGATGTGACACATCGGCCCA	4617
QY	4321	gttccccaagacatcatgagacctcttccaagaatggtgaactgtgacaatgcagaaccttca	4380
Db	4618	GTTCCTCCAGACCATCATGAGACCTTTCGAGAAATGGGAATGTGACATGTCAACAAACCTTCA	4677
QY	4381	ccgtcatgcaagtgtagcaacgcaacaaatcaagaagatgtagtgcctgtgtgtcccccagg	4440
Db	4678	CCGTGATGCCAGTGTAGCACACGACAAAATCAGGAAGATGTGCTGTGTGTCCCCACGGG	4737
QY	4441	gcagggggctgtccctccccaagaagaacaacaacacttgacatatalccttcaagacctg	4500
Db	4738	GCAAGGGGGCTGCTCTCTCCACAAAGAAAACAAACACGTGACAGATATTCCTTCAAGACCTG	4797
QY	4501	acagaagaacaacttgcgattatctgtgtgaagaagtatgtgcagatcaatagccaagaac	4560
Db	4798	ACAAGAAAGAAATTTTCGGAATTATCTGTGGAAGAGTGTGTGCAATCATAGCCAAAAGC	4857
QY	4561	ttaaagaacaagaatctgggtgaaatgattgagtagtgacgcttctccctgggtgtcaatt	4620
Db	4858	TTAAAGAAACAAGATCTGGGTGAATAGTGTTAGCTATGGCGGCTTTTCCCTGGGTGTCACT	4917

QY	4621	aagactcgaagccttcctccgagfccaagaagttaatgatgtccctaaacaatatgaagaa	4668
Db	4918	aaTACTCAAGCACTTCCTCCAGTCAAGAAAGATTAAATATGTCACCAAAACAAATGAAAGAA	4977
QY	4681	caactaaagctbfgccaagaagacagfctctgagatcgatattctcaagctctggaaattt	4740
Db	4978	CACTTAAAGCTGGCCAAGAGACAGTTTGACAGATCGATTTCTCAACAGCTTGGGAAGATT	5037
QY	4741	atgacaggaactbfgaacacagaataatgtaagatgttgltcaataacaaggctbfgaat	4800
Db	5038	ATGACAGGACtGTGACACAGAAATTAATGTCAGAGTGTGTCATTAATACAAAGGCTGGCAT	5097
QY	4801	gaatcaagctcttccctaaatgcatcaacaatgcaattctccggcccaactgtgaaag	4866
Db	5098	GCAATCAGTGCTTTTCTGTAATGTCATCAACATGCCATTCTCGGGCCAACTGCAAAAG	5157
QY	4861	gagagaaacctagccaattatgtaattactgtcttcaatcaatccctgaactcaacaag	4920
Db	5158	GGAGGAACCCCTAGCGCATTAATGGAATTAACGCTTTCAATCATCCCTGAAATTCACCAAG	5217
QY	4921	caagacgtctcaagaatgtgagctctbtaagaacacatcaagtgatgctctbfgcaactgt	4980
Db	5218	CAGCAGCTCTAGAGAGTGGCTCCGATACCACTACAGTGAATGTCTTGTGTCCATCTGT	5277
QY	4981	gtcaactcttgcaatgtccttcgtcccaagccagcttgtcglatctcgtatccagaagcgg	5040
Db	5278	GTCACTCTTGGAAATGTCTCTTGTCGCCAGCCAGCTTGTGTGCTTCTGTATCCAGAGCGG	5337
QY	5041	gtcagcaagaacaaacacctbcaattcaatgaatggatgaagcgtgtcaactacgtgttc	5100
Db	5338	GTCCACCAAGCAAAACACCTGCACTTATATAGTGGAGTAAAGCTGTCTACTACTGGCTC	5397
QY	5101	tctaaatttgctcggatagatgtgaattacgttgttccctgcgcacactgtaactaactc	5160
Db	5398	TCTAATTTTGTCTGGGAATATGTGCAATTAAGTGTGCCCTGCCACACTGGTATTAATATC	5457
QY	5161	ttcacctbgtctccagagaagctactatgttccctcaacaactctgcctgtgtctagccct	5220
Db	5458	TTCACTCTCTTCCAGCAGAAATCTTAATGTCTCTCCACCAAAATCTCTGTGTACCCCTT	5517
QY	5221	ctcaacttgcgttataagatggtcaatcaacacctctcatgtaccagacctccttgtgttc	5280
Db	5518	CTACTTTTGTGTATGGGTGGTCAATCACACCTCTATGACCAGCCTCTTGTGTGTCTC	5577
QY	5281	aagatccccacagaacctatagtgtgtgtctcacacagctgaacctcttcattgtgcaatt	5340
Db	5578	AAGATCCCCACACAGCCTATGTGTGTCTCACAGGCTGAACCTTTATTTGGCATTAAT	5637
QY	5341	ggcagcgtgcgcaacctcttgctcgtggagcgtgtacccgaacaataagctgaataataaat	5400
Db	5638	GSCAGCGTGGCCACTTTGTGTGTGTGGAGCTTTACCGACAAATTAACCTAATATATCAAT	5697
QY	5401	gatactcgtgaatcgtgtgtcttgatcttcccaattttgctcgtggagcgaaggctatc	5460
Db	5698	GATATCCCTGAAGTCCGTTCTTGATCTTCCACATTTTGGCTTGGGAGGGCTCATC	5757
QY	5461	gacatgtgaaaaaacaggaatgagctgtgtgtccctggaaagtttggggaataatcgttt	5520
Db	5758	GACATGTGTGAAAAACAGGAATAGTGTGTCCTGTGGAAAGTTTGGGGAATAATGCGCTTT	5817
QY	5521	gtgtcaacctatcttbggaactgtgtgtagacgaacaccttccgcatabgccgttggaaagg	5580
Db	5818	GTGTACCACTAATTTCTTGAGCTGTGGGAGCAAGAACCTTTTGCCATGGCCGTGAAGGG	5877
QY	5581	gtgtgtgttcttctcaattactgttctcgtacacagtaacagatcttcaatgaagccagaact	5640
Db	5878	GTGTGTGTCTTCTCAATTACTGTCTTGATCCAGTCAACAAATTTCTATCAGGCCAGACCT	5937
QY	5641	gtaaatbcaagactatctcctcgtgaatgtgaagaatgaagaatgtgtgagcgggaaagacg	5700
Db	5938	GTAATGCCAAGCATCTCTCTGTGAATGATGAAGATGTGAGCGCGGAAGACAG	5997
QY	5701	agaaattctgaatgtgtaggagccagaatgacatcttagaatalcaagaagtttgaacgaata	5760

Db	5598	AGATTCTTGATGTCGAGAGCCAGATGACATCTTAGAAATCAAGAGATTGACCAATATA	6057
Qy	5761	tataagaagaagagagagcctgcgtcttgacaggaatttgcgtggacatctccctcgtgtag	5820
Db	6058	TATAGAAGGAAGCGAAGCCTGCTGTGACAGAGATTTGCGTGGCATTTCCCTCGGTGAG	6117
Qy	5821	tgctttggcgcctctgggaattatgaggtcgtggaataatcaacttccaagtgtaca	5880
Db	6118	TGCTTTGGCTCTCGGAGATTATGAGGCTGGAAATATATACCTTCACAGATTTTAC	6177
Qy	5881	ggagataccaccttaccagagagaatgcttcccttaacaaataglatcttacaac	5940
Db	6178	GGAGATACCACTTTACAGAGAGATGCTTCTTAAACAGAAATAGTATCTTATCAAC	6237
Qy	5941	atccatgaagtatcatagaacaatggctactgcgcctcaagtttgatgcatacagaagct	6000
Db	6238	ATCCATGAATACATACAGAACATGGCTACTCCCTCGATTGTGATGGCATACAGACCTG	6297
Qy	6001	tttaacttgagagaacacgttgagttctcttgcctcttgagagagttccagaaaaaa	6060
Db	6298	TTGACTTGAGAGAACACTGCGATTCTTGCCCTTTTGAGAGGAGTCCAGAGAAAAAA	6357
Qy	6061	gttcgcaaggtcttgtagtggcgatctcgaaactcgtggcctgtgaagtalvgaaaaa	6120
Db	6358	GTTTGGCAAGTTTGATAGTGGGAGTTTCGAAACTGGCCCTCGTGAATGAGCAAAAA	6417
Qy	6121	tatgcttgtaactatgtagtggagcaaacagcaagctctcaagccaatgcttatgc	6180
Db	6418	TATGCTGTGTAACATATGATGAGGCAACACCAAGCTCTACAGGCATGGCTTTGATC	6477
Qy	6181	ggcggcgctcctctgtggtgtttcttcggaatgaaccacaaagagatgatacccaaacccg	6240
Db	6478	GGCGGGCCTCCTGGTGGTGTTCGATGAACCCACACAGCATGGATCCCAAGCCCG	6537
Qy	6241	cgggtctctggagaattgtgcccctaaagtgtgttgcagagggagagtcagtgtctaca	6300
Db	6538	CGGTTCTTGTGGAATTTGCTTAATGTGTTCAGAGAGGAGATGATGATGCTTAC	6587
Qy	6301	tctcatagtatggaagaatltgaagctcttgcactagatgtgcaatcatgtgcaatgga	6360
Db	6598	TCTCATGATATGGAAGATGTGAAGCTCTTTCAGTAGATGGCAATCATGGTCAATGA	6657
Qy	6361	aggttcaggtgaccttggtcagatgtgcagatctaaaaaataagtttggagatggtataca	6420
Db	6658	AGGTTCAAGGTGCTTGCAATGTTCAGCATCTTAAAAAATGAGTTTGGAGATGTTATCA	6717
Qy	6421	atagtttacaatagaaggttcacaaccggagacctgaagcctgtccagatctcttga	6480
Db	6718	ATAGTTTACCAAAATAGCAGSGTCCAAACCGGACCTTAACCCGTGCAGGATTTCTTGA	6777
Qy	6481	cttgcatctccgtgaagtgltcttaaaagaaaacaccggacaatgctataacacgctt	6540
Db	6778	CTTGCAATTCCTCGAAGATGTTCCAAAAAGAAACACCGAACAATGCTACAAATCACAGCTT	6837
Qy	6541	ccatcttcattatctcttcggccaagataatagaatctctccagagcgaaaaagga	6600
Db	6838	CCATCTTCATTATCTTCTGCGCAGGATATTTGCAATCCTCTCCAGACGCAAAAAGCA	6897
Qy	6601	ctccacatagaagaactactctgttcttcagacacaacacttgcacaagtatttgtgaactt	6660
Db	6898	CTCCACATAGAAGACTGCTCGTTTCAACACAACCTTGACCAGATTTTGTGAACCTT	6955
Qy	6661	gccaaagccaaatgtatgatgacacacttaaaagacctctcatcaacaanaaacagaca	6720
Db	6958	GCCAAAGCCAAATGTATGATGACCACTTTAAAGACCTCTCATTAACAAAAACACAGCA	7017
Qy	6721	gttagtggagcgttgaagttctcaactcttctcagagatbgagaagtgaagaagaagcat	6780
Db	7018	GTAAGTGAACGTTTGCACTTCTTCTTAACAGATGAGAAAGTGAAGAAGATGAT	7077
Qy	6781	gtatgaagaatcctgttctacaagg 6804	

[illegible]

QY 601 gaagagatgatactactggtgacaaagaagtcttgagcttggtgcttaccacaagag 660
| | | | |
Db 898 GAAGAGATGATTAACCTTGGTGAACAGAAAGTTCTGAGCTTTGGCCCTACCAAGGAG 957
QY 661 aaactggtctgacagagagagactcgttccacaatgacatcttgaaagccacccg 720
| | | | |
Db 958 AAAGTGGCTCAGAGAGAGAGTACTGTTCCATACATGACATCTCTGAAGCAATCCG 1017
QY 721 agaacactaaactctacatctcccttcccgaaagagctggtctgaagccacaaca 780
| | | | |
Db 1018 AGAACACTAAACTCTACATCTCCCTTCCGACAGAGAGCTGGCCGAAACCAAAAAA 1077
QY 781 ttgctgatagtcttgagactctgcccagagactgtttaagcatgagaagctgagtgac 840
| | | | |
Db 1078 TTGCTGATAGTCTTGGAGCTCTGGCCAGAGAGCTGTTCAGCATGAGAAAGCTGAGTGC 1137
QY 841 atgcgaagagaggtgatagttcttccacaatgttaacagctccagctcccaaccacaac 900
| | | | |
Db 1138 ATGCGAGAGAGAGTGAATGTTCTGACCAATGTGAACAGCTCCAGCTCCCAACCAATC 1197
QY 901 taccagagctgtgtctcgatgtctgacgggacatcccgagagagggggtgaaatcaag 960
| | | | |
Db 1198 TACCAGAGCTGTGTCTGTGATTTGTCTGCGGCAATCCGAGGAGGAGGGGCTGAAGATCAAG 1257
QY 961 tctctcaactggtatgaggaacaactacaagccctcttggagagaaatgagactgag 1020
| | | | |
Db 1258 TCTCTCACTGGTATGAGGACAACTACAAAGCCCTTTGGAGAGCAATGGCACTGAG 1317
QY 1021 gaagatgctgaacactcttactaagcaactcaacactcctactgacatgatttgaag 1080
| | | | |
Db 1318 GAAGATGCTGAACCTTTATATGACACTCTACACTCTTACTGCATATTTGATGAAG 1377
QY 1081 aatttgagatctagtcctcttcccgactatctggaagctctgaagccgtctgctgt 1140
| | | | |
Db 1378 AATTTGAGAGTCTAGTCTCTTCCGCAATCTGGAAGAGCTGTGAAGCCGCTGCTGTT 1437
QY 1141 gggaagatcctctatgactcctgacactccagccacaagcaagctatgctgagtgaa 1200
| | | | |
Db 1438 GGGAAATCTGTATACCTGACCTGACCTGACGACAAAGAGGATGAGCTGAGGTGAAC 1497
QY 1201 aagacactcaggaactgctgttctcaatgatactggaagagctggtggaagaaactcag 1260
| | | | |
Db 1498 AAGACTCTCCAGGAAGTGGCTGTGTTCCATGATCTGGAAGGATGAGGAGAACTCAAC 1557
QY 1261 cccaagatctggaactcctcaatggaagcaagcaagaatggaactgtccgagtgctgtg 1320
| | | | |
Db 1558 CCCAAGATCTGAGCTTCATGAGAAAGCCAAAGAAATGAGACCTTGTCCGAGATGCTGTTG 1617
QY 1321 gacagcagagagaatgacacactttggagacagagcttgatggtttagattggaagc 1380
| | | | |
Db 1618 GACAGAGGAGACAAATGACACTTTTGGGAACAGCAGTTGATGCTTGAATTTGACACGC 1677
QY 1381 caagacatcgtgtgttcttgccaagacccagagagatgtccagttcaatgttct 1440
| | | | |
Db 1678 CAAGACATGCTGGCTTTTGGCCAAGCACCCAGAGATGTCATTCAGATTAATGTTCT 1737
QY 1441 ggtgtaacctggaagagacttcaagagactaaacagagcaatccggacatctgc 1500
| | | | |
Db 1738 GGTGTACCTGGAGAGAGCTTTCAAGAGAGACTAACCGAGCAATCCGACATATCTCGC 1797
QY 1501 ttccagagagtggtcaacctgacaagcttagaacatagcaacagaaagcttggtac 1560
| | | | |
Db 1798 TTCAATGAGATGTTGTAACCTGAAAGCTAGAACCTATGAAACGAAGTCTGGGCTCAATC 1857
QY 1561 aacaagatcagagagctgtctgataagagaaagtcttggtgtatgtgttccactga 1620
| | | | |
Db 1858 AACAGATCCATGAGAGCTGCTGATGAGAGAAAGTCTGGGCTGATGTGTTCACCTGGA 1917
QY 1621 attactcagcagagctgagctgcccacatcatgtccaagtacaagatccgaatggaact 1680
| | | | |
Db 1918 ATTACTTCAGGAGCATGAGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGACATTT 1977
QY 1681 gacaaatgtgagagagagacaataaatacaaggaatggtgactgtggacctgtctcagct 1740
| | | | |
Db 1978 GACAAATGTGAGAGAGCAAAATAAATCAAGATGGTACTGGAGCCCTGGTCTCGAGCT 2037
QY 1741 gacctcttgagagacatcggttacgtctctgggggggacttcgactctgcaagatgtgt 1800
| | | | |
Db 2038 GACCCCTTTGAGAGACATCGGTACGTCTGGGGGGGCTTGGCTACTTGGCAGAGATGTGTG 2097
QY 1801 gacgaagcaatcaatcaaggtgtctgacgggacccagagaanaactggtgtctatataca 1860
| | | | |
Db 2098 GAGCAGGCAATCATCAGGGTCTGTGACGGGACCCGAAAGAAATAATGAGTATATCA 2157
QY 1861 cagatgccatctccctgttcaatgatacaatcttctgaggtgataagccggtcaatg 1920
| | | | |
Db 2158 CAGATGCCCTATCCCTGTAGTATGATCAATCTTTCGGGGGATGAGAGCCGCTCAATG 2217
QY 1921 cccctcttcaagacgtgacctgatttaccagtgctgagatcatcaagaggaatgtg 1980
| | | | |
Db 2218 CCCCTTTCATGACGCTGGCTGGATTTACTCAAGTGGCTGTGATCATCAAGGATGCTGTG 2277
QY 1981 tatgagaagagagcagggctlgaagagacatlgcgaatcatlggctgtgacaacagata 2040
| | | | |
Db 2278 TATGAGAGAGAGGACGGCTGAAGAGACATGGGATCATGGGCTGGAACACGATC 2337
QY 2041 ctctggtttagctgttcaatagtaagcctaattccctctctgtgagcgtgtgcgtcta 2100
| | | | |
Db 2338 CTCTGTTTACTGTGTTATATGATGACCTCATCTCTTCTTGTGAGAGCGCTGGCTCTTA 2397
QY 2101 gtgttcaatcctgaaggttagagaacactgtgcccagaagtgataccacggtgtgtgttc 2160
| | | | |
Db 2398 GTGGTCACTCTGAAGTTTAGAAACCTGCTGCTTACAGTATCCACAGCGGTGTGTGTC 2457
QY 2161 ttctgttccgtgttctgt 2220
| | | | |
Db 2458 TTCTGTCGCTGTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2517
QY 2221 tccagagcaaacctgagcagcagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2280
| | | | |
Db 2518 TCCAGAGCAACCTGGGACAGCGCTGTGGGGGATCATCTTCACTTCAAGCTGTACCTGCC 2577
QY 2281 taagtcctgt 2340
| | | | |
Db 2578 TACGTCTGT 2637
QY 2341 ctgtgtctcctgt 2400
| | | | |
Db 2638 CTGCTGTCTCTGT 2697
QY 2401 ggcattgagatgagctgt 2460
| | | | |
Db 2698 GGCATTGAGATGAGTGGGACAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2757
QY 2461 ctacacactctgactctcagatgactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2520
| | | | |
Db 2758 CTCACCACTTCGCTGT 2817
QY 2521 taactgaagctgtcttccagccagtlacggaattcccaagccctgtgtatcttctgtg 2580
| | | | |
Db 2818 TACATTGAGGCTGTCTTCCAGGCGCAGTACGAATTCAGGAGCCCTGTGTATTTCTCTTC 2877
QY 2581 accaagctctactggt 2640
| | | | |
Db 2878 ACCAAGTCTTACTGT 2937
QY 2641 aagaagatgcaagaatctcagcagagagagagagagagagagagagagagagagagagag 2700
| | | | |
Db 2938 AAGGAATATCAAAATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2997
QY 2701 attcagaacctgttlaaagcttaccagagatggaatgaaggtgtgtgtgtgtgtgtgtgtgt 2760
| | | | |
Db 2998 ATTACAGAACTGTGTAAGAGCTACCGAGATGGATGAAGTGTGCTGTGATGTGCTGGCA 3057
QY 2761 ctgaattttatgagggcagatcactctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2820

|||||
Db 3058 CTGATTTTATATAGAGGCCAGATCACCTCCTCTGGGCCACAAATGAGAGGGGAGAGG 3117
Oy 2821 accaccatgacatccctgacacgggttgctcccccacacctcggaacacgacatccctg 2880
Db 3118 ACCACCTGTGCAATCCTGACCGGGTTTCTCCCGACCTCGGGGACACCGCTACATCTG 3177
Oy 2881 ggaagaacacatcgctcctgagatgagacacatcccgcaaacctgggggtctgctcccg 2940
Db 3178 GGAAGAACATGCGCTGTGAGATGAGACCATCCGGGAGAACCTGGGGGCTCTGTCCCGAG 3237
Oy 2941 cataagtgctgtttgacatgctgactgctgaaagaacacatcgtgttctatgcccgtg 3000
Db 3238 CATACCTGTGCTTGTGACATGCTGACTGTGAAAGAACATCTGgttctatgcccgtg 3297
Oy 3001 aaaggtcctctgagaagacagctgaagcgagatgagacagatgagccctgagatgtgtgt 3060
Db 3298 AAAGGGCTCTGTGAGAGACAGTGAAGGGGAGATGAGACGATGGCCCTGTGATGTGGT 3357
Oy 3061 ttgcatcaagcaagctgaagaagcaaaacagccagctgtcaggttggaatgcaagagaag 3120
Db 3358 TTGCAATCAAGCAAGCTGAAGAAAGCAAGCCAGCTGTGAGTGAATGCAAGAGAAAG 3417
Oy 3121 ctatctgtgcccgtgacctgtgtcggggagatctaaagttgcatctctgagatgaaccaca 3180
Db 3418 CTATCTGTGCTTGTGCTTGTGCGGGGATCTAAGTTGTGATTTGTGATGAACCCACA 3477
Oy 3181 gctgtgtgagacccctactcccgcaagggaatatgaggagctgtcgtcgaataaccgaca 3240
Db 3478 GCTGTGTGAGACCTTACTCCCGCAGGGGAATATGGAGCTGTGTAATACCGCAAA 3537
Oy 3241 gggccgaacatattctctctacacacacacatgataagcgagcgtccctggggagag 3300
Db 3538 GGGCGACACATATTCTCTCTACACACACATGAGATGAAGGGAGGAGGCTGAGGGAGAGG 3597
Oy 3301 atigccatcatctcccatgaggaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3360
Db 3598 ATTGCATCATCTCCATGGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3657
Oy 3361 cagctgtggaacagctactactcctgtgctcaagaagaatgtggaatccctccctcagt 3420
Db 3658 CAGCTGGGACAGGCTACTACTCTGACCTTGTGTGAAGAAATGTGGAATCTCTCCCTCAGT 3717
Oy 3421 tctgtgcaaaacagtaagtagacgtgtgtcatactcgtgaagaagagagagagctgttc 3480
Db 3718 TCCTGCAAAACAGTAGTAGCACTGTGTCTAATCTGAAAAAGGAGAGAGAGTTCCTCAG 3777
Oy 3481 agcagttctgattgtgctgtgagcagcagacatgagatgagatgacacgtgtgacatcgt 3540
Db 3778 AGCAATTTGTATGCTGGGCTGGGAGCGACCATGAGATGACAGCTGACCATGATGTC 3837
Oy 3541 tctgcatctccaacatcatcaagaagcatgtgtcgaagccggctgtgtggaagacata 3600
Db 3838 TCTGTATCTCCAACTCATAGGAAGCATGTGTGTGAAGCCCGGCTGTGGAAGACATA 3897
Oy 3601 gggatgagctgacatagatgtgtcgcataaagatgtaagctgtgaagagagagagctgt 3660
Db 3898 GGGCATGAGCTGACCTATGTGTGTGCTCATATGAAGTGTCTTAAGAGAGAGAGCTTTGTGAA 3957
Oy 3661 ctcttctgagatgagacacgctcgaacacacacacacacacacacacacacacacac 3720
Db 3958 CTCTTTCATGAGATGATGATGACCGGCTGTGACACTGTGACATTTCTAGTTATGCA 4017
Oy 3721 gagacgacccctggaagaataatctcctcaagtgtgcccgaagagatgtgtgtgtgt 3780
Db 4018 GAGAGACCCCTGGAAGAAATATTTCTCAAGGTGGCCGAAGAGAGAGGTGTGATCTGAG 4077
Oy 3781 acctagatgtacctctcgaacagacagcaaaacagcgagccttcggggaacagagagc 3840
Db 4078 ACCTAGATGTACCTTGTGCGAGCAAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 4137
Oy 3841 tgtctccgccttactgaagatgattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3900
|||||

Db 4138 TGTCTTTCGCCCTTCACCTGAGATGATGCTGTGTATTCACAAATGATTCTGACATGACCA 4197
Oy 3901 gaatccagaagacagactgtctcagtgagatgatatgcaaaaggtcctaccagtgtaa 3960
Db 4198 GAATCCAGAGAGACAGACTGTCTCAGTGGAGATGTGCAAGAGGTCTCTACAGGTGAAA 4257
Oy 3961 ggtctgaaacttaacagaaagattgtgtgcccctttgtgtgaagaagactgtaattgc 4020
Db 4258 GGTGTGAACCTTACACAGACAGATTTGTGTGCCCCCTTTTGTGTGAAGAGACTGTAATTGCC 4317
Oy 4021 aagagagctcggaagaagatttttctcagatgtgtctgtccagctgtgtgtgtgtgt 4080
Db 4318 AGACGAGCTGGAAGAGATTTTGTGCTGATGTTGCTTCCAGCTGTGTGTGTGTGTGTGT 4377
Oy 4081 gccctgtgttaagctgt 4140
Db 4378 GCCCTGT 4437
Oy 4141 cctgt 4200
Db 4438 CCTGT 4497
Oy 4201 accctgt 4260
Db 4498 ACCCTGGAACCTTAAACCCCTCACCAAAAGACCCGTGTGTGTGTGTGTGTGTGTGTGT 4557
Oy 4261 ggaagacccatcccaagacagccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4320
Db 4558 GGAAGCCCATCCCAACACAGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4617
Oy 4321 gtltcccaagacatcaatggaactctctcagaatggaatggaatggaatggaatggaat 4380
Db 4618 GTTCCCAAGACATCATGTGAGCTCTTCCAGAAATGGAATGTGAGATGTGAGAACTTCA 4677
Oy 4381 cctgtatgcagt 4440
Db 4678 CTTGTATGTCCAGT 4737
Oy 4441 gcaaggggggt 4500
Db 4738 GCAAGGGGGGT 4797
Oy 4501 acaggaagaacatctcgaatltctgtgtgaagcgtatgtgcagatcaatgaacaaagc 4560
Db 4798 ACAGGAAGAAACATTTGT 4857
Oy 4561 ttaagaagaagaatctgt 4620
Db 4858 TTTAAAGAAAGATGT 4917
Oy 4621 aatactcaagcacttctcctcgaatcaagaagtttaatgattgattcaatcaatgaaga 4680
Db 4918 AATTAATCAACTTCTCTCGAGTCAAGAAATTAAATGATGCCCAACAAATGAAGAAA 4977
Oy 4681 cactcaagctgtgccaagacagcttctcagatcagatlttctcaacagctgtggaagatt 4740
Db 4978 CACTTAAGCTGGGCAAGAGACAGTGTGAGATCGATTTCTCAACAGCTTGGGAAATATT 5037
Oy 4741 atgaacagactgtgacacccaataatgtaaggtgtgtgtgtgtgtgtgtgtgtgtgtgt 4800
Db 5038 ATGACAGAGCTGTGACACCAAAATTAATGAAGTGTGTGTGTGTGTGTGTGTGTGTGT 5097
Oy 4801 gcaatcagccttctcgtgaatgtatcaatcaatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4860
Db 5098 GCAATGAGCTTTCCTGATGTATCAATAAAGGCCATTTCTGGGGCAACCTGCAAAAG 5157
Oy 4861 ggaagaagacccatgacatltggaatattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4920
Db 5158 GGAAGAAACCTTACCATCTTATGAAATATGCTTTCAATCATCCCTGATTCACCAAG 5217
Oy 4921 cagcagctctcagaaggt 4980
Db 5218 CAGCAGCTTCTAGAGGT 5277
|||||

QY	4981	gfcacatttgcaatgcttcctgcccagccaagcttgcgtatctctgtatccaggaacgg	5040
Db	5278	gtcattctttgcgaatgtcccttgctccacgacgcttgcgtatctctgtatccaggaacgg	5337
QY	5041	gtcagcaaaagcaaaacacctgcagtlcatcaagtgaggtgaagccttcaatacagctc	5100
Db	5338	gtcacaacaaagcaaaacacctgcattcatcagtgaggtgaagccttcaatacagctc	5397
QY	5101	tctaatcttgcctgggatagtgcattacatcgtttgccttcgcaactgtgtatcaac	5160
Db	5398	tctaatcttgcctgggatagtgcattacatcgtttgccttcgcaactgtgtatcaac	5457
QY	5161	ttcacctgcctccagcaagaagctcattatgttccccaacaactcctcgtgttagccct	5220
Db	5458	ttcacctgcctccagcaagaagctcattatgttccccaacaactcctcgtgttagccct	5517
QY	5221	ctaactttgcctgataagggtgtaacatacaccctccatgttaccagacccctctgtc	5280
Db	5518	ctaactttgcctgataagggtgtaacatacaccctccatgttaccagacccctctgtc	5577
QY	5281	aagatccccagcaaaccttatgtgtgtcaccagcgtgaacctctcaattgtgcaaat	5340
Db	5578	aagatccccagcaaaccttatgtgtgtcaccagcgtgaacctctcaattgtgcaaat	5637
QY	5341	ggcagcgtgagcacctttgtgcctggagcgtgttaccagcaataaactgaataataaat	5400
Db	5638	ggcagcgtgagcacctttgtgcctggagcgtgttaccagcaataaactgaataataaat	5697
QY	5401	gatacctgaagtcgcgtgtcttgcattctccacaattttgccttgagcagaggctatc	5460
Db	5698	gatacctgaagtcgcgtgtcttgcattctccacaattttgccttgagcagaggctatc	5757
QY	5461	gaactgtgtgaaaaacccggaaatggtgtatgacctgggaaagtttggggaaatcgcctt	5520
Db	5758	gaactgtgtgaaaaacccggaaatggtgtatgacctgggaaagtttggggaaatcgcctt	5817
QY	5521	gtctacacatlatcttbgagacttggtagtgtaggaacgaacctctgcacatgcgttgaaag	5580
Db	5818	gtctacacatlatcttbgagacttggtagtgtaggaacgaacctctgcacatgcgttgaaag	5877
QY	5581	gtgtgttcttctcatctactgtctgcataccagtaacagattctcaatgaagccagaact	5640
Db	5878	gtgtgttcttctcatctactgtctgcataccagtaacagattctcaatgaagccagaact	5937
QY	5641	gtcaaatgcaaaagctatctcctctgtaatgtatgaagaatgaagatgtgagcgagaaacag	5700
Db	5938	gtcaaatgcaaaagctatctcctctgtaatgtatgaagaatgaagatgtgagcgagaaacag	5997
QY	5701	agaattcttgatgtgtaggagccagaaatgacatctagaataatgaagaggttagcgaagata	5760
Db	5998	agaattcttgatgtgtaggagccagaaatgacatctagaataatgaagaggttagcgaagata	6057
QY	5761	tataagaagaagaaggaagcctgctgtgttgacagatttgcgtgggcatctctcctcgtgtgag	5820
Db	6058	tataagaagaagaaggaagcctgctgtgttgacagatttgcgtgggcatctctcctcgtgtgag	6117
QY	5821	tgctttgagctctcctgggaggttaatagggagcttgaaataatcaacttcaagaagttaaca	5880
Db	6118	tgctttgagctctcctgggaggttaatagggagcttgaaataatcaacttcaagaagttaaca	6177
QY	5881	ggagataccacgtttacacagaggaatgcttctccttaacaaataglatcttaacaac	5940
Db	6178	ggagataccacgtttacacagaggaatgcttctccttaacaaataglatcttaacaac	6237
QY	5941	atccatgaataatacaagaacatgggctgactgacccctgaattgtatgcatacaagagctg	6000
Db	6238	atccatgaataatacaagaacatgggctgactgacccctgaattgtatgcatacaagagctg	6297
QY	6001	ttgacttgagagagaacagtgtagtcttcttgcccttttgagagagtcctccagagaagaa	6060
Db	6298	ttgacttgagagagaacagtgtagtcttcttgcccttttgagagagtcctccagagaagaa	6357

QY	6061	attggcaaggttctgtagtgggagatcttgaaacttgacctctgtgaagtaatggagaataa	6120
Db	6358	gttggcagaagtttgtagtgggagatcttgaaacttgacctctgtgaagtaatggagaataa	6417
QY	6121	tatgctgtgaactatagtgagagcaacaacgcaagctctctcaagccatgagcttggatc	6180
Db	6418	ttatgctgtgaactatagtgagagcaacaacgcaagctctctcaagccatgagcttggatc	6477
QY	6181	ggcgggacctctgtgtgttcttgatgaaccacacagcagatgatacccaagcccg	6240
Db	6478	ggcgggacctctgtgtgttcttgatgaaccacacagcagatgatacccaagcccg	6537
QY	6241	cggttcttgtagaatgtgtccctaaatgtgtgtcgaaggaagggagatcagtagtcttaca	6300
Db	6538	cggttcttgtagaatgtgtccctaaatgtgtgtcgaaggaagggagatcagtagtcttaca	6597
QY	6301	tctcatagcatatggagaatgtgaagctctcttgcataggaatggcaatcgtgccaatga	6360
Db	6598	tctcatagcatatggagaatgtgaagctctcttgcataggaatggcaatcgtgccaatga	6657
QY	6361	aggttcgaatgtgcttgagcagtgctcagcaatcctaaanaataggtttgagaatggttaca	6420
Db	6658	aggttcgaatgtgcttgagcagtgctcagcaatcctaaanaataggtttgagaatggttaca	6717
QY	6421	atagttgtacgaatagcagaggtccaaacccggaccttgaagcctgtccaggaattcttga	6480
Db	6718	atagttgtacgaatagcagaggtccaaacccggaccttgaagcctgtccaggaattcttga	6777
QY	6481	cttgatattcccgcgaagtggtctttaaagaagaacccggaaatagtctaaataacagctt	6540
Db	6778	cttgatattcccgcgaagtggtctttaaagaagaacccggaaatagtctaaataacagctt	6837
QY	6541	ccatcttcattatctctctgagcaggaatatacagcatcctctccagagcaaaaagcga	6600
Db	6838	ccatcttcattatctctctgagcaggaatatacagcatcctctccagagcaaaaagcga	6897
QY	6601	cttccaatagaaagactactctgtttctcgaacaacacttgcacgaatttctgaactt	6660
Db	6898	cttccaatagaaagactactctgtttctcgaacaacacttgcacgaatttctgaactt	6957
QY	6661	gccaaaggccaagcgaatgatacacaacttaaagaacctctatcacaaaaccagaca	6720
Db	6958	gccaaaggccaagcgaatgatacacaacttaaagaacctctatcacaaaaccagaca	7017
QY	6721	gtatgtagcgttgcaggttctcaacatcttcttctaacagatgagaagtgaaagaagctat	6780
Db	7018	gtatgtagcgttgcaggttctcaacatcttcttctaacagatgagaagtgaaagaagctat	7077
QY	6781	gtataagaatccctgttcatagc	6804
Db	7078	gtataagaatccctgttcatagc	7101
RESULT	15		
LOCUS	AB055982	6786 bp	Linear
DEFINITION	Homo sapiens mRNA for ABCA1, complete cds.		PRI 18-AUG-2001
ACCESSION	AB055982		
VERSION	AB055982.1	GI:15212106	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;		
AUTHORS	Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.		
TITLE	1 (bases 1 to 6786)		
REFERENCE	Tanaka,A.R., Abe-Dohmae,S., Arakawa,R., Sadanami,K., Kidera,A.,		
AUTHORS	Kioka,N., Anachi,T., Yokoyama,S. and Ueda,K.		
JOURNAL	A new topological model of functional human ABCA1-Signal peptide		
REFERENCE	cleavage and glycosylation of a large extracellular domain		
AUTHORS	Unpublished		
TITLE	2 (bases 1 to 6786)		
	Ueda,K., Kioka,N. and Tanaka,A.R.		
	Direct Submission		

Dh 1201 AAGACCTTCAGAGAACTGGCTGTGTTCCATGATCTGGAAGGATGTGGAGAACTCAGC 1260
Qy 1261 cccaagatctggacctcatgagaaacagcagaagaatgacctgtccggatgctgtg 1320
Dh 1261 CCCAAGATCTGGACCTTCATGAGGAACAGCCAAAGAAATGACCTTGTCCGATGCTGTG 1320
Qy 1321 gacagaaggagcaatgaccacttttggagacagcaatgtgatggtctagatggagacc 1380
Dh 1321 GACAGAGAGGCAATGACCACTTTTGGAAACAGCACTTGATGGCTTACATTGGACAGCC 1380
Qy 1381 caagaaatcgtgacctttttggccaagcaccagaagatgtccagtcagtaatgttct 1440
Dh 1381 CAAAGAAATGCTGGCTGTGTTGGCAAGCACCCAGAGAGTCCAGTCCGTAATGTTCT 1440
Qy 1441 gtgtacacctggagagaagcttccaagagactaacagagcaatccggagcaatctgc 1500
Dh 1441 GTGTACACCTGGAGAGAACCTTTCACAGACTAACCCAGGCAATCCGGACCTATCTCC 1500
Qy 1501 ttcatgtgagtggttcaacctgaaacagctagaaaccatagcaacagaagtcgtgtc 1560
Dh 1501 TTCATGTGAGTGTCTCAACCTGAAACAGCTAGAACCCATAGCAACAGAACTGTGGCTCATC 1560
Qy 1561 aacaagatccatggagctgtctgtatgagagaagttctggctgtatgtgttcaatgga 1620
Dh 1561 AACAAATCCATGAGAGCTGCTGATGAGAGGAAGTTCTGGGCTGTGATGTGTCTCACTGGA 1620
Qy 1621 attactcagaagcaatltgagctgtcccaatcagtcagaaagtaagaatccgaatgtgacat 1680
Dh 1621 ATTACTCCAGGAGCATGTAGAGCTGCCCATTCATGTCAAGTACAAATCCGAATGAGACATT 1680
Qy 1681 ggaatgtgagagaagacaataaatacaagaatggtaactggagaccgtgtctcagact 1740
Dh 1681 GGAATGTGAGAGAGACAATAAATCAAGATGGGTACTGGGACCCGTGCTCTGAGACT 1740
Qy 1741 gacccttggagacatgagtgagctgtggggggtcttcgacctacttgcagatgtgtg 1800
Dh 1741 GACCCCTTGGAGACATGAGGATGACCTGTGGGGGCTTGGCTACTCTCAGAGATGTGTG 1800
Qy 1801 gaggcaggaatcaatcaagggtgtgagcgggacaggaagaactggtgtcatalatgcaa 1860
Dh 1801 GAGCAGGCAATCATAGGTTGCTGACGGGACCCAGAGAAACTGTGTCTATATGCA 1860
Qy 1861 cagatgacctatccctgttgaatgatacatcttctcggggtgtgagtaagccggtcaatg 1920
Dh 1861 CAGATGACCTTACCTGTGTAGCTGTATGACATCTTCTTGGCGGTGATGACCGGCTCAATG 1920
Qy 1921 cccctcttcaatgagcgtgacctgataatcaatcagtgagtgagtaatcaagggatcgtg 1980
Dh 1921 CCCCTCTTCATGAGCGCTGGCTGGATTTACTCAGTGGCTGTGATCATTAAGGGCATCTG 1980
Qy 1981 tatgagaaggaggaagcagcgtcaagaagacatgagatcagtgagtgagtgagcaacagata 2040
Dh 1981 TATGAGAAAGGAGGACGCGCTGAAGAGACCATGCGGATCATGGCGCTGAGAACAGCATC 2040
Qy 2041 ctctgtgttgaatgagttatagtaagctcatctctctctctgtgtgagagcgtgacctgta 2100
Dh 2041 CTCTGTGTGTACTGATGATTAATAGTACCTCATCTCTCTTGTGTGACGCGCTGCTGCTGA 2100
Qy 2101 gtgtgtacatccctgaagttagaagaacctgtgacctacagtgatcccaagcgtgtgtgtg 2160
Dh 2101 GTGTGATCCCGTAAGTTAGAAACCTGCTGCTTACAGTGTATCCCAAGGAGGTGTGTGTC 2160
Qy 2161 ttctgtgtcgt 2220
Dh 2161 TTCTGT 2220
Qy 2221 tccgaagcaaacctcgagcagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2280
Dh 2221 TCCGAGACCAACCTCGAGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2280
Qy 2281 taagtctgt 2340
Dh 2281 TACGTCTGT 2340

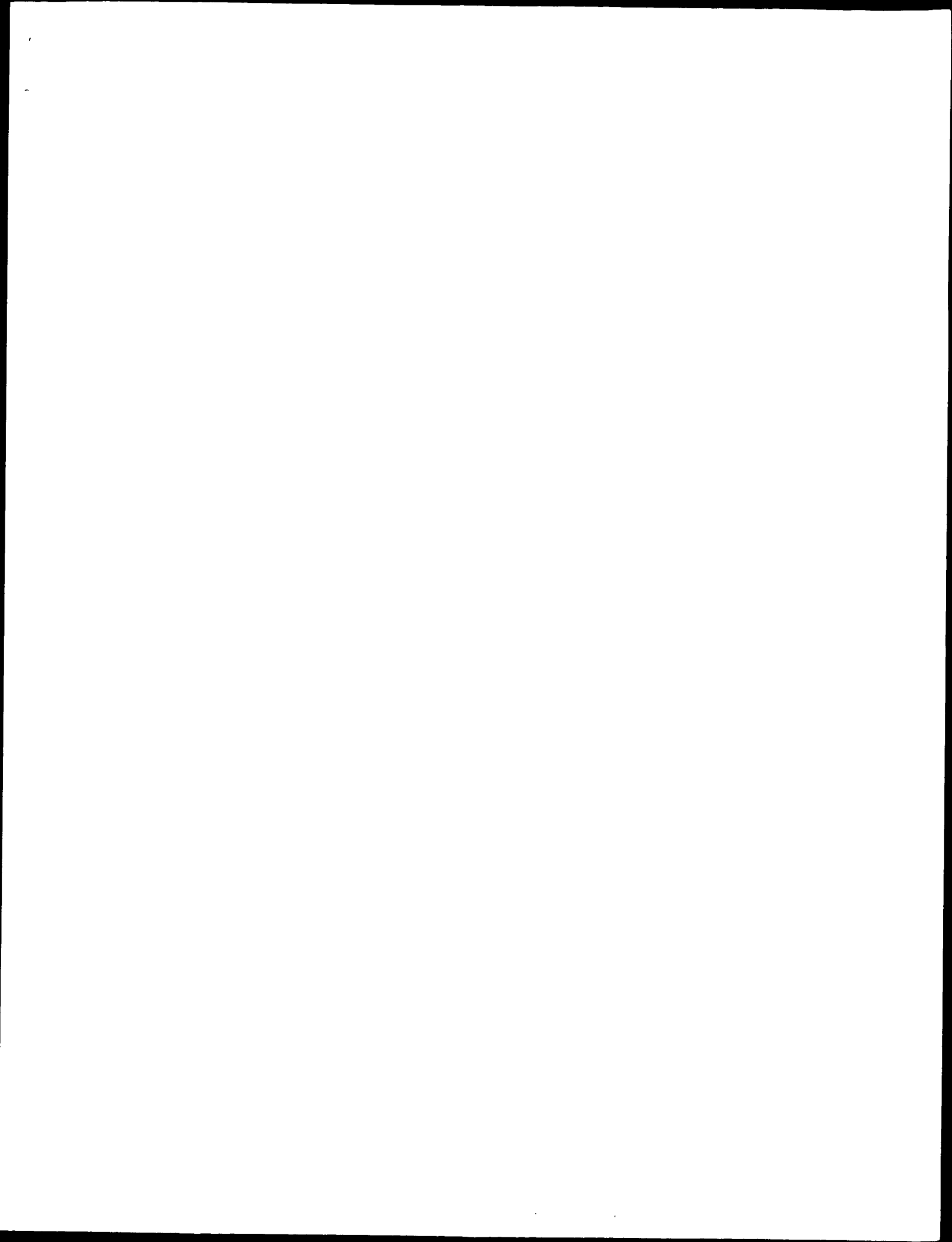
Qy 2341 ctgctgtctctgt 2400
Dh 2341 CTGCTGTCTCTGT 2400
Qy 2401 ggcatttgagtcagtgaggagacaacctgtgtgagtgctgtgtgtgtgtgtgtgtgtgtgt 2460
Dh 2401 GGCAATTGAGAGTCAGATGGGACCACTGTTTGAAGATCTGTGGAGAAATGGCTTCAAT 2460
Qy 2461 ctcaaccacttcagatccatgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2520
Dh 2461 CTCACCACTTGT 2520
Qy 2521 ttacattgagtgctgt 2580
Dh 2521 TTAATGTGAGCTGT 2580
Qy 2581 accaagtcctactgt 2640
Dh 2581 ACCAAGTCTACTGT 2640
Qy 2641 aagaagaatgcaagaatcagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2700
Dh 2641 AAGAGAAATATCAGAAATCTGATGAGAGGAACCCACCACTTGAAGCTGGCGTGTGC 2700
Qy 2701 attagaacctgt 2760
Dh 2701 ATTGAGAACTGT 2760
Qy 2761 ctgaatttttattgagggcagcaatcaactctctctgtgtgtgtgtgtgtgtgtgtgtgtgt 2820
Dh 2761 CTGAATTTTATGAGGGCCAGATCACCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2820
Qy 2821 accaagatgcaatcctgt 2880
Dh 2821 ACCAAGATGCAATCTGT 2880
Qy 2881 ggaagaagacatcgt 2940
Dh 2881 GGAAGAAACATTTGCTGT 2940
Qy 2941 cataagctgt 3000
Dh 2941 CATTAACGT 3000
Qy 3001 aaagggtctctgt 3060
Dh 3001 AAAGGCTCTGT 3060
Qy 3061 ttgcaatcaagcaagctgt 3120
Dh 3061 TTGCAATCAAGCAAGCTGT 3120
Qy 3121 ctatctgt 3180
Dh 3121 CTATCTGT 3180
Qy 3181 gctgt 3240
Dh 3181 GCTGT 3240
Qy 3241 ggcgcagcatattctctctacacacacacatgagatggaagcgaagctgtgtgtgtgtgtgt 3300
Dh 3241 GCGCGACCATTAATCTCTCTACACACACATGATGGAAGCGAGCTGTGTGTGTGTGTGTGT 3300
Qy 3301 attgcatcatctccatgt 3360
Dh 3301 ATTGCAATATCTCCATGT 3360
Qy 3361 cagctgt 3420
Dh 3361 CAGCTGT 3420

QY 3421 tcttgcagaacagtagtagcactgtgtcatacctgaagaagaagagcagtggttttcag 3480
|||||
Db 3421 tcttcgacaaacagtagtagcactgtgtcatacctgaagaagaagagcagtggttttcag 3480
QY 3481 agcagtttctgtctgtcgtcgttcgacgacacatagagtagacacgtcgcacatcgtatc 3540
|||||
Db 3481 agcagtttctgtctgtcgtcgttcgacgacacatagagtagacacgtcgcacatcgtatc 3540
QY 3541 tctgtatctccaacatcatcaggaagcagtggtctgaagcccggtctgtgtgaagacata 3600
|||||
Db 3541 tctgtatctccaacatcatcaggaagcagtggtctgaagcccggtctgtgtgaagacata 3600
QY 3601 gggcagatgagtagcactatgtgtcgcacataagaagctgtcgaaggaggagccttgttgaa 3660
|||||
Db 3601 gggcagatgagtagcactatgtgtcgcacataagaagctgtcgaaggaggagccttgttgaa 3660
QY 3661 cctcttcagtagatgtagcagcgtctcagacgtcggcagcttctgaatgatcagatcga 3720
|||||
Db 3661 cctcttcagtagatgtagcagcgtctcagacgtcggcagcttctgaatgatcagatcga 3720
QY 3721 ggaagacacctggaagaataatctcctcaaggctggccggaagagtgagggtgagtgag 3780
|||||
Db 3721 ggaagacacctggaagaataatctcctcaaggctggccggaagagtgagggtgagtgag 3780
QY 3781 accctagatgtagcacttgcagcagaagaacagcgagcgtccttcggggagacacagc 3840
|||||
Db 3781 accctagatgtagcacttgcagcagaagaacagcgagcgtccttcggggagacacagc 3840
QY 3841 tctcttcgacgttcaactgaagatgtgtctgtatcccaatgtagtgcagatgaccca 3900
|||||
Db 3841 tctcttcgacgttcaactgaagatgtgtctgtatcccaatgtagtgcagatgaccca 3900
QY 3901 gaatccagaagacagactgtctcagtgagatgagtgagcaaggctctaccaggtgaa 3960
|||||
Db 3901 gaatccagaagacagactgtctcagtgagatgagtgagcaaggctctaccaggtgaa 3960
QY 3961 ggtctggaacttacaagaagaagcttggcgcccttggtagaagaagctgtctaatctcc 4020
|||||
Db 3961 ggtctggaacttacaagaagaagcttggcgcccttggtagaagaagctgtctaatctcc 4020
QY 4021 agacgagatcaggaagaagcttctgtcagatgtctgtcgcagcagtggtgttgctgcac 4080
|||||
Db 4021 agacgagatcaggaagaagcttctgtcagatgtctgtcgcagcagtggtgttgctgcac 4080
QY 4081 ggccttggtctgaagcgtgtcgtgcacaccccttgagcaagtagaccagcgtgtgaactca 4140
|||||
Db 4081 ggccttggtctgaagcgtgtcgtgcacaccccttgagcaagtagaccagcgtgtgaactca 4140
QY 4141 cccctgagatgtagaagaagcagatgtgtcagatgtgtcagcaatgtagtccctgaagacagga 4200
|||||
Db 4141 cccctgagatgtagaagaagcagatgtgtcagatgtgtcagcaatgtagtccctgaagacagga 4200
QY 4201 accctggaacttctaaagcgcctcaccacaaagacccgtgtcgtggagcccgctgtatgaa 4260
|||||
Db 4201 accctggaacttctaaagcgcctcaccacaaagacccgtgtcgtggagcccgctgtatgaa 4260
QY 4261 ggaacacccatccacagacagcgtcgcagagagagagagagagagagagagagagagagag 4320
|||||
Db 4261 ggaacacccatccacagacagcgtcgcagagagagagagagagagagagagagagagagag 4320
QY 4321 gttccccaagacatcatgagcctctccagaaatgaggaactgagcaaatgagacaccttca 4380
|||||
Db 4321 gttccccaagacatcatgagcctctccagaaatgaggaactgagcaaatgagacaccttca 4380
QY 4381 cctgtacatgcaagtagagcagcagacaaatcaagaagaatgtctgtcgtgtgtgtgtgtgtgt 4440
|||||
Db 4381 cctgtacatgcaagtagagcagcagacaaatcaagaagaatgtctgtcgtgtgtgtgtgtgtgt 4440
QY 4441 gcaagggggggtcgtcctcctcacaagaagaagaagaacacacacacacacacacacacacac 4500
|||||
Db 4441 gcaagggggggtcgtcctcctcacaagaagaagaagaacacacacacacacacacacacacac 4500
QY 4501 acaggaagaacatcttcgagatctcgtgtgaagaagtagtgcagatcatagccaagaagc 4560
|||||
Db 4501 acaggaagaacatcttcgagatctcgtgtgaagaagtagtgcagatcatagccaagaagc 4560
QY 4561 ttaagaacaaagatcctggtgtgaatgtagtgaatgtagtgaatgtagtgaatgtagtgaatg 4620
|||||
Db 4561 ttaagaacaaagatcctggtgtgaatgtagtgaatgtagtgaatgtagtgaatgtagtgaatg 4620
QY 4621 aatctcagacacatctcctcagagtagcagaagtagtgaatgtagtgaatgtagtgaatgtag 4680
|||||
Db 4621 aatctcagacacatctcctcagagtagcagaagtagtgaatgtagtgaatgtagtgaatgtag 4680
QY 4681 caactaaagctggccaagaagtagtgcagatcagatcagatcagatcagatcagatcagatc 4740
|||||
Db 4681 caactaaagctggccaagaagtagtgcagatcagatcagatcagatcagatcagatcagatc 4740
QY 4741 atgacaagcagtagacacacagaatgaatgtagtgaatgtagtgaatgtagtgaatgtag 4800
|||||
Db 4741 atgacaagcagtagacacacagaatgaatgtagtgaatgtagtgaatgtagtgaatgtag 4800
QY 4801 ggaatcagctctctcctgaatgtagtgaatgtagtgaatgtagtgaatgtagtgaatgtag 4860
|||||
Db 4801 ggaatcagctctctcctgaatgtagtgaatgtagtgaatgtagtgaatgtagtgaatgtag 4860
QY 4861 ggaagaacacctagacatlatggaatgtagtgaatgtagtgaatgtagtgaatgtagtgaatg 4920
|||||
Db 4861 ggaagaacacctagacatlatggaatgtagtgaatgtagtgaatgtagtgaatgtagtgaatg 4920
QY 4921 cagacagctcagaagtgtagtgcagacacacacacacacacacacacacacacacacac 4980
|||||
Db 4921 cagacagctcagaagtgtagtgcagacacacacacacacacacacacacacacacacac 4980
QY 4981 gtagctctgcaatgtagtgcagacacacacacacacacacacacacacacacacacacac 5040
|||||
Db 4981 gtagctctgcaatgtagtgcagacacacacacacacacacacacacacacacacacacac 5040
QY 5041 gtagcagaagaac 5100
|||||
Db 5041 gtagcagaagaac 5100
QY 5101 tctaatcttgctggagtagtgcagacacacacacacacacacacacacacacacacacac 5160
|||||
Db 5101 tctaatcttgctggagtagtgcagacacacacacacacacacacacacacacacacacac 5160
QY 5161 tctaatcttgctggagtagtgcagacacacacacacacacacacacacacacacacacac 5220
|||||
Db 5161 tctaatcttgctggagtagtgcagacacacacacacacacacacacacacacacacacac 5220
QY 5221 ctaactcttgctggagtagtgcagacacacacacacacacacacacacacacacacacac 5280
|||||
Db 5221 ctaactcttgctggagtagtgcagacacacacacacacacacacacacacacacacacac 5280
QY 5281 aagatccccagac 5340
|||||
Db 5281 aagatccccagac 5340
QY 5341 gtagcagctggcagac 5400
|||||
Db 5341 gtagcagctggcagac 5400
QY 5401 gtagcagctggcagac 5460
|||||
Db 5401 gtagcagctggcagac 5460
QY 5461 gtagcagctggcagac 5520
|||||
Db 5461 gtagcagctggcagac 5520
QY 5521 gtagcagctggcagac 5580
|||||
Db 5521 gtagcagctggcagac 5580
QY 5581 gtagcagctggcagac 5640
|||||
Db 5581 gtagcagctggcagac 5640

Db 5581 GTGATGTTCTCCATTAAGTCTGATCCAGTACAGATTTCTTCAAGCCAGACCT 5640
QY 5641 gtaatgcaaaagctatctctctctgaaatgaagatgaagatgaagcaag 5700
Db 5641 gtaaatgcaaaagctatctctctgaaatgaagatgaagatgaagcaag 5700
QY 5701 agaattctatgagtgagagccagaaatgaacatctagaagaatgaagatgaagata 5760
Db 5701 AGAATTTCTGATGCTGAGAGCCAGAAATGACATCTTGAATATCAAGGATGACGAAGATA 5760
QY 5761 tataagaagaagcagaagccctgctgtgaagaattgctgtgagcattctctgtgag 5820
Db 5761 TATAGAGAGGAAGCGGAGAGCTGCTGTTGACAGGATTTGGTGAGCATTCCTCTGAGTGA 5820
QY 5821 tgcttgggctctctggagatgaatgagggctgagaaatctcaacttcaagaatgtaaca 5880
Db 5821 TGCTTTGGGCTCTCTGGAGATTATGGGGCTGAGAAATCATCACTTCAAGATGTTAACA 5880
QY 5881 ggaagataccactgttaccagaaggagatgcttcccttaacaaaatagatactatcaaac 5940
Db 5881 GGAGATACCACTGTTACAGAGAGAGATGCTTCCCTTAACAAAATAGTATCTTATCAAC 5940
QY 5941 atccatgaagatcatcagaacatgagctactgacctcaagttgatgcatcacaagactg 6000
Db 5941 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCACTTGTATGCCATCACAGAGCTG 6000
QY 6001 ttgactgagagaagaacagtgagatcttctgaccttgaagagagatcccaagaagaag 6060
Db 6001 TTGACTGGGAGAGAACACCTGAGATCTTTGCTTTGAGAGAGATCCCAAGAGAAAGAA 6060
QY 6061 gttgcaaggttggtagagtgagatcagaaactgggctcgtgagatlatgagaagaaa 6120
Db 6061 GTTGGCAAGGTGGTAGAGTGAGGCGATGCGAAACTGGGCTGTCGAGATGAGAGAAAAA 6120
QY 6121 tatgtctgaactatagtgagagcaaaagcaagctctctacagccatgcttgatc 6180
Db 6121 TATGCTGGAATATAGTGGAGGCAACAGCAAGCTCTTACAGCCATGAGCTTTGATC 6180
QY 6181 ggcgggacctctgtgtgttctctgatagaacccacacagcatgatacccaagcccg 6240
Db 6181 GCGGGGCTCTGTGTGTCTGTGATGACCCACACAGGATGATCCCAAGCCCGG 6240
QY 6241 cggctctgtggaattgtgacctgaagtgtgtcaagaaggagatcagtagtcttaca 6300
Db 6241 CGGCTCTGTGGAATTGTGCTTAAGTGTGTCAAGGAGGAGATCAGTAGTCTTACA 6300
QY 6301 tctcatatagaaagatgtgaagctcttgcactagatgagcaatcatgtgtcaatgga 6360
Db 6301 TCTCATATAGGAAGAGATGTGAAGCTTTTGCACTAGGATGCAATCATGTCAATGGA 6360
QY 6361 aggtcagggtccttgagcagtgatccagcatcctaaataagtttgagatggttataca 6420
Db 6361 AGGTCAGGTCCTTGGCAGTGTCCAGCATCTAATAAATAGGTTGGAGATGTTATACA 6420
QY 6421 ataattgagaagaatgaggggttcaacccggagactgaagctgtccaggatcttctgga 6480
Db 6421 ATAGTTGACGAATGACGAGGCTCAACCCGAGCCTGAAAGCTGTCCAGGATTTCTTGA 6480
QY 6481 ctgtcattctctggaagtgttcttaaaagaagaacacccggaacatgctacaaatcaccat 6540
Db 6481 CTGTGATTTCTCTGAGAGTGTCTAATAAGAGAAACCCGGAATGCTTACAAATACCAAGCTT 6540
QY 6541 ccaatctcatatctctctgagcagatatcagcatcctctccagagcaaaaaagcga 6600
Db 6541 CCATCTTCAATATCTCTCTGGCCAGGATATTCAGCATCTCTCTCCAGAGCAAAAAAGCGA 6600
QY 6601 ctccacataagaagactactcgttctcagacaacacttgaaccaagatattgtgaactt 6660
Db 6601 CTCACATAGAGAGCTACTCTGTTTCTCAAGACAACTTGAACAGATTTGTGAACCTTT 6660
QY 6661 gccaaaggaacaaagtgaatgaaccacttaaaagacctcattacacaaaaacagaca 6720
Db 6661 GCCAAGGACCAAGTGTGATGACCACTTAAAGACCTCTCATTTACCAAAAAACAGACA 6720

QY 6721 gtagtgaagcttgcaagttctcacatcttctctacagatgagaaagtgaagaagctat 6780
Db 6721 GTAGTGAAGCTTGCAGTCTCTCACATCTTTCTACAGGATGAGAAAGTGAAGAAGCTAT 6780
QY 6781 gtagta 6786
Db 6781 GTATGA 6786

Search completed: September 14, 2002, 07:35:05
Job time: 76873 sec



Query Match 100.0%: Score 10438: DB 6: Length 10442:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 10442: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ggcggagaccgagagccgagccgacctctctccgggctgagcgagcgagcg 60
Db 1 GGC GGAGACCCGAGAGCCGAGCCGACCTCTCTCCGGGCTGCCGCGAGGGCG 60
QY 61 gggagctcgagacccaacagagccgggtctcaggcgcttgctctgttttcccg 120
Db 61 GGAAGCTCCGACACCAACAGAGCGGTCTCAGAGGGCGCTTCTCTGTTTTTCCCG 120
QY 121 gttctgtttctccctctccggagagctgtgcaagggtgaggaagaagcaaac 180
Db 121 GTTCTGTTTTCTCCCTTCTCCGGAAGGCTGTGCAAGGGGTGAGGAAGAACCCAAAC 180
QY 181 acaaaagtgaaaacagtttaagaccagccagcgccctgctgtgagcttgccgc 240
Db 181 ACAAAGTGAAAAACAGTTAATGACACGCGGGGCTCTGCTGTGAGCTCTGGCCGC 240
QY 241 tgcctccagagctcccgagccagccagcgtgctgctgagctgaggaacatggctt 300
Db 241 TGCTTTCAGAGGCTCCCGAGCCACAGCTGGGCGTGTGCTGAGGGAACATGGCTTGT 300
QY 301 ggcctcaagctgaggtgtgctgtgtggaagaacctcaacttccagaagaacacatg 360
Db 301 GGCCTCAGCTGAGGTGTGCTGTGTGGAAGAACCTCACTTTCAGAGAAGAACAAACATGTC 360
QY 361 agctgtactggaagtgagctgacctatattctctgactgactgctgttgcgc 420
Db 361 AGCTGTACTGGAAGTGAGCTGTGTGGAAGAACCTCACTTTCAGAGAAGAACAAACATGTC 420
QY 421 tgaagctaccacccctatgaaacacaaatgacatcttccaaataaagcaatgcccctg 480
Db 421 TGAGCTACCCACCCCTATGAAACAAATGACATGTCCTTTCGAATTAACCAATGCCCTCTG 480
QY 481 caagaaaccttctgtgtgtgctgaggaatattctgtaatgcaaacacccctgttccgt 540
Db 481 CAGGAACACTTCTGTGGGTTCAGGGGATTAATCTGTAATGCCAACACCCCTGTTCGGTT 540
QY 541 acccgactcctggagagctcccgagctgtgtggaacctttaaacaactccatctgctc 600
Db 541 ACCCGACTCTGGGAGGCTCCCGAGCTGTGTGGAACCTTTAAACAAATTCATGTGGCTC 600
QY 601 ggccttctcagaatgctcgagagctcttatacagccagaaagacacacagatgaag 660
Db 601 GCCTGTCTCAAGATGCTCGAGGCTTCTTTATACAGCCAGAAAGACACCGCATGAAGG 660
QY 661 acatgcgcaaaagtcttggaacattacagcagatcaagaataatccagctcaacttgaag 720
Db 661 ACATGCGCAAAAGTCTTGGAACATTACAGCAGATCAAGAAATTCACAGCTCAAACTTGAAGC 720
QY 721 ttcagaatttccctgtgtgacaatgaacacctctctggttccctatatacaacctctc 780
Db 721 TTCAGATTTCTCGTGTGACAATGAACCTTCTGTGGGTTCTTATACACACACTCTCTCTC 780
QY 781 tcccaaatctactgtggaacaaagtgtcgagagctgtatgtcatctccacaagatatt 840
Db 781 TCCCAAACTCTACTGTGGAACAAAGATGCTGAGGCTGATGTCATCTCCACAAAGTATTTT 840
QY 841 tgaagagctacagttatcaatttgcaagctgtgtgcaatgtaataaatacgaagaatga 900
Db 841 TGCAAGGCTTACAGATTATTTGCAAGCTGTGTGCAATGATCAAAATTCGAAGAATGA 900
QY 901 ttcaactgtgtgacaaagaatttctgagctgtgtgcttaccacaagaagaagatgctg 960
Db 901 TTCAACTGTGTGACAAAGATTCTGAGCTTGTGTGCTTACCAAGGAAGAAATCTGGCTG 960
QY 961 cagcagagcagatctctcttccacaatgacatccctgaagccaaatccctgagaagactaa 1020
Db 961 CAGCAGAGCAGTACTCTCTCTCCACAATGACATCTTGAAGCCAAATCTGAGAACACTAA 1020

QY 1021 acctacatcccttcccgagcaagagctgtgtgaaagccacaacaaacattgtgtcata 1080
Db 1021 ACTCTACATCTCCCTTCCGAGCAAGAGCTGGCTGAAGCCACAAACATTTGCTGCATA 1080
QY 1081 gtttggagctcgtgcccgagagctgttcaagatagaagcttgagtgacatgcgaag 1140
Db 1081 GTTCTGGAGCTCTGGCCCGAGAGCTGTTCAAGCATGAGAAGCTGGAGTACATGGGACAGG 1140
QY 1141 aggtgaatgttctgaccaaagtgaacagctccagctcccaacccaatactaccagctg 1200
Db 1141 AGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCTCCACCAATCTACCAAGCTG 1200
QY 1201 tgcctgatttctgtcgagagctcccgagagaggggctgaagatcaagtcttcaact 1260
Db 1201 TGCTGTATGTGTGCGGGGCATCCCGAGGAGGGGGCTGAAGATCAAGTCTCTCAACT 1260
QY 1261 ggtatgagacaacaactcaagaccctcttggaggaatggaacatgagaagaatgtctg 1320
Db 1261 GGTATGAGACAACAACCTCAAGAGCCCTTTGGAGGCAATGGCACTGAGGAATATCTG 1320
QY 1321 aaactctctatgaacactctacaactccctactgcaatgattgataagaattggagt 1380
Db 1321 AAACCTTCTATGACAACCTCTACAACTCTTACTGCAATGATTTGATGAAGAAATTTGGAGT 1380
QY 1381 ctgactccttcccgacatctatctgaaagctctgaaagcgtctctgttggagaatcc 1440
Db 1381 CTAGTCTCTTCCCGCATTTATCTGAAAAGCTCTGAAGCCGCTCTGTGGGAAGATCC 1440
QY 1441 tglataacctgtacacatccagccacaagcagatgactgtgtaagtgtaaaagacctcc 1500
Db 1441 TGLATACACTGTACACCTCCAGCCACAAGCAGGTCATGGCTGAGAGTAACAAAGCTTCC 1500
QY 1501 aggaagctgtgttccatgatctggaagcagatgtgtggagaaactaagcccaagatct 1560
Db 1501 AGGAAGCTGTGTCTCATGATCTGGAAGCATGTGGAGAACTTCAAGCCCAAGATCTC 1560
QY 1561 ggaacttcaatggaagacagcaagaatggaactgtgcccagatgtgttgagacagag 1620
Db 1561 GGACCTTCAATGAGAAAGCAAGCAAGAAATGAGACTTGTCCGATGCTTTTGGACACAGG 1620
QY 1621 acaatgacacacttltgggaacagcaatgtgagttaagttggaacagcccaagacatcg 1680
Db 1621 ACAATGACACACTTTLTGGGAACAGCAGTTGATGATGATGATGATGATGATGATGATG 1680
QY 1681 tggcgttlttggccaagaccagagagatgtccagctccagtaatgttctgttacaact 1740
Db 1681 TGGCTTTTGGCCAGAGACCCACAGATGTTCAGTCCAGTAATGATGATGATGATGATGAT 1740
QY 1741 ggaagaaagcttcaacagagactaaccaagcaatccggaacataatcgtctcatgagt 1800
Db 1741 GGAGAAAGCTTTCACAGAGACTTAACAGCAATCCGAGCATATATCTCGCTTATGAGAT 1800
QY 1801 gtgtcaacctgaaagaagtgtgaaccatagcaagaagctctgtgtcatcaacaagtcca 1860
Db 1801 GTGTCAACCTGAAGAGGTGAACCCATACCAACGAAGCTGTGTGTATCAAAATTCOA 1860
QY 1861 tggagctgtgtgagatgaggaagatgtctgagctgtgattgtgttccacttggaattactccag 1920
Db 1861 TGGAGCTGTGTGAGAGGAGGAGTGTGGGCTGTGATGTGTTCATCTGGAATTTACTCCAG 1920
QY 1921 gcaagataggctgtgcccatcatgtcaagatccgaatggaacatggaacatgtg 1980
Db 1921 GCAGCATTTGAGCTGCCCATCATGTCAAGTACAAAGTCCGAATGAGCATTTGCAATGTGG 1980
QY 1981 agagacaataataaataaagatggttactgggaacctgtgtctgagctgaccccttg 2040
Db 1981 AGAGACAATAATAAATAAAGATGGTACTGGGACCTGTCTCTGAGCTGACCCCTTTG 2040
QY 2041 aggacatgagctacgtctgtggggggtctcgcttacttggaagatgtgtgtggagcgaa 2100
Db 2041 AGGACATGCGGTAGCTGTGGGGGGCTTGGCTTGTGAGGATGTGTGTGGAGGAGGCA 2100
QY 2101 tcatcaggtgtctgagcggaacccgagaagaacactgtgtctatatgaaacagatgccc 2160

```
|||||
Db 2101 TCATCAGGGGTGACGAGGACCGAGAAACCTGCTCTATATGCAAGATAGCCCT 2160
Qy 2161 atcccggttaacgttgaatgacatcttcctgaggtgatagccggtcaatgccccctca 2220
Db 2161 ATCCCTGTTACGTTGATGACATCTTTCTGCGGGGTATGAGCCGGTCAATGCCCCCTTCA 2220
Qy 2221 tgaagctgagccttgatcttaacatgagctgctgcatcaaggagcaatgcatgaagaag 2280
Db 2221 TGACGGGTGGCGGTGATTTACTCAGTGGCTGTGATCATCAAGGCGCATCGTGTATGAGAAG 2280
Qy 2281 aggcacagctgaaagagaccatgacgcatatgagccttgagcaacagcctactctggtta 2340
Db 2281 AGGCACGGCTGAAAGAGACCATGCGGATCATGGCTTGAGCAACAGCATCTCTGTTTA 2340
Qy 2341 gctggttcaatgaatgacccatctctctctctctgtagcctgagcctgctagtgtaccc 2400
Db 2341 GCTGCTTCATTAATGATACCTCATTTCTCTTGTGAGCGCTGCGCTGGTGGTGGTATCC 2400
Qy 2401 tgaagtgaagaaacctgctgagccctacagtgatcccaagcgtgtgttctctctccg 2460
Db 2401 TGAAGTTAGGAAACCTGCTCCCTACAGTATCCAGCGCTGGTGTGTTCTTCCGTCCG 2460
Qy 2461 tttttgtgtgtgaaacatctgcaatgcttctctgtagttagcaactctctcagaagcca 2520
Db 2461 TGTGTGCTGTGTGACATCTCTCACTGCTTCTGTATGACACTCTTCTCAGAGCCA 2520
Qy 2521 acctggaagacgctgtgaggagcatcatctactcaagctgtaacctgacctgacctgt 2580
Db 2521 ACCTGGACAGACGCTGGGGGATCATCTACTTACGCTGTATCCGCTTACGCTCTGT 2580
Qy 2581 gtgtgagatgagcagctagctgaggttcaactcaagcttctgtagcctgctgctc 2640
Db 2581 GTGTGAGATGACAGGATGATGAGGCTTCACTCAAGATCTTCTGCTTACCTGCTGCTC 2640
Qy 2641 ctgtgctcttgaggttgctgctgtagtacttgcccttcttgagagcagggagcttgag 2700
Db 2641 CTGTGCTCTTTGGGTTTGGCTGTGATGACTTTCCTTTTGGAGAGCAGGCAATGAG 2700
Qy 2701 tgcagtgagacaacctgttctgagagctccctgtagagaaatgagcttcaatctcaacct 2760
Db 2701 TGAGTGGGACACCTGTTTGAAGTCTGTGAGGAAAGTGGCTTCAATCTCACCACTT 2760
Qy 2761 cgaatccatgagctgttctgacaactctctctataggggtgtagaactgtatcatgag 2820
Db 2761 CGATCTCTCATGATCTCTTTGACACTTCTCTATGGGGTGAAGACTGGTACATTTGAG 2820
Qy 2821 ctgtcttccagcagtaagaaatctccagccttgatattctctgcaaccaagctct 2880
Db 2821 CTGCTTCCAGGCGCATAGCAATCCAGGCGCTGGTATTTTCTTGCACCAATCTCT 2880
Qy 2881 actggttctgagaaagatgagtagaagagcaacctgttctcaaccagaagaatgt 2940
Db 2881 ACTGGTTTGGGAGAAAGTATGAGAGACCACTGCTTCCACCAACAAAGAAATGT 2940
Qy 2941 cagaatctgcatgagagagaaaccccaactgaaagctgaggcgtgctcatcagaacc 3000
Db 2941 CAGAAATCTGATGAGAGAGAACCCACACTTGAAGCTGGGGTGTCCATTCAGAAC 3000
Qy 3001 tggtaaaagtctaccgagatgagatgaaagtgtgtcgatgagctgtgcaactaattttt 3060
Db 3001 TGGTAAAGTCTACCGAATGAGATGGAAGGTGCTGTGATGCTGGCACTAATTTT 3060
Qy 3061 atgaagggcagatcacctctctctctgagccaaatgagaggggaaagaaagacaatgt 3120
Db 3061 ATGAGGGCCATACCTCTCTCTCTGAGCCAAATGAGAGGGGGAAGAGACACACATGT 3120
Qy 3121 caatctgacgggtgtgttcccccagactgagcagcctacatccctgagaaagaca 3180
Db 3121 CAATCTGACGGGTTGTTCCTCCCGACCTTGCGCACCGCTCATCTCTGGGAAAGACA 3180
Qy 3181 ttcgctctgagatgagacccatccgcaagaacctgggggctgtgtccccaacataagctg 3240
|||||

Db 3181 TTGCTCTGAGATGAGACCATCCGAGAACCTGGGGGTCTGTCCACGATTAAGCTGC 3240
Qy 3241 tgttgacatgctgactgtcgagaacacatctgttctatgcccgtctgaaaggtct 3300
Db 3241 TGTGTACATGTGCTGATGCTGCAAGAACATCTGTGTTATGTCCCGCTTGAAGGGCTCT 3300
Qy 3301 ctgagaaacacttgaagggagagatgagagacatgagccctgtagtgtgtcttgcatcaa 3360
Db 3301 CTGAGAAAGCATGTGAAGGGCGGAGATGAGACAGATGGCCCTGGATGTTGTTGGCATCA 3360
Qy 3361 gcaagctgaagaaacaaagccagctgtcagtgagatgcaagaaagctatctgtg 3420
Db 3361 GCAAGCTGAAGAAACAAACAGCCAGCTGTAGTGAATGAGAGAAAGCTATCTGTGG 3420
Qy 3421 ccttgacctgttcggggagatctaagtgtgtatctctgtagaacccaacactgtgtg 3480
Db 3421 CCTTGGCCCTTGTGCGGGGATCTAAGTGTGTATTTCTGGATGAACCCACAGCTGTGTGG 3480
Qy 3481 acccttactccgcaagggaataatgagagctgtcgtgaatataccgaagaagccgcaaca 3540
Db 3481 ACCCTTACTCCCGCAGGGGAATATGGAGCTGTCTGTAAATACCGAAGCGCCGACCA 3540
Qy 3541 ttaatctctacacaacacatgagatgaaagcgtctgaggagaaagatgcatca 3600
Db 3541 TTATTTCTCTACACACACATGAGATGAAGCGAGCTCTTGGGGACAGGATTGCAATCA 3600
Qy 3601 tctcccaatggaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3660
Db 3601 TCTCCCATGGGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3660
Qy 3661 caagctactaccttgagcttgtagaagaatgtagaactctccctcaagcttctgtcagaa 3720
Db 3661 CAGGCTACTACCTGACCTTGTGTCAAGAAAGATGTGAATCTCCCTCACTTCTCAAAA 3720
Qy 3721 aagtagtagacactgtgtgtagaacttgaagaaagagagagagttctccagagcaattctg 3780
Db 3721 ACAGTACTACACTGCTGTCTATACCTGAAGAAAGAGAGACAGCTGTTTCTAGACACTTCTG 3780
Qy 3781 atgtctgcttgagcagagcaatgagatgagacagctgacatcgatgtctgtatct 3840
Db 3781 ATGCTGGCTGGGGACGACCATGAGATGACAGCTGACCTATCGATGCTCTGTATCT 3840
Qy 3841 ccaactccatcaaggaagcatgtgtctgaaagcccggtgtgtgaaagcataagagcatgtgag 3900
Db 3841 CCAACTCATACAGGAACCATGTCTGAAGCCCGGCTGGGGAAGACATAGGGCATGAGC 3900
Qy 3901 tgaactatgtgtgtcctatgaaagctgtgaaagagagccttgtgtgaaacttctcatg 3960
Db 3901 TGACCTATGTGCTGCTCATATGAAGCTGTGAAGAGGAGAGCTTTGTGGAATCTTTCAATG 3960
Qy 3961 agattgtagacggtctctcagacctgggcatctctagatagcatgcatcaagaagacc 4020
Db 3961 AGATTGATGACCGGCTCTCAGACCTGTGGCATTTCTGTATGTGCAATCTAGAGACACCC 4020
Qy 4021 tggaaagaatacttctcaaggtgagcgaagaagatgaggtgtgtgtgtgtgtgtgtgtgtgt 4080
Db 4021 TGGAAGAATATTTCTTAAGGTGGCCGAAAGAGACTGGGGTGTGCTGTGACACTTGAGATG 4080
Qy 4081 gtaccttgccagcaagaacgaacagcgagcctctgaggagcaagcagctgtctgtcc 4140
Db 4081 GTACCTTGCCAGCAAGACGAAGACAGCGGCGCTTGGGGGCAAGAGAGAGCTGTCTGTGAC 4140
Qy 4141 cgttcaactgaagaatgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4200
Db 4141 CGTTCACTGAAGATGATGCTGTGATCTCAATATGATTTGTGATAGACCAAGAAATTCAGAG 4200
Qy 4201 agacagactgtctcagtgagatgagatgcaaaagttctcactcaggtgtgaagagctgtgaac 4260
Db 4201 AGACAGACTTGTGCTAGTGTGATGTGATGCAAAAGGCTCTACAGAGTGAAGAGCTGTGAAC 4260
Qy 4261 ttacacagcaacagttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4320
Db 4261 TTACACAGCAACAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4320
```

OY 4321 ggaagagatltttgtcagatgtcttgcacgtgtgttgcctgcatgtccctgtgt 4380
|||||
Db 4321 ggaagagatltttgtcagatgtcttgcacgtgtgttgcctgcatgtccctgtgt 4380
OY 4381 tcagcctgcatgtgcacaccccttggcagatgaccccgccctggagactgaagcctgtgt 4440
|||||
Db 4381 tcagcctgcatgtgcacaccccttggcagatgaccccgccctggagactgaagcctgtgt 4440
OY 4441 acaagaacagtatcacatltgtcagcaatgtgtcctctgaggaacgagggagccctggaac 4500
|||||
Db 4441 ACAAGGAACAGTACACATTGTGACGATGATGCTCTTGAGGACACAGGGAACCCCTGAGAAC 4500
OY 4501 tcttaagcccttcacccaagaagaccctgtgtctggagcccgctgtatgtgaagaaaccaa 4560
|||||
Db 4501 TCTTAAAGGCCCTTCACCAAGAACCCCTGTGGACCCGCTGTATGGAAGGAACCCCA 4560
OY 4561 tcaccaagacgcccctgcagagcagggaggaagaagtgagccacactgcccagatltcccca 4620
|||||
Db 4561 TCCAGAGACGCCCCCTGCGACGAGGGAGGAAGAGTGGACACACTGCCCATGTTCCCA 4620
OY 4621 ccatcatgtgaccccttcacgaatgggaactgtgacaaatgacaaaccccttaccctgtatgc 4680
|||||
Db 4621 CCATCATGAGACCTCTTCACAAATGGGAACCTGGACATGCAGAACCCCTTCACCTGCATGCC 4680
OY 4681 agtgaagcagcagaataatcaagaatgtctgcctgtgtgtccccaagggcagggggc 4740
|||||
Db 4681 AGGTGACAGCAGCAAAATCAAGAGATGCTGCTGTGTGTCTCCACAGGGGAGGGGGC 4740
OY 4741 tgcctcctcacaaagaaacaaacacatgcagatalcccttcaggaacccctgacaggaaga 4800
|||||
Db 4741 TGCTCTCTCCACAAGAAACAAACACCTGCAGATATCTTACGAGCCCTGACAGCAAGAAA 4800
OY 4801 accttgcagatctcgtgtggaagacgtatgtgcagatcatagccaaagcttaaaagaa 4860
|||||
Db 4801 ACATTTGGGATTAATCTGGTGAAGACGTATGTACATCATACCCAAAGCTTAAAGAACAA 4860
OY 4861 agatctggtgtgaatgaatgaatgaatgtgtgtccctgtgtgtcagatataactgaag 4920
|||||
Db 4861 AGATCTGGGGTGAATGAGTTAGGTATGGGGCTTTTCCCTGGGTGTGAGTAACTACTAAG 4920
OY 4921 caacttcccgagtcagaagaagttaatgatgtccatcaaaacaaatgaaagaaacactaaagc 4980
|||||
Db 4921 CACTTCTCCGAGTCAAGAGTTAATGANGCCATCAACCAATGAAAGAACACCTAAAGC 4980
OY 4981 tggccaagagacagttctgacagatcgaattctcaagacgttggagatlttgaagagac 5040
|||||
Db 4981 TGGCCAAGGACAGTTCTGCAAGATCGATTTTCTCAACAGCTTGGAGAGATTTATGACAGGAC 5040
OY 5041 tggacacccaagaataatgtcaagtggtgttcaataacaaggtgtgcatgtcaactgaact 5100
|||||
Db 5041 TGGACACCGAATAATATGTCAAGGTGTGTTCATATACAAAGGGCTGGCATTCATTCAGCT 5100
OY 5101 ctcttcgaaatgtcaacaatgtccatcttccgggccaacactgcaaaaggaagaac 5160
|||||
Db 5101 CTTTCTGAAATGTCAATCAACATGTCATTTCTCCGGGCCAACCTCGAAAAGGGAAGAAC 5160
OY 5161 ctgacacatattggaattactgtcttcaatcactccctgtaatctcacaagaagcagctct 5220
|||||
Db 5161 CTAGGCAATATGGAATTAATGCTTCAATTCATCCCTGTAATCTCACCAAGAGGAGCTCT 5220
OY 5221 gaggagtgctgtgtgacacatcagtgagatgtccctgtgtcactgtgtcatgtgtcatcttg 5280
|||||
Db 5221 CAGAGGTGCTGTGATGACCAATCAGTGAATGTCCTTGTGTCCATCTGTGTCATCTTTTG 5280
OY 5281 caatgtcctcgtcccaagcagcttgcgtatccttcgatccagaagcagggatgagcaag 5340
|||||
Db 5281 CAATGCTCTGTGTCACAGCAGCTTTGTGATTTCTGATTCAGAGGAGGAGGCTACGCAAG 5340
OY 5341 caaaacacctgagttcatcagtgagtgagtgagcctgtcatctactgtgtcttaatttg 5400
|||||
Db 5341 CAAAACCTGTGATTCAGTGAAGTGAAGCTGTGATCTACTGTGCTCTTAATTTTG 5400

OY 5401 tctggagatgtgaattacgttgccttgcacacactgtgtcatatcatcttcatctgt 5460
|||||
Db 5401 TCTGGGATGATGTCAATTAAGCTGTGTCTCCGCCACACTGGTCAATTATCATCTTCACTCTCT 5460
OY 5461 tccagagaagtcctatgtgttcttcacacaaatcgtcgtgtgtatgaccccttactgtgc 5520
|||||
Db 5461 TCCAGCAGAAGCTCTATGTGTCTCCACCAATCTGCTGTGATGAGCCCTTACTTTTGGC 5520
OY 5521 tgtatgtgtgtgaatcaaacctctcatgttacccagcccttctgttcaagaatcccca 5580
|||||
Db 5521 TGTATGGGTGTGAATTCACACTCTCTATGTACCCAGCCCTCTTGTGTCAAGATCCCA 5580
OY 5581 gcaagcctatgtgtgtcctcaacagcgtgaaccccttcatltgtgcatltatgtgcagcgtg 5640
|||||
Db 5581 GCACAGCCTATGTGTGTGTCTACACAGCGTGAACCTCTTCAATTGAGCATTAATGGACGCTGG 5640
OY 5641 ccaaccttgtgtcgtgagcgtgtcaccgacaataaagctgaataatacaatgatatcctga 5700
|||||
Db 5641 CCACCTTTGTGTGAGAGTGTTCACCGACAAATTAAGCTGAATTAATGATATATCTCTGA 5700
OY 5701 agtgcgtgttctgtatcctccacatlttgccttggagcagaggtgtatgagatgtga 5760
|||||
Db 5701 AGTCCGTGTCTTGATCTTCCACATTTTGTGCTGGAGAGAGGCTCATTCACATGGTGA 5760
OY 5761 aaaacaggaatgtgtgtatgtcccttgaagaaaglttggggagaatcgtcttgttcaacat 5820
|||||
Db 5761 AAAACAGGCAATGCTGTATGCTGTGAAGAAAGTTTGGGAGAAATGCTTTGTGTGCACCAT 5820
OY 5821 tatcttggagactgtgtgtgaagaagaaccccttgcacatgctgcgtgtgaaggggtgtctc 5880
|||||
Db 5821 TATCTTGGGACTGTGGTGGAGCAAAACCTTTCGCATGAGCCGTGGAAAGGGTGTGTCT 5880
OY 5881 tcccatlactgttctgtatccagtaacagatcttcatcagcccaagcccttaaatgcaa 5940
|||||
Db 5881 TCCATTAATCTGTGTGATTCAGTACAGTATCTTCTCATCAGGCCACAGACCTTAATGCAA 5940
OY 5941 agctatctcctctgtatgtatgaatgaatgtgaagtcgagggcgggaagacagaaatcttg 6000
|||||
Db 5941 AGCTATCTCTCTGTGAATGTGAAGATGTGAGCGGGGAAAGACAGAAATTCCTTG 6000
OY 6001 atgtgtgaagcagaatgtacatctagaatcaagaagttgaagaagatatagaagga 6060
|||||
Db 6001 ATGTGTGAAGCAGAAATGACATCTAGAAATCAAGAGATTACCAAAATATATAGAAAGA 6060
OY 6061 agcggagacccgtgtgtgaagatgtgcgtggacatccctcctgtgtgagtgcttggc 6120
|||||
Db 6061 ACGGGAAGCCTCTGTGACAGGATTTGCGGGCATTTCCCTGTGAGATGCTTTGGGC 6120
OY 6121 tccctggagttaatgtggcgtggaataatcaacttccaagatgttgaaggagatacca 6180
|||||
Db 6121 TCTGGGAGTTAATGGGCTTGAAAAATCATCACTTTTCAGATGTTAACAGGAAATACCA 6180
OY 6181 ctgtttacagaagagatgtcttcccttaacaaaataglatcttcatcaaacatccatgaag 6240
|||||
Db 6181 CTGTTACCAAGAGAGATCTTCTTAAACAAAATATATCTTAATCAACATCATGAAG 6240
OY 6241 tacatcagaagaatgt 6300
|||||
Db 6241 TACATCAAAATGAGGCTACTGCTCAGTTGTGATGCAATACAGAGCTGTGAGTGA 6300
OY 6301 gagaacagctgtgagttcttgccttlttgagagagtcaccaagaagaagaagttgtgaag 6360
|||||
Db 6301 GAGAACAGCTGTGAGTTCTTTCCTTTTGAAGAGAGTCCAGAGAAAGAAAGTTGGCAAG 6360
OY 6361 ttgt 6420
|||||
Db 6361 TTGT 6420
OY 6421 actatagtgagagcacaacagcagctctcacaagcagtggttggatcggggccctc 6480
|||||
Db 6421 ACTATAGTGAAGGAGCAAAAGCAAGCTCTCTACAGCATGAGCTTTGATCGGGGCTCTC 6480
OY 6481 ctgtgtgtgttctgtatgtgaacccaacaggaatgtatcccaagcccggtgttctgt 6540

QY	9781	ACTGAAGAATGCTTTGTGACATATTAATGTTGGACATCAATTCATTACATGTTATATA	9840
QY	9781	actggaagaacaatgctttgtgacattaaatgttgacaatcatcttaacgtatagta	9840
QY	9841	accattgactaaagccattgctgctgttctctctctgtggnlgnatatacagtaaat	9900
QY	9901	atttccaaagagccatgctgcatgtaatactgaacccttgatatgaagaaatttt	9960
QY	9901	attttccaaagagccatgctgcatgtaatactgaaccctttgatatttgagcatttaatt	9960
QY	9961	ggacccttggtattactactactagaataatgtaactgnaagaatactgcttaattctt	10020
QY	9961	ggacccttggtattactactactagaataatgtaactgnaagaataatgcttaattctt	10020
QY	10021	tcaaaatgctgcatccccccttaaaagttctatattccataaagattgctgcttatcc	10080
QY	10021	tccaaatgctgcatccccccttaaaagttctatattccataaagattgctgcttatcc	10080
QY	10081	cttctatacccttaagaatgaagctgttttctgtctctgtgttcaatcatgagccctcattc	10140
QY	10081	cttctatacccttaagaatgaagctgttttctgtctctgtgttcaatcatgagccctcattc	10140
QY	10141	caagcactttagcgtctgctgtaatggatctatltttgcactggaatactggaattgc	10200
QY	10141	caagcactttagcgtctgctgtaatggatctatltttgcactggaatactggaattgc	10200
QY	10201	aaactagacaaaagtttccacaacagatcttcaagttaatcatlttcatlaaaggaaa	10260
QY	10201	aaactagacaaaagtttccacaacagatcttcaagttaatcatlttcatlaaaggaaa	10260
QY	10261	aaagaaaaaaatttgtatgtaataactttatatgaagttaaaatgacataattcta	10320
QY	10261	aaagaaaaaaatttgtatgtaataactttatatgaagttaaaatgacataattcta	10320
QY	10321	tgttctaataatgagtcacaataaagcgtgacagttctgttaaaaaaa	10380
QY	10321	tgttctaataatgagtcacaataaagcgtgacagttctgttaaaaaaa	10380
QY	10381	aaa	10440
QY	10381	aaa	10440
QY	10441	aa	10442
QY	10441	aa	10442
Db	10441	AA	10442
RESULT	2		
AX060892		10442 bp	DNA
LOCUS			
DEFINITION	Sequence 1 from Patent WO0078971.		
ACCESSION	AX060892		
VERSION	AX060892.1		
KEYWORDS			
SOURCE			
ORGANISM	human.		
REFERENCE	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 10442)		
REFERENCE	Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.		
REFERENCE	Alp binding cassette transporter protein abcl polypeptides		
REFERENCE	Patent: WO 0078971-A 1 28-DEC-2000;		
REFERENCE	CV THERAPEUTICS, INC. (US)		
FEATURES	Location/Qualifiers		
FEATURES	1..10442		
FEATURES	/organism="Homo sapiens"		
FEATURES	/db_xref="taxon:9606"		
BASE COUNT	2898 a	2297 c	2408 g
ORIGIN	2835 t	4 others	

Query Match	100.0%;	Score 10438;	DB 6;	Length 10442;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 10442; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;	
Oy 1	gacccgagaccccgagacccgagccgacccctctctcccgagctcgcgcagagagcgcg 60				
Db 1	GGCCGGGACCCGCGAGCGCGAGCCGACCTCTCTCCGGGGCTGGCGCAGGCGGCG 60				
Oy 61	ggagctccgcgcacacaagagcggtctcgaaggcgcttgctcctgttttcccg 120				
Db 61	GGAGCTCCGCCACACACAGAGCGGTTCTCAGGCGCCTTGGCTTCGTTTTCGCCG 120				
Oy 121	gttcgttttccctctcccgaaagcgctgtcaagggatgaggaagaagacgcgaac 180				
Db 121	GTTCGTTTCTCCCTTCTCCGGAAGCGCTGTCAAGGGGTAGAGAAAGACGCAAC 180				
Oy 181	acaaaagtggaaaacaglttaatgaccagccagcgcgctccctgtgtagctctgcgc 240				
Db 181	ACAAAAGTGGAAAACAGTTAATGACCAACCCAGCGCGCTCCCTGCTGTAGCTCTGGCCG 240				
Oy 241	tgccctccaggggtcccgagccacacgcttgagcgctgtcgtcgttgagggaatagctggt 300				
Db 241	TGCCCTTCCAGGGCTTCCGAGCCACACGCTGGCGTGTGCTGAGGGAACATGGCTTGT 300				
Oy 301	ggcctcaagctaggtgtgtcgtgtgtaagaaactcaacttcaagaagaacaaatgtc 360				
Db 301	GGCCTCAGCTAGGTTGTCGCTGTGAGAACCTCACTTCAGAAAGACAAACATGTG 360				
Oy 361	agcgttactgtgaagtgtgcctgacctattatcttcctatcctgtatctcttcggc 420				
Db 361	ACCTGTACTGTGAAGTGGCTGTGGCTCTATTATCTCTGATCTGTACTGTGTGTGGC 420				
Oy 421	tgagctaccaccccatgacacaca tgaatgcatcttccaaatlaaagccatlgccctgt 480				
Db 421	TGAGCTACCCACCCATATGACAAACATGAATGCATTTTCCAAATTAAGCCATGCCCTGTG 480				
Oy 481	caggaaacctctcttgggttcaagggatatctgtaatgtgcaaacacccctglttcgt 540				
Db 481	CAGGAACACTTCTCTGGGTTTCAGGGGATTATCTGTAATGCCAACACCCCTGTTTCCGTT 540				
Oy 541	accgcactctcgggagaggtcccgaggtgtgtgtgaaacttaacaatccatctgtgtc 600				
Db 541	ACCCGACTCTTGCGAGAGGCTCCCGAGTGTGTGGAACCTTAAACAATTCATGTGGGCTC 600				
Oy 601	gacctgtctcagaatgtctcgaggtctcttcttatacagccagaagaacacagcatgaag 660				
Db 601	GCCTGTTCTCAGATGCTCGAGGCTCTTATTATACAGCCAGAAAGACACACATGAAGG 660				
Oy 661	acatgtgcgaagtctcgaacaattacagcaatcaagaataccaggtcgaacttggaagc 720				
Db 661	ACATGTGCGAAAGTTCTGGAAMACTTTCACAGCAATCAAGAAATCCAGCTTAAACTTGAAC 720				
Oy 721	ttaacaatctccctggtgagcaatgaaacctctctgtgttccctatacaaacctctctc 780				
Db 721	TTCAGATTTCCTGSHGGAACAATGAACCTCTCTGGGTTCTATATACAACTCTCTC 780				
Oy 781	tcccaaatctactgtggacaagaatgtctgaaggctgtatgtcaattctccacaagratitt 840				
Db 781	TCCCAAAAGTCTACTGTGTGACAAAGATCTGAAGGCTGATGTCTATCTCCACAAGGATTTT 840				
Oy 841	tgcgaagctacccgattacatttgaacaagctgtgcataatgatacaaatagaagaatga 900				
Db 841	TGCAAGCTACCAATTACATTTGACAAGTCTGTGCAATGGAATGCMAAATCAGAAAGATGA 900				
Oy 901	ttaaaactgtgtgacaaagaagttctgtgagcttgtgtgctaccaaagggaactgtgctg 960				
Db 901	TTCAACTTGTGTGACAAAGATTTCGTGAGCTTGTGTGGCTTACCAAAAGGAACATGTGCTG 960				
Oy 961	cagaagcgagatgactctgttccaactgtgacatctctgaagccaatccctgagaacataa 1020				
Db 961	CAGAGCGAGATCTTCTGTCCACACATGACATCTCTGAAGCCAATCTGTAGAAACACTTA 1020				
Oy 1021	acttcaatctccctccgagcaagagactgtgcgtgaagccacaacaaacattgtctcata 1080				

Db	1021	ACTCTACATCTCCCTTCCCGAGACAGAGACTGGCTGAAGCCACCAAAACATTGCTGCATA	1080
Oy	1081	gtcttgagactctcgagccagagagctgttctcagatctagaagcttgatgtacatgagcagag	1140
Db	1081	gtcttgagactctcgagccagagagctgttctcagatctagaagcttgatgtacatgagcagag	1140
Oy	1141	aggtgatgtttctcgaccaatctgaaacagctccagctctctccaccaaattaccagctg	1200
Db	1141	AGGTGATGTTTCTCGACCAATGTGAACAGCTCCAGCTCTCCACCAATATCTACAGAGCTG	1200
Oy	1201	tgctctgatctgtctcgagagcaccagagaggggagctgaagaatcaagtcctctaact	1260
Db	1201	TGCTCTGATTTGTTCTGGGGCATCCCGAGAGGGGGCTGAAGATCAAGTCTCTCACT	1260
Oy	1261	ggtatgaggaacaacaactatacaagccctcttggagagcaatgagcaatcgaggaagatgctg	1320
Db	1261	GGTATGAGGACAAACATCAAAAGCCCTTTGGAGGCAATGGCACTGAGAGAGATGCTG	1320
Oy	1321	aaacctctatagaacaactctacaaccccttactgcaatgattgatgaagaatltggagt	1380
Db	1321	AAACCTTTATGACAACTCTACAACTCTTACTGCAATGTTGATGAAGATTGGAGT	1380
Oy	1381	ctgagtcctcttcccgcatatctggaagaactcgaagcgcgtcgtctgttggagaatcc	1440
Db	1381	CTAGTCCTCTTCCCGCATTTATCTGGAAGAGCTGTAAAGCCGTGCTGCTTGGAGATCC	1440
Oy	1441	tgataaacctcgaaactccagagcaagcagatgatgactggaagtgaacaagacctcc	1500
Db	1441	TGTATACCTGAGACATCCAGCCCAAGAGAGGTCAATGGCTGATGATGAACAAAGACTTCC	1500
Oy	1501	aggaaactgagctgtgttccatgatlctggaagcaatgtaggaagaaactcagcccaagatc	1560
Db	1501	AGGAACCTGGCTGTCTCCATGATCTGGAAAGCATGAGGAGAACTCAGCCCCAAGATCT	1560
Oy	1561	ggaccttcaatgagaaacagccagaagaatgagcttgtccggaatgtgtgttgaacgcagg	1620
Db	1561	GGACCTTCAATGAGAAACAGCCCAAMAAATGACCTTGTCCGATGCTGTGGACAGCGAGG	1620
Oy	1621	acaatggaacacttctggaaacagagtttgatgtgtctatgtgaacagcccaagacaatcg	1680
Db	1621	ACAAATGACACTTTTGGGAACAGAGTGTGATGGCTTAATTGGACAGCCCAAGCATCG	1680
Oy	1681	tggagcttlttggccaagcaccagagaatgttccagtcagtaatgtgtctgtgtacacct	1740
Db	1681	TGGCGTTTTTGGCCACAGCACCCAGAGATGTCCAGTCACGATATGTTCTGTGATACCT	1740
Oy	1741	gagagagaagcttcaaagagacttaacagagcaatccagagcaatctcgtcttcaatggagt	1800
Db	1741	GGAGAAACACTTTTCAACGAGACTAACCAAGCAATCCGGACATATCTGCTTCATGAGGT	1800
Oy	1801	gtgtcaacctgacaagcttagaaccacaatgaacaagaatctgtgctatcaacaagaatcca	1860
Db	1801	GTTCAACCTGAAACAGCTTAGAACCCATPACACAAAGCTGTGGCTCATCAACAAGTCCA	1860
Oy	1861	tggagctctgtgaaatgaagaggaagttctgggctgtgattgtttcaactggaattactcag	1920
Db	1861	TGGAGCTGCTGGATGAGAGGAAGTTCTGGCTGTGATTTGTTCACTTGSAAATTACTCCAG	1920
Oy	1921	gagagactgagctgcccatactgttcaagtatacaagaatccgaatgagcaattgacaatgtg	1980
Db	1921	GCAGCAATTAGCTGCCCATCATATGTCAAAATCAAAATCCGAATGCAATTCGACATGTGG	1980
Oy	1981	agaagacaataataatcaaggaatggtgtactvggagccctgtgtctcgagtvgaccccttg	2040
Db	1981	AGAGGACAAATTAATTAAGATGGGTACTGGGACCTGTGATCTTCAGAGCTGACCCCTTTG	2040
Oy	2041	agaagactgagatgactctcgagggagcttgcgctaacttgcaggaatgtgtgtgtagcagga	2100
Db	2041	AGAGCAATGCGGTACGTCTGGGGGGCTTCGCTACTTGCAGAGATGTGTTGGAGAGGCAA	2100
Oy	2101	tctacagggctgctgacgagcaccgagaagaactgtgtctatatagtcaacagatgacct	2160

Db 2101 TCATCAGGCTCTACGCGGACCGAGAAAGAACTGGTGTCTATATGCAACAGATGCCCT 2160
QY 2161 atccctgttactgtatgatacattcttcggtgtatgagccggtcaagcccccttca 2220
Db 2161 ATCCCTGTTAGCTTGATGACATCTTTCTGGGGGATGAGACCGGTCAATGCCCTTTCA 2220
QY 2221 tgaagcttgcttgatattactcaatgagctgtatgatacagaagcatcgtatgaaag 2280
Db 2221 TGAGCTGGCTGGATTACTCACTGGCTGTGATCATCAAGGGGCAATCGTATGAGAAAG 2280
QY 2281 agcaacgctgaagagacatgagatcaatgagccctgagcaacagacatacttggtta 2340
Db 2281 AGGACGGCTGAAGAGACCATGGGATCATGGGCTGGACACACATATCTTGTTTA 2340
QY 2341 gctgttcaatagtacacctaatcctctcttctgtagcagctgagctgagtgtatcc 2400
Db 2341 GCTGTTCAATTAGTAGGCTTATTCCTCTCTGTGAGCGCTGGCTGCTAGTGTATCC 2400
QY 2401 tgaagttagaagaacctgtccctacagtgatccagcgtgtgtgttctcctgtccg 2460
Db 2401 TGAAGTTAGGAACCT 2460
QY 2461 ttttctgt 2520
Db 2461 TGTTTGT 2520
QY 2521 acctgagcagcctgt 2580
Db 2521 ACCTGAGCAGCCTGT 2580
QY 2581 gttgt 2640
Db 2581 GT 2640
QY 2641 ctgt 2700
Db 2641 CTGT 2700
QY 2701 tgcagtgaggaacacctgt 2760
Db 2701 TGCAGTGAGGAACACCTGT 2760
QY 2761 cgaatccatgagctgt 2820
Db 2761 CGAATCCATGAGCTGT 2820
QY 2821 ctgtcttccagccagtaacggaatcccaagccctgtgtgtgtgtgtgtgtgtgtgtgt 2880
Db 2821 CTGTCTTCCAGGCCAGTACGGAATCCAGGCCCTGTGTGTGTGTGTGTGTGTGTGTGT 2880
QY 2881 actgt 2940
Db 2881 ACTGT 2940
QY 2941 cagaatactgcatgagaggaacccacccacttgaagcttgagcgtgtgtgtgtgtgtgt 3000
Db 2941 CAGAAATCTGCATGAGAGGAGAACCCACCCACTTGAAGCTGGGGCTGTGTGTGTGTGT 3000
QY 3001 tggtaaaagtctacccagatgagatgagatgagatgagatgagatgagatgagatgag 3060
Db 3001 TGGTAAAGTCTACCCAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3060
QY 3061 atgagagccagatgagatgagatgagatgagatgagatgagatgagatgagatgag 3120
Db 3061 ATGAGAGCCAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3120
QY 3121 caatccctgagcgt 3180
Db 3121 CAATCCCTGAGCGGTTGT 3180
QY 3181 ttcgctctgagatgagatgagatgagatgagatgagatgagatgagatgagatgag 3240
Db 3181 TTCGCTCTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3240

QY 3241 ttttgaacatgctgagctgt 3300
Db 3241 TTTTGAACATGCTGAGCTGT 3300
QY 3301 ctgagaagcagctgt 3360
Db 3301 CTGAGAAGCAGCTGT 3360
QY 3361 gcaagctgt 3420
Db 3361 GCAAGCTGT 3420
QY 3421 ccttgagcctgt 3480
Db 3421 CCTTGAGCCTGT 3480
QY 3481 acccttactccgcaaggt 3540
Db 3481 ACCCTTACTCCCGAAGGGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3540
QY 3541 ttattctctac 3600
Db 3541 TTATTCTCTAC 3600
QY 3601 tctcccatggaagctgt 3660
Db 3601 TCTCCCATGGGAAGCTGT 3660
QY 3661 caggtctactaacctgt 3720
Db 3661 CAGGTCTACTAACCTGT 3720
QY 3721 acsagt 3780
Db 3721 ACAGT 3780
QY 3781 atgt 3840
Db 3781 ATGT 3840
QY 3841 ccaactctacaggaagcgt 3900
Db 3841 CCAACTCTACAGGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3900
QY 3901 tgaacctgt 3960
Db 3901 TGAACTGT 3960
QY 3961 agatgt 4020
Db 3961 AGATGT 4020
QY 4021 tggagaagaatctctcaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4080
Db 4021 TGGAGAAGAATCTCTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4080
QY 4081 gtaaccttgccaagaagaaagagagagagagagagagagagagagagagagagagag 4140
Db 4081 GTAACCTTGCCAGCAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4140
QY 4141 cgttcaactgaagatgt 4200
Db 4141 CGTTCAACTGAAGATGT 4200
QY 4201 agacagactgt 4260
Db 4201 AGACAGACTGT 4260
QY 4261 ttacaacgaacagttgt 4320
Db 4261 TTACACGACACAGTTGT 4320

```
QY 4321 ggaagagatlttctgcaagatgtctgcaagctgtgttctgcatgtccctgtgt 4380
|||||
Db 4321 ggaagagatlttctgcaagatgtctgcaagctgtgttctgcatgtccctgtgt 4380
QY 4381 tcaagctgagtgctgcaagctgtgcaagatgccccagctggaattcgaagctgtgt 4440
|||||
Db 4381 tcaagctgagtgctgcaagctgtgcaagatgccccagctggaattcgaagctgtgt 4440
QY 4441 acaagcaagatgacatlttgcaagcaatgtctcctggaagcaaggaacctgtgaac 4500
|||||
Db 4441 acaagcaagatgacatlttgcaagcaatgtctcctggaagcaaggaacctgtgaac 4500
QY 4501 tcttaaacgccccccaagaaagccctgtgctggaagccccgtgtatgtgaagaaacccaa 4560
|||||
Db 4501 tcttaaacgccccccaagaaagccctgtgctggaagccccgtgtatgtgaagaaacccaa 4560
QY 4561 tcccaagacgccccccaagaaaggaaggaaggaaggaaggaaggaaggaaggaaggaagga 4620
|||||
Db 4561 tcccaagacgccccccaagaaaggaaggaaggaaggaaggaaggaaggaaggaaggaagga 4620
QY 4621 ccatcagacgtctctccagaaatggaaactgacaatgcaagaaacctcactgcatgac 4680
|||||
Db 4621 ccatcagacgtctctccagaaatggaaactgacaatgcaagaaacctcactgcatgac 4680
QY 4681 agttagcagcgaacaatacaagaagatgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4740
|||||
Db 4681 agttagcagcgaacaatacaagaagatgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4740
QY 4741 tgcctccccaagaagaacaacaacactgcaatatacctcagaagccctgacaggaagaa 4800
|||||
Db 4741 tgcctccccaagaagaacaacaacactgcaatatacctcagaagccctgacaggaagaa 4800
QY 4801 accttcgcatatctgctggaagagctatgtgcatgatacgaacaagacttaagaaca 4860
|||||
Db 4801 accttcgcatatctgctggaagagctatgtgcatgatacgaacaagacttaagaaca 4860
QY 4861 agatctgagtgaaatgagttatgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 4920
|||||
Db 4861 agatctgagtgaaatgagttatgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 4920
QY 4921 caactcctccagtgcaagaagttaatgagtgagtgagtgagtgagtgagtgagtgagtgag 4980
|||||
Db 4921 caactcctccagtgcaagaagttaatgagtgagtgagtgagtgagtgagtgagtgagtgag 4980
QY 4981 tggccaagagcagctgtgcaagatgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 5040
|||||
Db 4981 tggccaagagcagctgtgcaagatgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 5040
QY 5041 tggcaacagagaataatgtcaagatgtgtgtcaatacaagaagctgtgcaatgcaatgcaatgca 5100
|||||
Db 5041 tggcaacagagaataatgtcaagatgtgtgtcaatacaagaagctgtgcaatgcaatgcaatgca 5100
QY 5101 cttctcctggaatgcaacaataatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgca 5160
|||||
Db 5101 cttctcctggaatgcaacaataatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgca 5160
QY 5161 ctgagcattatggaattactgcttcaatcatcaccctggaatgcaatgcaatgcaatgcaatgcaatgca 5220
|||||
Db 5161 ctgagcattatggaattactgcttcaatcatcaccctggaatgcaatgcaatgcaatgcaatgcaatgca 5220
QY 5221 caagagtgagctgtgcaacacatcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 5280
|||||
Db 5221 caagagtgagctgtgcaacacatcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 5280
QY 5281 caatgtcctgctcccaagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5340
|||||
Db 5281 caatgtcctgctcccaagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5340
QY 5341 caaaacacctgagtgatcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 5400
|||||
Db 5341 caaaacacctgagtgatcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 5400
QY 5401 tctggagatgtgcaatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 5460
|||||
```

Db 6481 CTGTGTTTCTTGATGAACCCACGACGATGATCCAAAGCCCGGCTTCTGT 6540
Qy 6541 ggaatttgccttaagtggttcaagaaggagatcagtaagtgttacctatcaatga 6600
Db 6541 GGAATGTGCTTAAGTGTGTCAAGAGGAGATCACTAGTGTCTTACATCTCATAGA 6600
Qy 6601 tgaagaatltgaagctcttctgcataggaatgaatcagtcagtcagtcagtcagtc 6660
Db 6601 TGAAGAATGTGAAGCTCTTGTGACATGATGATGATGATGATGATGATGATGATG 6660
Qy 6661 gcccttgcaatgtcccaagatcctaaataagtttggagatggttatcaatagttgac 6720
Db 6661 GCCCTTGCAATGTCCCAAGATCCTAAATAAGTTTGGAGATGTTATACAAATAGTTGAC 6720
Qy 6721 gaataagaggtcccaagcctgaagcctgctcagagatcttcttgacttgatctc 6780
Db 6721 GAATAGAGGCTCCCAAGCCTGAAGCCTGCTCAGAGATTTCTTGGACTTGCAATTC 6780
Qy 6781 ctggaagatgtctaaagaagaacacaggaacatgtctacatacagcttccatctcat 6840
Db 6781 CTGGAAGATGTCTTAAAGAGAAACACGAGACATGCTACATATACAGCTTCATCTTCAT 6840
Qy 6841 tatcttctcagcagatatacagatctctcctcagagacaaagcagactcacaatag 6900
Db 6841 TATCTTCTCGCCAGATATTCAGATCTCTCCAGAGCAAAAGGACTCCACATAG 6900
Qy 6901 aagaactactgttctcagacaacacttgaccagatattgtgaacttggcagaagcc 6960
Db 6901 AAGACTACTGTCTTCTCAGACAACACTTGACCAAGTATTTGTGAACCTTGCCAAAGACC 6960
Qy 6961 aagtgatgaatccactaaagaacctctctctacacaaacacagacagtaagtgaag 7020
Db 6961 AAGTGATGATCCACTAAAGAAAGCTCTCTCTACACAAAACACAGACACTAGTGGACG 7020
Qy 7021 ttgcaatltcacaatcttctcagagatgaagaagtgaagaagcctgatatgaaga 7080
Db 7021 TTGCAATCTTCACATCTTCTTACAGAGATGAGAAAGTAAAGTAAAGTAAAGTAA 7080
Qy 7081 tctgttctcagaggtgtgctgaagaatgaagaagcagacttcttcttgaccatgtg 7140
Db 7081 TCTGTCTCTTACAGGCTGTGCTGAAGTAAAGAGAACTAGACTTTCCTTGCACATCTG 7140
Qy 7141 aagtgcttggaagaagaagcagagaagtgtgtgtggaagaagaatcagatcagctac 7200
Db 7141 AAGTGCTTGGAAGAAAGCCAGAGATGATGAGGAGAAAGTAAAGTAAAGTAAAGTAA 7200
Qy 7201 tgaatactatcagcaatgtcaatcagatgaagaagaacaaatctcattacagggca 7260
Db 7201 TGATACTATTCATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 7260
Qy 7261 gfgccttggtagcctatgtctgtatgtctcagtgcaagtgaagaactgaattagtttt 7320
Db 7261 GFGCCTTGGTAGCCTATGTCTGTATGTGCTGCTCAAGTGAAGACTTTAAATTTAGTTT 7320
Qy 7321 acctatacctatgtgaacatctatatagaaccacatgagacatagggttgaactaca 7380
Db 7321 ACCATACCTATGTGAACCTATATATGAGAACCAATGAGACATATGAGTTGAACAC 7380
Qy 7381 ctttttttttttttttctgtctgtgtatctcattggggtgtgacaataatcattcaag 7440
Db 7381 CTTTTTTTTTTTTTTTGTCTGTGTATTCATTTGGGGTGGCAACAATAATTCAACAG 7440
Qy 7441 taatcatggcagcagatattgatcaaatcaaatgaaggtaatgacatccctacatca 7500
Db 7441 TAATCATGGCAGAGATATATGATCAAAATCAAAAGTAAATGACATCCCATTCATCA 7500
Qy 7501 gccatgcatgcccagagagactgttcccggtgacacatcactgtcgtgcaatgagtg 7560
Db 7501 GCCATGCGATGCCAGAGAGACTGTTCGCGGTGACACATTCATGCTGGCAATGAGTGT 7560
Qy 7561 gccagagttatagtgccaagttttcagaagaattgaagacacatggtgtcagtgctc 7620
Db 7561 GCCAGAGTTATAGTGCCAAAGTTTTCAGAAAGTTTGAACACCAATGATGTGTGATGCTC 7620

Qy 7621 acttttgaaagctgtctcgtcagagatcctacacattgaataatcagttgacagaatg 7680
Db 7621 ACTTTTGTGAAGCTGTCTGCTGACAGCTCTATCAACATGATATGATGATGATGATG 7680
Qy 7681 gtcacatgctgtgctacacatcctgcttgaatccctcgtataagctgtctgtgagat 7740
Db 7681 GTCCATGCTGTGCTGAACATCTGCTTGTATTCCTCTGATTAAGCTCTTGTGGGAGT 7740
Qy 7741 aacatgcaacaaatggtgtgtcctcagagaggaagactgttctcattgtatatt 7800
Db 7741 AACATGCAACAAATAGTGGTGTCTCTAGCAGCGGAACCTGCTTCATGTTATAT 7800
Qy 7801 gtccatgcttcagacatgggtctcagaggtcactcattagactcctlaataact 7860
Db 7801 GTCCATGCTGTGAGGCAAGGCTCTACAGGCTCATCTTATGAGACCTCTTAATATAC 7860
Qy 7861 agatcctgtgaagagcagaagaatcaacagccaactgtgtggtctgcaagctgtgaag 7920
Db 7861 AGATCCTGTGAAGAGCAAGATCAACAGCCAACTGCTGGGCTGCAACCTGCTGAAG 7920
Qy 7921 ccagggcatgggattaaagaatgtgtcgtcaaacctagaagagcctgtgcccattgt 7980
Db 7921 CCAGGCAATGGGATTAAGAGATGTGGCTTCAAACTAGGGAAGCCGTGGCCATTTGT 7980
Qy 7981 cctgactgtctgtacatgtgtacactgtcactcaagaatgttactcgtacacaaagtat 8040
Db 7981 CCTGACTGTCTGTCAACATGATGATCACTCATCTCAAGATGTTTATCGACAAAGTCTAT 8040
Qy 8041 tatlcttgcttcttgaatlaactcagaataatgaataatgaatgttatatttgaacaaa 8100
Db 8041 TATTTCTGCTTTTGAATTAATCTAGAAATGAAGAATGAGATTTATTTTACAAAA 8100
Qy 8101 atgttctgacttcttaagtatttgaatttcaagttcactcaagtgactctgaaacct 8160
Db 8101 ATGTTTGAATCTTTTAAAGTTATTTGGAATTTTAAAGTTTATCATGATCTTGAATCT 8160
Qy 8161 tagaatggcctcttctgaagaccctgtgtgtatagaagaatgacacacacacatt 8220
Db 8161 TAGAATGGCCTCTTTGTGAACCTGTGTGTATAGAGAGATATGGCCCTGCCACCTAAT 8220
Qy 8221 ttatcttctatgtaagtgtgacatcagatcagactgtgactgaagaagaatgtat 8280
Db 8221 TTTATTTCTTATGAATGATTTGATATCAGATCAGTACTAGTGCCTAGAAAGCAATGTAT 8280
Qy 8281 ggtcagagatctcagacatctatattgaatttcttcttaagatcattgaactctaat 8340
Db 8281 GGTCAAGATCTCAGATCTATATTTAGATTTCTTTCAGATCTATTAAGATCTTAAAT 8340
Qy 8341 ctcaatcacaatcaaatatttcttgatgtatgtcgtgacgtgaagaagatgtatcgt 8400
Db 8341 CTCACCTTCATCAATCAATATTTTGTGATGATGATGATGATGATGATGATGATGATG 8400
Qy 8401 cgtataagacactagagatataatgaatcagatcagactcctgtgcaatglatcaagtc 8460
Db 8401 CGTATAAGACACTAGAGATATTTAGTCTCAGTACACTTCTGTGCCATGTATTTAGCTC 8460
Qy 8461 actggttacaataatagatgtgtctgtgtgtgtagaagccactgttaacaatatgggc 8520
Db 8461 ACTGTTTACAAATATAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8520
Qy 8521 agcctttttttttttttttaaattgcaacaaatgcaaaagccaagaagaatataaggtcac 8580
Db 8521 AGCCTTTTTTTTTTTTTTAAATTGCAACAAATGCAAAAGCAAGAAAGTAAAGGCTCAC 8580
Qy 8581 aagttlaaacaatgaatctcacaaggggaacacagctgttgaataactgtcgaataa 8640
Db 8581 AAGTTTAAACAATGAATTTCTTCAACAGGGAACACCTAGCTTGAAACCTTCTGAAAAA 8640
Qy 8641 cacactgtgttattagcaatcttgaactcacaataatgtgcttgcagatattgata 8700
Db 8641 CACAACCTGTGTATTAGGCAATTTAGTACCTTCAAAATATTTGGCTTTGCAAGATATTGATA 8700

Qy	8701	ccccatbaactcgacagctctcgaatttttcaattctcttcaataccacgctcagaagaaaaata	8760
Db	8701	ccccattaaatcgacagctcgaatttttcaattctcttcaataccacgctcagaagaaaaata	8760
Qy	8761	taaaacaacaatacttcacatcgagacattttccagatttctcaaccgagctctat	8820
Db	8761	taaaacacacaaatcttcacatcgagacattttccagatttctcaaccgagctctat	8820
Qy	8821	tttcctagtcagtaaacatttctgaanaaatactggtttccaaatactactactgtaactgctt	8880
Db	8821	tttctagtcagtaaacatttctgaanaaatactggtttccaaatactactactgtaactgctt	8880
Qy	8881	tggagagaaaaaataatagagagacattggtttggagagtcgaatgtaacttccat	8940
Db	8881	tggagagaaaaaataatagagagacattggtttggagagtcgaatgtaacttccat	8940
Qy	8941	atactactactctctccacatttcccaaaatttgtaatactaaagcgtaaagtgtaaga	9000
Db	8941	atactactactctctccacatttcccaaaatttgtaatactaaagcgtaaagtgtaaga	9000
Qy	9001	cttcagatctcaaatcttaactcttcatatttttaaatcttcagaataatataccca	9060
Db	9001	cttcagatctcaaatcttaactcttcatatttttaaatcttcagaataatataccca	9060
Qy	9061	ctctgtaaaaaaagaanaattgatttcttgaagaagttaagccaatltgttttaaat	9120
Db	9061	ctctgtaaaaaaagaanaattgatttcttgaagaagttaagccaatltgttttaaat	9120
Qy	9121	aagtaatgaagcatalcttccaaataactgtaataatggcactgctgttgcgaatttcagat	9180
Db	9121	aagtaatgaagcatalcttccaaataactgtaataatggcactgctgttgcgaatttcagat	9180
Qy	9181	ttcaaaatacgaattatagataaattcccccattataatttccaaatacgaag	9240
Db	9181	ttcaaaatacgaattatagataaattcccccattataatttccaaatacgaag	9240
Qy	9241	ttatgttccatcttctactaaatcgtatcttaattcttcaattatagtaatactatga	9300
Db	9241	ttatgttccatcttctactaaatcgtatcttaattcttcaattatagtaatactatga	9300
Qy	9301	gcaactcttactcctcggttctctctgatttccaagcgacataattttaaanaatacaaggcac	9360
Db	9301	gcaactcttactcctcggttctctctgatttccaagcgacataattttaaanaatacaaggcac	9360
Qy	9361	tgtgactactatttgaagaaaaacagacatttcaatcagatgtgaaggacctcttcgaa	9420
Db	9361	tgtgactactatttgaagaaaaacagacatttcaatcagatgtgaaggacctcttcgaa	9420
Qy	9421	gctagaacaacatctatgattataoacttcattataacgigtgttacccttttaaatgta	9480
Db	9421	gctagaacaacatctatgattataoacttcattataacgigtgttacccttttaaatgta	9480
Qy	9481	acttttctacatttcccggttgaaccctaatttgytgaagaatttttaccacactatact	9540
Db	9481	acttttctacatttcccggttgaaccctaatttgytgaagaatttttaccacactatact	9540
Qy	9541	caataagcaaaaatttctgtatcttccctgttgaatgtaatacctatgttggatttgaanaat	9600
Db	9541	caataagcaaaaatttctgtatcttccctgttgaatgtaatacctatgttggatttgaanaat	9600
Qy	9601	ctcaaaatacgttctcaaaaatttctgcttcttcgacttcttggagacccctcagaanaacta	9660
Db	9601	ctcaaaatacgttctcaaaaatttctgcttcttcgacttcttggagacccctcagaanaacta	9660
Qy	9661	cttaacaactgtgtaataatgagaatacagaagaaaaataatgaagccctctataataatgac	9720
Db	9661	cttaacaactgtgtaataatgagaatacagaagaaaaataatgaagccctctataataatgac	9720
Qy	9721	ccagacacatcattgtttaaanaaacacacaaacctcaacactatgtaatttcaattcgt	9780
Db	9721	ccagacacatcattgtttaaanaaacacacaaacctcaacactatgtaatttcaattcgt	9780
Qy	9781	actgaaagcaaatgcttctgtgactattaaatgltgacacatctcaatctcaactgatagtga	9840

Db	9781	ACTAAAGCAATCTTTGACTATTAAATGTGGCAGTCATTCATTCACGTATAGTA	9840
Oy	9841	atcatgactaaagccattgctgtgttcttccttgtygnfnatatatcaggtaa	9900
Db	9841	ATCATTTAGCTAAGCCATTGCGTGTGTTTTCTTCTTGNTGNATATACAGGTAAA	9900
Oy	9901	attltcaaagaaccatgltcatgttaactgaaccccttgttatggaagttaatt	9960
Db	9901	ATTTTCCAAAAGCCAGTGTGCATGTATACTGGAACCTTTGATTTGAGAATTAA	9960
Oy	9961	ggaccttggatattatcacagaataatgyaacacgnagaalatgtctcaattctt	10020
Db	9961	GGAACCTTGGATATTATCTACTAGATAATATGTAAATACGNGMAATATTCCTAAT	10020
Oy	10021	tcaaatggtgatcccccttaaanngttctattccaataaggaattagcttctatcc	10080
Db	10021	TCAAATAGTGTCATCCCCCTTAAAAANGTTCTATTTCATAGGAATTTAGCTTAATCC	10080
Oy	10081	cttcttatacccttaagatggaagctgttttgctccttggtcatcatgtgccctatlc	10140
Db	10081	CTTCTTATACCTTAGATGAAGAACGCTTTTTTGCTCTTTGTTCACTCAFTGGCCCTAATTC	10140
Oy	10141	caagcacttacgcgtctgtcataaggatctattttgacctggaatcatctgaattgc	10200
Db	10141	CAGGACTTTACCGCTGCTGTGTAATGGATCTATTGTTTGCACGTGAATATCTGAAATTTGC	10200
Oy	10201	aaaactagacaagaatgcacaaagelttctaagtaaacattccattccataaaggaaa	10260
Db	10201	AAAAGTACGCAAAATTTTCACACAGATTTCTTAAGTTAAATCATTTTCATTTAAAGGAAA	10260
Oy	10261	aaagaanaaaatlgtgatgtlcaataacttataatgaagattaanaatgcatttctca	10320
Db	10261	AAGAGAAAAAATTTGTATGTCATTAATTAATGAAGATTAATAAATGCATATTCTTA	10320
Oy	10321	tgttgtataataatgaatgcacaaataaagctgtgacagcttcgtttaaaaaaa	10380
Db	10321	TGTTGTAAATATATGATGTCACAAAATTAAGCTGTGACGTTCTGTTAAAAA	10380
Oy	10381	aaa	10440
Db	10381	AAA	10440
Oy	10441	aa 10442	
Db	10441	AA 10442	
RESULT	3		
AF285167		10442 bp	mRNA linear PRI 09-AUG-2000
LOCUS	AF285167	Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA,	
DEFINITION		complete cds.	
ACCESSION	AF285167		
VERSION	AF285167.1	GI:9755158	
KEYWORDS			
SOURCE		human.	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE		1 (bases 1 to 10442)	
AUTHORS		Schwartz,K., Lawn,R.M. and Wade,D.P.	
TITLE		ABCA1 gene expression and apoA-I-mediated cholesterol efflux are regulated by LXR	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 10442)	
AUTHORS		Lawn,R.M., Wade,D.P., Garvin,M.R., Wang,X., Schwartz,K., Porter,J.G., Seilhamer,J.J., Vaughan,A.M. and Oram,J.F.	
TITLE		Direct Submission	
JOURNAL		Submitted (06-JUL-2000) Discovery Research, CV Therapeutics Inc., 3172 Porter Drive, Palo Alto, CA 94304, USA	
FEATURES		Location/Qualifiers	
source		I..10442	

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/map="9q31"
/cell_type="fibroblast"
/tissue_type="skin"
1..10442
/gene="ABCA1"
291..7076
/gene="ABCA1"
/codon_start=-1
/product="ATP-binding cassette transporter 1"
/protein_id="AAP8175.1"
/db_xref="GI:975159"
/translation="MACPQLRLKLNTRRROTCOLLVAMPFIPLILSVRL
SYPPYDHECHPNKAMPAGTLPMVGGITCANPCCRYPGPGAPVONFKSIV
ARLSDARLLYSQKDTSKDMKRLRLQOIKKSSSLKQDLVNFSEFGLYH
NLSPLKSTVDKMLRADVILAKYVLOGYLHLSLNGSKSEMIQLOEYSELGLP
KEKLAAREVILNSMDILKPLRLTNSGPPSKELAEATTLHSLGTLAOLPSMR
SMDSMEVYVFLTNVSSSTOIOAVSRIVCGPEGGLKIKSINYEENRKALF
GNGTEDEAETPYDNSTPYCNLMKLNESPLSKITKALPKLVGKILYPTPAT
ROYMAVNTPOELAFHDLRSGMEELSKMTFENSQEDVLMILDSNDHNEF
OQLDIDMTAODIYAFIAKHEDVOSNGSVYTWENAEENNOALRTISRMEDVNI
KLEPIATEVWLINSMELDERKFWAGIVGTITPSTELPHHYKIRMDIDVERT
NKIKDYMPPGRADPEEDMRVWVGFAIADYEOALITVLTGHEKKGYMOOMY
PCYVDIPLRVASRMLPMTLAWISVAVILKGIYVEKELKETMIMGLDSILM
SFWEISLILPLVASGLVILKLGILNIPSPSVVPEFLSFVAVITLQCFLLSLF
SRANLAAAGGCIYETLYIPLYLCVAMODYGTFLTKITASLSPVAFGCEYALFE
BOGIVQMDNLESEVEEDGENTLTSISMLFDFLVGMVWYIEAVPOGYIPRW
YFPECTKSYWGESEDESKSHPSNOKRMEIEEPEPLKLGVSIONLVKRYRGMVY
AVDGLANPVEGOILTSFLHNGAGKTTMSILTGPEPTSTAYILKQDISEMSTR
ONAGVCPQHNVEFDMIVVEHIMFYARLGLSEKVKAMEOMALDYGPSKIKST
SOLSGMOKRLSVALAFAGSKVYVLTDEPTAGVDYPSRGITWELLIYRORTILST
HMDADVGLDRILATISHGKLCQVSSIFLNQGLTYTLVLKVDVSSILSRNS
STVSYLKKEDSYOSSSPAGUSDHESPLTIVSALSNIIRKHVSARLVEDGHL
TYVLEPEAKBEAEVELHEIDRLSDIGISSYGISETLEELIKVAESGVDAETS
DGTLPARRRRRAFGDKQSLRPFEDDAADNDSDIPESRETDILSGMGKGYQVK
GKMLTQOQFVALMLKRLIARSKRGFAQIYLAPEVCIALVSLVPPGKPSYK
LOPMYNEQYVFNDAPEDEGTLELALNALKRDPGEGRCMEGIPIDPFGAEEPM
TAPVORTMDLFGNMNTMONSPACCCSDIKKMLPVCPPAGASITOPKORONTA
DILQDITGNISDLYVKTVOIYIAKSLKNKTWNEPVGSGFSNCGTQALPSOEVN
DAIKMKKIKAKSSADRPLNSIGRMTGLDRNNVKFWFNKGMHAISSFLNVN
NALIRANIQKGNESHGTTAFNPHNLITKQOLESVALMTSVVLAISIVIPMSFV
PASEVVEILOEKVSKAKHLOFISGVPIVWLSNFWMDCNVYVPAVLVILITCFO
KSYVSTNLPVIALLLDLYMSITPLPASFVKRIPSTAAVLTIVLIGNGSVA
TVELEFTDNKLNINILKSVFLIPFHCGRGLIMVGNOMAAALAEFGNGRREVS
PLSMDLVGNLFAVAVEGVFLLTVLOYRFRIRPRAVNAKSLINDDEVDYRERO
RLDGGGNDILEIKELIKYIRRRKRPAVDICVGPPEGCEGLLGNCAKGSSTRKM
LTGDTTVRGDAFLNKNISINIHBYONNGYCOFDATITELINGRHVEFALLGCV
PEKBYGKYGMAIKRLGLYKIGEKYAGNYSGNRKSTAMAILGGPVVLEDEPTG
MDPKARRLMLCALSVKESVVLTSHMEECALCTRAIWNNGFRCLGVSOLK
NREGGYITIVRIAGSNPDLKPVODPFGFLAFKPEKERNMLQOLPSSLSLARI
FSLISQSKRLHIEDYSVSQTTLDQVFNKAKDQSDDDHLKLSLHKNQVVVDVAVLT
SFLQDEKKESEYV"
BASE COUNT      2898 a      2297 c      2408 g      2835 t      4 others
ORIGIN
Query Match      100.0%; Score 10438; DB 9; Length 10442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
181 acaaaagtgtgaaacagtaataaccagcgacggggtccctgtgtgtgagctctggcgc 240
181 ACAAAGTGTGAAACAGTTAATGACACGCGGGGGTCCCTGCTGTGAGCTTG6CCGC 240
241 tgccttcgaaggtcccgagcaacacgctgggagctgtgctgaggaagcaatgagctgt 300
241 TGCTTCGAGGGCTCCGAGCCACACGCTGGGCTGCTGGAGGGAACATGGCTTGT 300
301 ggccttcgaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 360
301 GGCCTTCAGCTGAGGTGTCTGTGTGAAGAACCTCACTTTCAGAGAACAAACATGTC 360
361 agctgttactgtgaagtgtgctgtgctcttatactctgtctgtctgtctgtctgt 420
361 AGCTGTACTGTGAAGTGGCTGGCCCTATTATCTCTGTGATCTGTGATCTGTGCGC 420
421 tgagctaccacccctatgaacaacatgacatlttccaaataaagccatgtccctgt 480
421 TGAAGCTACCCACCCCTATGAACAACATGACATTTTCCAAATTAAGCATGCCCTGTG 480
481 caggaacactcctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 540
481 CAGGAACACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
541 acccgactcctgtggaggtcccgagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
541 ACCCGACTCCTGTGGAGGCTCCCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
601 gctgtgtcgaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 660
601 GCTGTGTCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
661 acatgtgcaaaagtctgtgaacaacatlaacagcaataaagaatcagctcgaactgaagc 720
661 ACATGCGCAAAAGTGTGAAACATTACAGCAATCAAAATCCAGCTCAAACTTGAAGC 720
721 ttcaagaattctcgtgtgtgaacaatgaacctctcgtgtgtgtgtgtgtgtgtgtgt 780
721 TTCGAATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
781 tcccaagctcactgtgtgaacaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 840
781 TCCCAAGCTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
841 tgcgaagctcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 900
841 TGCAGGCTACCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
901 ttcacactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 960
901 TTCACACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
961 cagcagagcgaagtaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1020
961 CAGCAGAGCGAGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
1021 actctaacctccctcctcccgagcaagagctgtgtgtgtgtgtgtgtgtgtgtgtgt 1080
1021 ACTCTAACCTCTCTCTCCCGAGCAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
1081 gctctggagactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1140
1081 GCTCTGGAGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
1141 aggtgagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1200
1141 AGGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
1201 tgtctgfatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1260
1201 TGTCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
```


QY 1261 ggtatgaggaacaaactaacaaagccctcttgaggagcaatggcactgaggaagaatgctg 1320
|||||
Db 1261 ggtatgaggaacaaactaacaaagccctcttgaggagcaatggcactgaggaagaatgctg 1320
QY 1321 aaacctctatbaaactatagaactccttactgcaatgatattgaggaattggagat 1380
|||||
Db 1321 aaacctctatbaaactatagaactccttactgcaatgatattgaggaattggagat 1380
QY 1381 ctatgctctcttcccgcatlacttggaaagctctgaaagcgcgtgctcgttgggaagatcc 1440
|||||
Db 1381 ctatgctctcttcccgcatlacttggaaagctctgaaagcgcgtgctcgttgggaagatcc 1440
QY 1441 tgtataacctgaactccaagccaaggaatgcaatgctgtaagtggaaagaccttcc 1500
|||||
Db 1441 tgtataacctgaactccaagccaaggaatgcaatgctgtaagtggaaagaccttcc 1500
QY 1501 aggaactggtctgtctcactgactggaagcattgaggaggaactcaagcccaagatct 1560
|||||
Db 1501 aggaactggtctgtctcactgactggaagcattgaggaggaactcaagcccaagatct 1560
QY 1561 ggaactctatggaagcaagccaagaatggaactgtccgagatgctgttggagagagag 1620
|||||
Db 1561 ggaactctatggaagcaagccaagaatggaactgtccgagatgctgttggagagagag 1620
QY 1621 acaatgacacactttgggaagcaagcttgatggtctgagatgagacagcccaagacatcg 1680
|||||
Db 1621 acaatgacacactttgggaagcaagcttgatggtctgagatgagacagcccaagacatcg 1680
QY 1681 tggcgttcttggccaagcaagccagagagatgctcagtcagtaatggtctgttctgtaacct 1740
|||||
Db 1681 tggcgttcttggccaagcaagccagagagatgctcagtcagtaatggtctgttctgtaacct 1740
QY 1741 gggagagaagcttccaagcagacttaacaggaatctcgagacatattctgcttaatgagt 1800
|||||
Db 1741 gggagagaagcttccaagcagacttaacaggaatctcgagacatattctgcttaatgagt 1800
QY 1801 gttcacaacctgaagcaagctgaagcccaatagaacagaagctgtgctcatalcaaacatgcca 1860
|||||
Db 1801 gttcacaacctgaagcaagctgaagcccaatagaacagaagctgtgctcatalcaaacatgcca 1860
QY 1861 tggagctgctgagatgagagaagttctggcgtgattgttctcacttggaaattaccag 1920
|||||
Db 1861 tggagctgctgagatgagagaagttctggcgtgattgttctcacttggaaattaccag 1920
QY 1921 ggcagcatggagctggcccatcatgctcaagatgcaagatccgaatggacattgacaatgttg 1980
|||||
Db 1921 ggcagcatggagctggcccatcatgctcaagatgcaagatccgaatggacattgacaatgttg 1980
QY 1981 agaggaacaaataaatacaagatgagtgactgggaacccctgttctcgagctgaaccccttg 2040
|||||
Db 1981 agaggaacaaataaatacaagatgagtgactgggaacccctgttctcgagctgaaccccttg 2040
QY 2041 aggaactgctgagatgctgggggggcttgcctacttgcagaagatgtgggtggagcagagca 2100
|||||
Db 2041 aggaactgctgagatgctgggggggcttgcctacttgcagaagatgtgggtggagcagagca 2100
QY 2101 tcaatcaagatgctgagagggagccaggaagaaactgtgtctatataccaagatgacct 2160
|||||
Db 2101 tcaatcaagatgctgagagggagccaggaagaaactgtgtctatataccaagatgacct 2160
QY 2161 atccctgttaactgtagacatcttctgaggtgtagaagccggttcaatgacctcttca 2220
|||||
Db 2161 atccctgttaactgtagacatcttctgaggtgtagaagccggttcaatgacctcttca 2220
QY 2221 tggagctgagctgagatgctgaggtgctgtagatcatcaaggaatcgtgtatagagaag 2280
|||||
Db 2221 tggagctgagctgagatgctgaggtgctgtagatcatcaaggaatcgtgtatagagaag 2280
QY 2281 aggaagagctgaaggaagcaatgagatgagctggagcctggagcaaaagatactcgtgtta 2340
|||||
Db 2281 aggaagagctgaaggaagcaatgagatgagctggagcctggagcaaaagatactcgtgtta 2340
QY 2341 gctggttcaatgtagcctcaatctctcttcttgagcgcgtgctgtagtggtaacc 2400
|||||

Db 2341 gctggttcaatgtagcctcaatctctcttcttgagcgcgtgctgtagtggtaacc 2400
QY 2401 tgaagttagaagaaactgctgcccctacagtagtaccagctgtgtgttcttctctgctg 2460
|||||
Db 2401 tgaagttagaagaaactgctgcccctacagtagtaccagctgtgtgttcttctctgctg 2460
QY 2461 tgttggctgtgtgtagaactcctgcaatgctcctgtagatgaacactctctccagagca 2520
|||||
Db 2461 tgttggctgtgtgtagaactcctgcaatgctcctgtagatgaacactctctccagagca 2520
QY 2521 acctggcagcagcctgtgggggcaatcacttaactcaagcgtgtaactgacctgctgt 2580
|||||
Db 2521 acctggcagcagcctgtgggggcaatcacttaactcaagcgtgtaactgacctgctgt 2580
QY 2581 gttgtgcaatgaggaactcaagctgtggtctcaacatcaagatcttctgtagcctgtgtctc 2640
|||||
Db 2581 gttgtgcaatgaggaactcaagctgtggtctcaacatcaagatcttctgtagcctgtgtctc 2640
QY 2641 ctgtgcttcttgggtctgtgctgtgtagtacttgccttcttggaggaagcaatggag 2700
|||||
Db 2641 ctgtgcttcttgggtctgtgctgtgtagtacttgccttcttggaggaagcaatggag 2700
QY 2701 tgcagtgaggacaacctgttgaagatctctgtggaggaatgcttaactcaacct 2760
|||||
Db 2701 tgcagtgaggacaacctgttgaagatctctgtggaggaatgcttaactcaacct 2760
QY 2761 cgaatcctatgtagtctgttgaacactcctctatgggtgtagatgacctgtagattag 2820
|||||
Db 2761 cgaatcctatgtagtctgttgaacactcctctatgggtgtagatgacctgtagattag 2820
QY 2821 ctgtcttccaagcagtagaagatctccagcctgtlatlcttcttccagcaagtcct 2880
|||||
Db 2821 ctgtcttccaagcagtagaagatctccagcctgtlatlcttcttccagcaagtcct 2880
QY 2881 actggttggcaggaagatgtagaagagccacccctgtgttccaacaggaaggaatgt 2940
|||||
Db 2881 actggttggcaggaagatgtagaagagccacccctgtgttccaacaggaaggaatgt 2940
QY 2941 cagaatctgcaatggagaggaagcaacccacttgaagcctgtgctgttccatccagacc 3000
|||||
Db 2941 cagaatctgcaatggagaggaagcaacccacttgaagcctgtgctgttccatccagacc 3000
QY 2941 cagaatctgcaatggagaggaagcaacccacttgaagcctgtgctgttccatccagacc 3000
|||||
Db 2941 cagaatctgcaatggagaggaagcaacccacttgaagcctgtgctgttccatccagacc 3000
QY 3001 tggtaaaagctacacagatgtagatgtagatgtagatgtagatgtagatgtagatgtagat 3060
|||||
Db 3001 tggtaaaagctacacagatgtagatgtagatgtagatgtagatgtagatgtagatgtagat 3060
QY 3061 atgagggccagatcacctctcttccctgggccaatgagagcggggaggaagcagccacatgt 3120
|||||
Db 3061 atgagggccagatcacctctcttccctgggccaatgagagcggggaggaagcagccacatgt 3120
QY 3121 caatctgacccggtgtgttcccccgaacctgggagccgctacatctctggggaaagaca 3180
|||||
Db 3121 caatctgacccggtgtgttcccccgaacctgggagccgctacatctctggggaaagaca 3180
QY 3181 ttcgctctgtagatgagacacatccgagcaagacctgggggtgtgttcccaagcaatagctgc 3240
|||||
Db 3181 ttcgctctgtagatgagacacatccgagcaagacctgggggtgtgttcccaagcaatagctgc 3240
QY 3241 tgtttgacaatgctgactgtcgaagaaacacatctgttctatagcccgcttgaagaggctct 3300
|||||
Db 3241 tgtttgacaatgctgactgtcgaagaaacacatctgttctatagcccgcttgaagaggctct 3300
QY 3301 ctgagaagcagctggaagagtagagatgtagacagatgagccctgtgattgttgcacataa 3360
|||||
Db 3301 ctgagaagcagctggaagagtagagatgtagacagatgagccctgtgattgttgcacataa 3360
QY 3361 gcaagctgaagaaagcaaaacagccagctgtcaggtggaatgtagagaagatctatctgtg 3420
|||||
Db 3361 gcaagctgaagaaagcaaaacagccagctgtcaggtggaatgtagagaagatctatctgtg 3420
QY 3421 ccttggccttgtcggggatctaaagttgtcaatcttctgtagaagcaacccagctgtgtgg 3480
|||||

QY 5641 caacccttgactgagcgttccaccgacaataaactgaataataatcgaatcctgca 5700
|||||
Db 5641 CCACCTTGTGCTGAGCGCTGTTACCGACAAATAGCTGATATATATCAATGATATCTCGA 5700
QY 5701 agtccgctgtcttgatctctccacatttttgccctggagagaggtctcagacatgta 5760
|||||
Db 5701 AGTCGCTGTTGTAATCTTCCACATTTTGGCTGGAGAGGGCTCATCGACATGTGTA 5760
QY 5761 aaacacagagcaatgctgtatgctcccgaaaggtttggggagaaatcgcttgatccat 5820
|||||
Db 5761 AAAACACAGCAATGCTGTATGCTTGGAAGGTTGGGGAATGCTTGTGTACCAAT 5820
QY 5821 tatctggagactgtgtggagcaaacctcttcgcaatgacgtggaggggtgtct 5880
|||||
Db 5821 TATCTTGGGACTTGTGGGACCAAACTCTTGCCATGGCCGTGGAAGGGGTGTGTCT 5880
QY 5881 tccctacatcgtcttgatccaglacagatctctcagcccgagacctgtaaatgcaa 5940
|||||
Db 5881 TCCTCATCTGTTGATGATCCAGATCTCTCATCAGGCCCAAGCCTGTAAATGCAA 5940
QY 5941 agctatcctcctgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaat 6000
|||||
Db 5941 AGCTATCTCTCTGAAATGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGAT 6000
QY 6001 atgttgagagccagaaatgacatctcagaaatcagaaatgagatgagaaatagaaagaa 6060
|||||
Db 6001 ATGCTGAGAGCCCAATGATGATCTTGAATCAAGAGATGTAAGAGATATATAGAGAA 6060
QY 6061 aagcgaagacctgtcttgacagagatttgcgtggacatccctcctgttgatgctttggc 6120
|||||
Db 6061 AGCGAAGCCTGCTGTGAGAGATTTGGCGGCAATTCCTCTGCTGTGATGCTTTGGCG 6120
QY 6121 tctctggagatgaaatgggctcggaaatcctcagctcagctcagctcagctcagctcag 6180
|||||
Db 6121 TCCTGGAGATTAATGGGCTGGGAAATCATCACTTTCAAGATGTTAAAGAGGATACCA 6180
QY 6181 ctgtaccagagagatgctcttctccttaacaaataglatctatcacaatcagatgaag 6240
|||||
Db 6181 CTGTTACCAAGAGATGCTTCTTACCAAAATAGTATCTATCAAAATCATCATGAAG 6240
QY 6241 tacatcagaacatgagctactgctcctcagtttgaatgcatcagagagctgttgatggga 6300
|||||
Db 6241 TACATGAGAACATGGGCTACTGCTCTCAGTTGATGATCCATCAGAGCTGTGTACGGGA 6300
QY 6301 gaaacacgtagagctcttctcctccttggagagagctcccaagaaagaaatgtggcaag 6360
|||||
Db 6301 GAGAACACGTGGAGTCTTGGCTTTTGAGAGAGATCCAGAGAAAGAGATGGCAAG 6360
QY 6361 ttggtgagtgagcgtatcgaagaactggcctcgatgaatgagagaaataatgctgta 6420
|||||
Db 6361 TTGGTGAATGGGAGATTCGGAACACTGGGCTCGTGAAGATGAGAAATATGCTGGTA 6420
QY 6421 actatagtgagagcaacaacagcaagctctcagcaatgcttgaatgcgagggcctc 6480
|||||
Db 6421 ACTATAGTGAGGCAACAAACGCAAGCTCTACAGCCATGCTTGTGATGGGCGGCTC 6480
QY 6481 ctgtgtgttcttgatgaaacccacacagagatgatalcccaagcccgagcttctgt 6540
|||||
Db 6481 CTGGGGTGTCTTGATGAACCCACACAGGATGATGCCAAAGCCCGGCTTCTGT 6540
QY 6541 gaaatctgcccctaagtgtctcagaagagagagatcagtagtctacatccatagta 6600
|||||
Db 6541 GGAATTTGCTGCTTAAGTGTGTCAGAGAGGGGAGATCAGTAGTCTTACATCATAGTA 6600
QY 6601 tggagaagaatgaaagcctcttgacatgagatgagatcagatcagatgagaaagttcaagt 6660
|||||
Db 6601 TGGAGAGATGAGAGCTCTTTGCACTAGGATGCAATCAGTCAATGGAAGGTCAAGT 6660
QY 6661 ggccttgacgtgctcagacatcctaaataagtttggagatggttatacaatggtttac 6720
|||||
Db 6661 GCCTTGGCAGTGTCCACATCTTAAATAATAGGTTTGAGAGATGTTATACATATGTTTAC 6720
QY 6721 gaataagcaggttccaccggagacctgaagcctgacagagattccttgagactgcatlc 6780
|||||

Db 6721 GAATAGAGGGTCCACACCGGACCTGAAGCCTGCCAGATTTCTTGGACTTGCAATTC 6780
QY 6781 ctggaagtgtcttaagaagaacaacgaggaatgcttaacatccagatccatcttca 6840
|||||
Db 6781 CTGGAAGTCTTAAAGAGAAACCGGAACAGTGTACATATACCACTTCCATCTTCAT 6840
QY 6841 tatctctctggcagagatctcagcatcctcctccagagcaaaagcagctccacaatg 6900
|||||
Db 6841 TATCTTCTGTGGCCAGATATTACGATCTCTCCAGAGCAAAACGATCCACATAG 6900
QY 6901 aagactcctgttctcagaacaacttgacaaatgatttgaacttggcaagagc 6960
|||||
Db 6901 AAGACTACTGTTCTTCAGAACAACTTGACCAAGATTTGTGAOCTTGGCCAAAGACC 6960
QY 6961 aaagatgatgagcacttaagaacctctatcacaacaaacagagatgagag 7020
|||||
Db 6961 AAAGATGATGACCACTTAAGACCTCTCATACACAAACCAACAGACTAGTGGACG 7020
QY 7021 ttgcagtctcacaatcttctcagagatgagaaagtgaagaaagctatgtaagaa 7080
|||||
Db 7021 TTGCAGTCTCACATCTTTCTACAGATGAGAAAGTGAAGAAAGCTATGTATGAAGAA 7080
QY 7081 tccgttcaatcaggggtgctgaaagtgaagaaagtaagacttctcttgacacatgtg 7140
|||||
Db 7081 TCCTGTATACGGGGTGTGCTGAAGATGAAGAGCAATGACTTCTTGCACCATGTG 7140
QY 7141 aaggttgagaaagaagcagcaagtttgaatgaggaagaagtgaactgtatctac 7200
|||||
Db 7141 AAGTGTGTGGAGAAACAGCCAGAGTTGATGTGGAGAGATGAACCTGATCTGTAC 7200
QY 7201 tgatactatcatalgcaatgcaatcgaatgaaatgaagaacaaatccatcagaaggca 7260
|||||
Db 7201 TGATCTATTTCAATGCAATGCAATTCATGCAATGAATAAATTCATATACAGGGCA 7260
QY 7261 gtgccttgtagcctatgtctgtatgagctcgaagtgaagacttgaattgaatttt 7320
|||||
Db 7261 GTGCTTTGTACCTATGCTTGTGTGAGCTCTCAAGTGAAGACTGTAATTTAGTTTTT 7320
QY 7321 acctaacctatgaaactctatatagaaacccaaatgagatagtttgaactcaca 7380
|||||
Db 7321 ACCATATACCTATGTAACACTCTATATGGAACCCATGACATATGCGTTGAACTGCA 7380
QY 7381 ctttcttcttcttctgtcctgtatctcctatcaggttgggttgaacaaatcacaag 7440
|||||
Db 7381 CTTTTTTTTTTTTTTGTTGCTGTATTCATTTGGGGTGAACATATATTCATCAAG 7440
QY 7441 taatcatgagcagatattgatacaaaatcaaaagtgaatgacatccatcactaa 7500
|||||
Db 7441 TAATCATGGCCGCGCATTAATGATCAAAATCAAAAGTATGACATCTCATTTCACTAA 7500
QY 7501 gccatgcaatgcccaggaagctgttcccggttgcacatccatctgctggcaatgagt 7560
|||||
Db 7501 GCCATGCCATGCCAGAGACAGTGTTCGCCGTGACACATCATGCTGGCAATAGAGT 7560
QY 7561 gccagatgatagtgccaagtttctcagaagtttgaagcaatggtgtgcatgctc 7620
|||||
Db 7561 GCAGAGTTATATAGGCCAAAGTTTTCAGAAAGTTGAAGCCCATGTGTGTCTGCTC 7620
QY 7621 accttgtgaaagcgtcctgctcagaggtctatacaaatlgaatatcagttgagagagt 7680
|||||
Db 7621 ACTTTTGTAAAGCTGCTGTGCTGACAGCTATCAACATTTGAATGAGTTGACAGATG 7680
QY 7681 gtgcacgtcgtgagcaatccctgctgtatccctctgataagctgtcttggttgagcgt 7740
|||||
Db 7681 GTGCCATGGCTGTGCTTAACATCTGCTGTGATTCCTGTGATAGCTGTGTGGTGGCAGT 7740
QY 7741 aaatgcaacaaatggtgtgtctctgagcagggaaactgtgtccatgtgtatct 7800
|||||
Db 7741 AACATGACCAAAATAGTGGGTGTCTGTAGCGACGGAAACTTGGTTCATTTGATATTT 7800
QY 7801 gtccatagcttgagcagatgggtctacaggggtacatccatataagactttaaataact 7860
|||||

Db 7801 GTCTTATGCTTGAAGCCATGAGGCTATCTTATGAGACTTTAAATATACCTT 7860
Qy 7861 agatccctgtaagagcaagaalcaacagcaaacctgctgggctgcaagctgctbaag 7920
Db 7861 AGATCTGCTGTAAGAGCAAGAAATCAACAGCAACCACTGCTGGGGCTGCAAGCTGCTGAAG 7920
Qy 7921 ccagggcatgggataaagaagatgctgctcaaacctgaaggagccctgctccattgt 7980
Db 7921 CCAGGGCATGGGATTAAGAGATTTGCTTCAACCTAGAGGAAGCCCTGCTCCATTTGT 7980
Qy 7981 cctgacgtctgctaacatgctgacgtcctccaaagatgttatctcgacacaaagtgtat 8040
Db 7981 CCTGACGTCTGCTAACATGCTGACACTGCAATCTCAAGATTTTATCTGACACAAAGTGTAT 8040
Qy 8041 tattctgctgctttggaatcaactagaanaaagaagaatgagctgtgtatttgaacaaa 8100
Db 8041 TATTCTGGCTTTTGGATTAATCTGAAAAATGAAAAAGATGAGTGTATTTGACAAAA 8100
Qy 8101 atgttctgcttttaagtgtatgtaattggaatttgaattctcaatgactgactgacttct 8160
Db 8101 ATGTTTCTACTTTTAAATGTTATTTGGAATTTTAACTTCTATGATGACTTCTGAATTCCT 8160
Qy 8161 tagaagagcctcttctgtagaacctgctgtaagaagatgagccactgctccactat 8220
Db 8161 TAGAATGGCTCTTGTGAGAACCTGTGTATGAGAGATGAGGCACTGCCCCACTAT 8220
Qy 8221 ttatttctctatgtaagttgcatatcagtaagtaagctgctgaagaagaactgtat 8280
Db 8221 TTTATTTTCTTATGTAAGTTTGTGATATCACTCAATGATGCTTGAAGCAATGTGTAT 8280
Qy 8281 ggtcagagatcctgacatataatgagtttcttccagatcttgaagataacttcaat 8340
Db 8281 GGTCAAGATCTCAATGATTAATTTGAGTTTCTTCAATCATTTAGATTTACTTTAAT 8340
Qy 8341 ctcaattcacaatcaaatatlttttgagtgatgctgtagagctgaaagatgtagctga 8400
Db 8341 CTCAATCTCAATCAATTAATTTTGTGAGTATGCTGATGCTGAAGAGTATGTCGTA 8400
Qy 8401 cgtataagactagaagataatgaagctgacactcctgctgacatgttataagctc 8460
Db 8401 CGTATAAGACTAGAAGATTAATTAAGTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 8460
Qy 8461 actggtttcaaatatagctgctgctgctgctgtagagagccactgtaacaatattggc 8520
Db 8461 ACTGGTTTCAAAATATAGGTTGCTTGTGTGTATGAGACCCCACTGTAAATATTTGGGCT 8520
Qy 8521 agccttt 8580
Db 8521 AGCCTTTTtt 8580
Qy 8581 aagtttaacaatgaattcctcaacaggaanaaagaagctgaagctgtaaacctgctgaana 8640
Db 8581 AAGTTTAAACAATGAATTTCTTCAACAGGGAACCAACCTGATGAAACTTGTCTGAAAA 8640
Qy 8641 cacaacttgctttagagatttagacttcaaatgaattgcttggcagatattggata 8700
Db 8641 CACAACCTTGTGTTTATGGATTTAGTACTTCAAAATATTTGGCTTGGCAATTTGGATA 8700
Qy 8701 ccccatlaaatctgacagctcacaatttttcaatcctcctcaatcactagcaagaanaata 8760
Db 8701 CCCCATTAATCTGACAGCTCAAAATTTTCACTCTTCAATCACTAGTCAAGCAAAAAATA 8760
Qy 8761 taanaacaacaatctccatataagagcatttccagaagtttcttaaccagacttatt 8820
Db 8761 TAAAAACAACAATCTCTCATATGAGCATTTTTCAGAGTTTTCAGCCAGTCTTAT 8820
Qy 8821 ttcttagtcaagtaaacattgttaaaaatactttcactcaactactactgtaactgtct 8880
Db 8821 TTTCTAGTCAAGTAACATTTGTAATAATCTTTCACTAATTAATCTTACTGTTAACTGCT 8880
Qy 8881 taagaagaaagaaataatagagaactatgttgggagaaagtccaagtacttcaat 8940
Db 8881 TAGAGAAAGAAATAATATGAGAGAACTATGTTGGGGAAGTTCAAGTACTTTCAT 8940
Qy 8941 atcattactaacttctccacttctccaaaattggaatattgaacgctaaaggtgaaga 9000
Db 8941 ATCATTACTAATCTTCTCCACTTTTCCAAATTTGAATATTAACTGTAAGAGGTGAAGA 9000
Qy 9001 ctccagatttcaaatatcttctctataatltttaaattcaagaataatataaaccca 9060
Db 9001 CTTCAGATTTCAAATTAATCTTTATATTTTAAATTTTACAGAAATATTTATTAACCCA 9060
Qy 9061 ctgctgaaanaaagaaataatgattttagaagtaagtaagcaatattgattttaaata 9120
Db 9061 CTGCTGAAANAAGAAATAATGATTTGTTTGAAGTTAAAGCAATATGATTTTAAATAT 9120
Qy 9121 aagtaatgaagcatatttccaatlaactagatgataagcactgctgcaattacagatc 9180
Db 9121 AAGTATGAAGCATATTTCCAAATTAAGTATGATTTGCACTGTTCAATTTACAGATTC 9180
Qy 9181 ttcaaaaatacagaatttataagaataatcttctcattataatlttcaaatcaag 9240
Db 9181 TTTCAAAAATACGAATTTATGAAATATTTCTCCATTTAATATTTTCAAAAATCAAG 9240
Qy 9241 ttaagtttccatatttactaanaacgtatctcaatctcattatagtaaatctatga 9300
Db 9241 TTATGTTTCCATTTTACTAATAATGCTATTTCAATTTCTCATTAATATGATTAATCTATGA 9300
Qy 9301 gaaactccttactcctgctcctctgatttcaagagcacaattttaaataaagaagcac 9360
Db 9301 GCAACTCTCTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9360
Qy 9361 tctgaactatcttgaagaacacagacatttaatacagattgaagaagcctctcgaa 9420
Db 9361 TGTGAATATTTTGAAGAAACAGSACATTTTATTAAGATTTGAAGAGCCTCTTCTGAA 9420
Qy 9421 gctagaacaactatagatatacatctcaatlaactatgctgttacctttaaataagla 9480
Db 9421 GCTAGAAACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 9480
Qy 9481 atttttcaatttctctgctgtaaacctaatattggtgaagaaattttaaacaacttact 9540
Db 9481 ATTTTTCAATTTTCTGCTGTAACCTTAATTTGCTGTAACCTTAATTTTCAATCTTAATCT 9540
Qy 9541 caatcaagaacaattctctgataatctccctgtagaagctgacatgtagttcagaat 9600
Db 9541 CAATCAACCAAAATTTTGTATTTTCTGTAATTTCTGTAATTTCTGTAATTTCTGTAATTT 9600
Qy 9601 ctcaaaaagctgcttcaaaaattctctcttcttgaacttcttggagacactcagaanaactta 9660
Db 9601 CTCAAAAATACGTGTTCAAAAATTTCTGCTTGTGATCTTGGGACACTCAGAAAACTTA 9660
Qy 9661 ttaacaactgtaatatgagaataacagaagaanaataaagccctctataataatgct 9720
Db 9661 TTAACAACTGTGAATATGAGAAATATACGAAGAAATATTAAGCCCTTATTAATTAATGTC 9720
Qy 9721 ccagacaaatcattgtttaaaaaaaccaaacctcaactactgtaatttcatattctgt 9780
Db 9721 CCAGCAAAATTCATTTGTTAAAAAACCAAACTCTCACTAGTGTATTTCAATTAATCTGT 9780
Qy 9781 actgaagcaaatgcttctgtaactataaagtgtgacacatcattcaacttactatagta 9840
Db 9781 ACTGAAGCAAAATCTTTGTGACATTAATTTGTCACATCACTTCACTGCTGTAATGTA 9840
Qy 9841 atcatgactaagaagcatttctgctgttcttcttcttcttcttcttcttcttcttcttct 9900
Db 9841 ATCATTTGACTTAAGCCATTTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 9900
Qy 9901 atttccaaagagcactgctgctatgtaatactgaaaccttctgtaattagaaactatt 9960
Db 9901 ATTTTCCAAAGAGCAGTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 9960
Qy 9961 ggaaccttggtatatactactagaataatgtaataactgnaagaataatgcttcaattct 10020
Db 9961 GGACCTTGTGATTAATCTACTAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10020

QY	10021	tcaaat	tgatgccccccttaaangtctattccaaagagattgacttgctatcc	10080
Db	10021	TCAAAAATGGTCATCCCCCTTTAAANGTCTATTTCATTAAGATTACCTGGCTTATGC		10080
QY	10081	cttcttaacccttaagatgaagctgfttttgagctcttgcttcattgcattgcccctcattc		10140
Db	10081	CTTCTTATACCTTAAGATGAAGCTGTTTTTGTCCTTTGTTTCATATTGGCCCTCATTC		10140
QY	10141	caagcacttaagctgctctgtaayggatctattttgacatggaatctcgagaatgc		10200
Db	10141	CAAGCACTTACCGCTGCTGTATGGAGACTATTTTGTGACATGGAATATCTGGAATTCG		10200
QY	10201	aaaactgacaaaagttccacacgatttctaaglttaatacttttcgttaaaagaaa		10260
Db	10201	AAAATGACAAAAAGTTTCACACAGATTTCTAAGTTAAATCTTTTCATTTAAAGGAAA		10260
QY	10261	aagaataaaaaatttgaatgataacttataatgaaglatataaagcatattctta		10320
Db	10261	AAAGAAAAAAATTTTGTATGTGCATTAACCTTTATGAAGTATTAAAGCATATTTCGA		10320
QY	10321	tgttgtaataatagtagtccaaataaagctgtgacagttcgttaaaaaa		10380
Db	10321	TGTTGTAATATTAAGACTGCACAAATTAACCTGTGACAGTTTGTAAAAA		10380
QY	10381	aaa		10440
Db	10381	AAA		10440
QY	10441	aa	10442	
Db	10441	AA	10442	
RESULT	4			
AX060719		10474 bp	DNA	linear
LOCUS	AX060719			PAT 22-JAN-2001
DEFINITION	Sequence	7 from Patent WO0078972.		
ACCESSION	AX060719			
VERSION	AX060719.1	GI:12406108		
KEYWORDS				
SOURCE		human.		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE		Law, R.M., Wade, D. and Garvin, M.		
JOURNAL		Regulation with binding cassette transporter protein abcl		
		Patent: WO 0078972-A 7 28-DEC-2000;		
FEATURES		CV THERAPEUTICS, INC. (US)		
source		location/Qualifiers		
		1. 10474		
BASE COUNT		/organism="Homo sapiens"		
ORIGIN		/db_xref="taxon:9606"		
		2906 a 2305 c 2416 g 2843 t 4 others		
Query Match		99.9%; Score 10429; DB 6; Length 10474;		
Best Local Similarity		100.0%; Pred. No. 0;		
Matches 10436; Conservative		0; Mismatches 5; Indels 0; Gaps 0;		
QY	2	gccggagaccgcagagccgagcgcgaaccttctccgggctgcgcgacggcgagggcg	61	
Db	34	GGCAGAGACCCGACAGCGCGAGCCGACACCCCTTCTCCGGCTGCGGACAGGGCGGG	93	
QY	62	gagctccgagccacaaagagccggtctcagggcgcttgcctcctglttttcccg	121	
Db	94	GAGCTCCGCGCACACAGAGCCGGTTTTCAGGGCGCTTCTGCTGTTTTTCCCGG	153	
QY	122	ttctgttttctcccttccggaagctgttcaagggttagsgaagagaca	181	
Db	154	TTCTGTTTTTCTCCCTTCTCCGGAAGCCTTGTCAAGGGGTGAGAAAGACGCCAACA	213	

OY	182	caaaagcggagaaacaaattaaatbaacaagcagaggggtccctcgtctgtatgcctgtgcgcgt	241
Db	214	caaaagcggagaaacaaagttatntacacagccacggccgtccctcgtctgtatgcctgtgcgcgt	273
OY	242	gctctccagaggtcccgagccacaagctgtggcgtgtgcctgtatggagaaatgtcgtgtg	301
Db	274	gccttccaggggctccgagccacacgctggggctgctggctgaggaagaaatgtgctgttg	333
OY	302	gctctcagctgaagttgtcgtctgtgtggaagaactcaactcttcgaagaagacaaatgtca	361
Db	334	gccctacactgaagcttgctgtgtgtggaagaaaccttcattgcaagaaacaaacatgttca	393
OY	362	gcgttctactggaagtgtgcgcgtatctatcttcctgtatccctgtatcctgtctgtgcgt	421
Db	394	gctgtttacttggaagtgtgcctgcgcctcttattttattttccgtgattccgtgattctgttcggcgt	453
OY	422	gagctaccaccaacctatgaacaacaatgaatgtcaattccaaataagccatgtccctgtc	481
Db	454	gagctaccaccaacctatgaacaacaatgaatgtcaattttccaaataagccatgtccctgtc	513
OY	482	aggaaccttccttggtttgaaggaggtatctgttaatgccaacaaacctgttccgtta	541
Db	514	aggaacaccttcttggtttgaaggaggtatctgttaatgccaacaaacctgttccgtta	573
OY	542	ccgcacctcctggaggaggtcccgagtttgtgaaactttaaacaatccattgtgtcgtg	601
Db	574	ccgcacctcctggaggaggtcccgaggtgtgtgaaacctttaaacaatccattgtgtcgtg	633
OY	602	ccgtgtctcagaatcgtcgtgaggtcttcttatacagccgaagaagcaccagcatgaaga	661
Db	634	cctgtttccacaatctctggagggcttctttttatcacccgaagaaacccagcatgaaga	693
OY	662	catgagcaaatctcttggaacatctacagcagatcgaagaatccagctcaacttgaagct	721
Db	694	catgagcaaatctcttggaacatctacagcagatcgaagaatccagctcaacttgaagct	753
OY	722	tcaagaattcctgtgtgacaatgaacactctctgtgttccctatatcaaacctctctct	781
Db	754	tcaagaatttctgtgtgacaatgaacacttctctgtgttccctatatcaaacctctctct	813
OY	782	cccaagactctatcttgacaagaatagtcgtgaaggtctgtatctctccacaagaatttt	841
Db	814	cccaagactctatctgtgtgacaagaatagtcgtgaaggtctgtatctctccacaagaattttt	873
OY	842	gcaaggtcaccaagttacatttgacaagtctgtgtcaatggatcaaaatccagaagatgat	901
Db	874	gcaaggtcaccaagttacatttgacaagtctgtgtcaatggatcaaaatccagaagatgat	933
OY	902	tcaactgtgtacaaccaagaagtctctgtggtcttctgtccacaagaaggaanaactgtgcgc	961
Db	934	tcaactgtgtgtacccaagaagaagtcttctgtggtcttctgtccacaagaaggaanaactgtgcgc	993
OY	962	agcagagagagtaactgtcttccaacatgacatcccttgaagccaactccttgagacactaaa	1021
Db	994	agcagagagagtaactgtcttccaacatgacatcccttgaagccaactccttgaagacactaaa	1053
OY	1022	ctctacatctccctcccgagcaagaggtcgtgtgaagccacaanaaacttgtcttatag	1081
Db	1054	ctctacatctccctcccgagcaagaggtcgtgtgaagccacaanaaacttgtctctatag	1113
OY	1082	tcttggagactctggccagagaggtcttccaacatgagaagctctgagatgtcgcacaga	1141
Db	1114	tcttggagactctggccagagaggtcttccaacatgagaagctctgagatgtcgcacaga	1173
OY	1142	ggatgagttcttgaccaatgttgaagaagctccaagctcctccaaccaatctacagagctgt	1201
Db	1174	ggatgagttcttgaccaatgttgaagaagctccaagctcctccaaccaatctacagagctgt	1233
OY	1202	gtctcgttatctgtcgcggacatcccgaggagaggggctctgaagaataagctctcaactg	1261
Db	1234	gtctcgttatctgtcgcggacatcccgaggagaggggctctgaagaataagctctctcaactg	1293
OY	1262	gtatbgaggaacaacatacaagccctcttctggaagcaatgtgcactgaggaatgtctga	1321

Db 1294 GTATGAGACACACTACAAAGCCCTTTGGAGCAATGAGCACTGAGAAATGCTGCA 1353
QY 1322 AACCTTATGAAACCTCTCAACCTCTTACTGCAATGATTTGAAAGATTTGAGTC 1381
Db 1354 AACCTTATGAAACCTCTCAACCTCTTACTGCAATGATTTGAAAGATTTGAGTC 1413
QY 1382 TAGCCCTCTTCCCGCAATCTGGAAGCTCGAAGCCGCTGCTGTTGGAAAGATCC 1441
Db 1414 TAGTCTCTTTCCCGCAATCTGGAAGCTCGAAGCCGCTGCTGTTGGAAAGATCC 1473
QY 1442 GTATACACCTGACACTCCACCAAGGAGTCATGGCTGAGGTGACAGACCTTCCA 1501
Db 1474 GTATACACCTGACACTCCACCAAGGAGTCATGGCTGAGGTGACAGACCTTCCA 1533
QY 1502 GGAAGCTGGCTGTCTCATATCTGGAAGGCTGGAAGGAACTCAGCCCAAGATCTG 1561
Db 1534 GGAAGCTGGCTGTCTCATATCTGGAAGGCTGGAAGGAACTCAGCCCAAGATCTG 1593
QY 1562 GAACCTATGAGAGAACAGCAAGAAATGACCTTGCAGATCTGTTGACAGCAAGGA 1621
Db 1594 GAACCTATGAGAGAACAGCAAGAAATGACCTTGCAGATCTGTTGACAGCAAGGA 1653
QY 1622 CAATGACCACTTTGGGAAACAGAGTGGATGGCTTAGATTGAGACAGCCCAAGATCTG 1681
Db 1654 CAATGACCACTTTGGGAAACAGAGTGGATGGCTTAGATTGAGACAGCCCAAGATCTG 1713
QY 1682 GAGCTTTTGGGCAAGCAAGCAAGATGTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1741
Db 1714 GAGCTTTTGGGCAAGCAAGCAAGATGTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1773
QY 1742 GAGAGAAGCTTCAACAGAGACTAACCAAGCAATCCGACATATCTCGCTCATGAGTG 1801
Db 1774 GAGAGAAGCTTCAACAGAGACTAACCAAGCAATCCGACATATCTCGCTCATGAGTG 1833
QY 1802 TGTCACCTGAAACAACTGAAACCTTACCAAGCAAGTTCATGATGATGATGATGATG 1861
Db 1834 TGTCACCTGAAACAACTGAAACCTTACCAAGCAAGTTCATGATGATGATGATGATG 1893
QY 1862 GAGCTGCTGAGAGAGAGAGAGTCTGAGCTGATGATGATGATGATGATGATGATG 1921
Db 1894 GAGCTGCTGAGAGAGAGAGAGTCTGAGCTGATGATGATGATGATGATGATGATG 1953
QY 1922 CAGCATTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1981
Db 1954 CAGCATTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 2013
QY 1982 GAGGACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2041
Db 2014 GAGGACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2073
QY 2042 GAGCATTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 2101
Db 2074 GAGCATTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 2133
QY 2102 CAGCATTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 2161
Db 2134 CAGCATTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 2193
QY 2162 TCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2221
Db 2194 TCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2253
QY 2222 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2281
Db 2254 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2313
QY 2282 GAGCAGGCTGAG 2341
Db 2314 GAGCAGGCTGAG 2373
QY 2342 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2401
Db 2374 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2433
QY 2402 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2461
Db 2434 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2493
QY 2462 GTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2521
Db 2494 GTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2553
QY 2522 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2581
Db 2554 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2613
QY 2582 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2641
Db 2614 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2673
QY 2642 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2701
Db 2674 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2733
QY 2702 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2761
Db 2734 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2793
QY 2762 GATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2821
Db 2794 GATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2853
QY 2822 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2881
Db 2854 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2913
QY 2882 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2941
Db 2914 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2973
QY 2942 AGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3001
Db 2974 AGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3033
QY 3002 GGTAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3061
Db 3034 GGTAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3093
QY 3062 TGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3121
Db 3094 TGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3153
QY 3122 AATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3181
Db 3154 AATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3213
QY 3182 TGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3241
Db 3214 TGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3273
QY 3242 GTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3301
Db 3274 GTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3333
QY 3302 TGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3361
Db 3334 TGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3393
QY 3362 CAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3421
Db 3394 CAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3453
QY 3422 CTG 3481
Db 3454 CTG 3513

OY	3482	cccttaccctccgcaaggagataatggaagctgctgtctgtcaataaccgaacaaggccgcacat	3541
Db	3514	cccttactccccgagggggaatattggagctgctgtctgaaataccgaagaaggccgacat	3573
OY	3542	tattctctcaaccacacatgatgaagccgaagctctgtggagacaggaattgccaat	3601
Db	3574	tattctcttaccacaccacatgatgatgaacccgagactccttgggggacagagattgcattat	3633
OY	3602	ctcccatlggaaagctgtgctgtgtgtggctctctccctgtttcttgaagaaccagctggagac	3661
Db	3634	ctcccatlggaaagactgtgctgtgtgtggctctctccctgtttcttgaagaaccagctggagac	3693
OY	3662	aggctactactgaacctgtgtcaagaanaatgttgaaatccccccctcagttctctcaaaa	3721
Db	3694	aggctactactgaacctgtgtcaagaanaatgttgaaatccccccctcagttctctcaaaaa	3753
OY	3722	cagtagtagactgtgtcatalactctgnaaaaaggagacagtglttctcaagcagttctga	3781
Db	3754	cagtagtagactgtgtcatalactctgnaaaaaggagacagtggtttctcagacagttctga	3813
OY	3782	tgctgcgcttggcagcgaccatgagagtgtaacgcttgacccttgatgctgtatctc	3841
Db	3814	tgctgcgcttggcagcgaccatgagagtgtaacgcttgacccttgatgctgtatctc	3873
OY	3842	caacctcatgaagaagacatgtgtctbaagcccgcgctgtgtgnaagacataaggaatgact	3901
Db	3874	caacctcatgaagaagatgtgtctbaagcccgcgctgtgtgnaagacataagggactgagct	3933
OY	3902	gaacctatgtctgcacatalgaagcctgtcgaaggagaccttgttgaaactcttcatga	3961
Db	3934	gacctatgtctgtccatattgaattgaactctcttaaggaggagcgtttgtgaaactcttcatga	3993
OY	3962	gattgatgaacgggctctcagaactgtgcaattcttaagtagcatctcaagaagacacct	4021
Db	3994	gattgatgaacgggctctcagaactgtgcaattcttaagtagcatctcagaagacacct	4053
OY	4022	ggaagaaatatctctcaaggctggcgcgaagaagtggtgtgtagtctgaagcctaagatg	4081
Db	4054	ggaagaaatatctctcaaggctggcgcgaagaagtggtgtgtagtctgaagcctaagatg	4113
OY	4082	tacctgtccagaagaagcaagacagcgggccttcgggacaagacagatcttctgcgcc	4141
Db	4114	tacctgtccacacagagaaagaaagggggccttcggggacaaagcagactgttctgcgcc	4173
OY	4142	gttcactgaagaatgaatcctgcacccaatgatcttgcacatagaccagaatccagaga	4201
Db	4174	gttctactgaaatgatattctctgatccaaatgatcttgcacatagaccagaatccagaga	4233
OY	4202	gacagaactgtctgaatgtggatgtgatgcaaaaggctctcaacagtgtaaaagcttgaact	4261
Db	4234	gacagaactgtctgaatgtggatgtgatgcaaaaggctcttaccagtgtaaaagcttgaact	4293
OY	4262	tacagaagaacagtttgttggcccttttgttgaaagagactgtcaatttgcagaacyagatg	4321
Db	4294	tacacagacacagattgttgcccttttgttgaaagagactgtcaatttgcacagcagatgc	4353
OY	4322	gaagaagatlltttgtctcaagatgtgtcttgcacagtgatgtgtgtctgattggccctgttt	4381
Db	4354	gaagaagatllttttctcagattgtgtcttgcacagtgatgtgtgtgtctgattggccctgttt	4413
OY	4382	cagcctgtatctgcaaccccttgttcaagtagtaccacagccttgaacttcaagccctgtatga	4441
Db	4414	cagcctgtatctgcaaccccttgttggcagatgaccacagccttgaacattcagccctgatgta	4473
OY	4442	caagaacacgtacacatttgtcagaatgatgtcctctgaagacacggggaacccttgaact	4501
Db	4474	caacacaaacgtatcaaatatttgttcaacaaatgatgtcctctgaagacacgggaacccttgaact	4533
OY	4502	cttaagacccctcaacaaagccttggcttcgggaacccgctgtatgtatgaagaaacccat	4561
Db	4534	ctttaaagccctctacacaaagaccccttgcttcgggaccccgctgtatgtatgaagaaacccat	4599

QY	4562	ccccgaacagccctcgtccaggcagggaagaaagtgcgacacctgcgccagttccccaagc	4621
Db	4594	cccgagacacgcgcccgtccagccagccgaggaamaagtgagcaccctccacgttcccacga	4653
QY	4622	catcatgacctcttccagaatggaacccggagcaatgcaagacctcaactgcatcca	4681
Db	4654	catcatggacctcttccagaaatggaaatcggaacatgcgaamaaccttaccctgatccca	4713
QY	4682	gtgtagcagcgacaatatcaagaatgctgcctgtgtgtccccaaggcgagggggct	4741
Db	4714	gtgtagcagcgacaaaatcaagaagaatgcgtgcctgtgtgtccccaaggcgaggggct	4773
QY	4742	gacctctccaaaagaacaaaacacccctgcagatctcccttaagaccctggacaggaagaa	4801
Db	4774	gcctctctccaaaagaamaaaacacctgcagatctcttccagagacctgcagagaaamaa	4833
QY	4802	catctcgatcatctgtgtgaagacgtatglugagatcatagccaagaactaaagaacaa	4861
Db	4834	catctcgatcatctgtgtgaagacgatatgcagatcatagccaamaaccttaagaacaa	4893
QY	4862	gactcgggtgaatgaagtttagtatagtgacgctttccctgggtgcagtaatactaaagc	4921
Db	4894	gattctgggtgaatgaatttagtatagtgacgcttttccctgggtgcagtaataactaaagc	4953
QY	4922	acttccctccgagtcgaagaaatlaatgaatgcataccaacaaatgaaagaacccataagct	4981
Db	4954	acttctctccgagtcgaagaagttaatgaatgcataccaamaaaatgaagaamaacctaaagct	5013
QY	4982	ggccaagaacagttctgcagatcgattctccaacagcttgggaagattatgacagact	5041
Db	5014	ggccaaagacagcttctgcagatcgattctccaacagcttgggaamaatttatgacagact	5073
QY	5042	ggaccacgaagaaatgaatgcaagtggtgtgttccaataacaaaggctggcaatgcaagctc	5101
Db	5074	ggaccacgaaatgaatgaatgcaagtggtgtgttccaatacmaaggctggcaatgcaagctc	5133
QY	5102	tttccctgaatgcatcaacaatgccaattctccgggccaacctgcaaaagggaagaaacc	5161
Db	5134	ttttcctgaatgcatcaacaatgccaattctccgggccaacctgcaaaagggaagaaacc	5193
QY	5162	tagcctaataatgaatgaatgaatgcttccaatactccctggaaatccaacaagcagacgtc	5221
Db	5194	tagcctaataatgaatgaatgaatgcttccaatactccctggaaatccaacaagcagacgtc	5253
QY	5222	agaagtgagctcgtabgacacatacgaatggaatgctcctgtgtccatcgtgtcaactgtgc	5281
Db	5254	agagtgagctcgtabgacacatacgaatggaatgctcctgtgtccatcgtgtcaactgtgc	5313
QY	5282	aattgtccttcgtcccaagcagcttgtgcgattctccgataccagggcgagttcaagaagc	5341
Db	5314	aattgtccttcgtcccaagcagcttgtgcgattctccgataccagggcgagttcaagaagc	5373
QY	5342	aaaacacccgagttccaacgattggaatggaagcctgtcaatactactggtctcctaattgt	5401
Db	5374	aaaacacccgagttccaacgattggaatggaagcctgtcaatactactggtctcctaattgt	5433
QY	5402	ctggagatagtgcaatacgaattgtcctcctgcacaactcgtgcatatcatatcttaactgct	5461
Db	5434	ctggagatagtgcaatacgaattgtcctcctgcacaactcgtgcatatcttaactgctgct	5493
QY	5462	ccgaaggaagtctaatgtgtctccaacaatcgcgcctgtgctagccctctcaacttgcct	5521
Db	5494	ccgaaggaagtctaatgtgtctccaacaatcgcgcctgtgctagccctctcaacttgcct	5553
QY	5522	gtatgggtgtgcatcacacctcctcatgtaaccaagcctccttgtgtccaagaatcccaag	5581
Db	5554	gtatgggtgtgcatcacacctcctcatgtaaccaagcctccttgtgtccaagaatcccaag	5613
QY	5582	caaaagcctatgtgtgtcctccaacacgtgaagcctctcaattggaataaaggagcgtggc	5641
Db	5614	caaaagcctatgtgtgtcctccaacacgtgaagcctctcaattggaataaaggagcgtggc	5673
QY	5642	caaccttggctcggagcgtgttccacgcgaataaagctgtaataatacataatgataatcctgaa	5701

QY 7862 gatccgtgtaagaggcaagaatcaacagccaaactgctgaggctgcaagctgctgaagc 7921
 |||||
 Db 7894 GATCCGTGTAAGAGGCAAGAAATCAACAGCCAAACTGCTGGGGCTGCAAGCTGCTGAAGC 7953
 QY 7922 caggagcaaggagtaagaagatctgctgctcaaacctagggaagctgtgcccatttgc 7981
 |||||
 Db 7954 CAGGGGATGGGATTAAGAGATTTGCCCTCAACCTAGGGAGAGCCCTGGCCATTTTCTC 8013
 QY 7982 cgaactgctgtaacacatgtaacacgctcgaagaatgtaattctgacacaaagtatt 8041
 |||||
 Db 8014 CTGACGTCTGCTACATGATGTAAGTCACTGCTCAAGATGTTATCTGACACAGTGAT 8073
 QY 8042 attctgagctttagaataatcagaanaaagaaagatgagatgtgattttgacaaaaa 8101
 |||||
 Db 8074 ATTTGCGCTTTTGAATTAATCTGAAAAATGAAAAAGATGAGTGTATTTTGAACAAAA 8133
 QY 8102 tgttgaacttttaagtatttgaatttaagtctacagtgactctgaatccct 8161
 |||||
 Db 8134 TGTTGTACTTTTAAATGTTATTTGAAATTTTAAAGTTCTATAGTACTTGAATCCCT 8193
 QY 8162 agaatgacctcttgtaagaccctgtaagagagagatgagccactgcccactattt 8221
 |||||
 Db 8194 AGAATGGCCTCTTTGTAAGAACCTGCTGATAGAGAGATAGGCCACTGCCACTATTT 8253
 QY 8222 ttatttcttaagagtttgcatalcagtcagtaagtgccctagaagaatgtgatg 8281
 |||||
 Db 8254 TTATTTCTTATGATTAAGTTTGAATATCACTGACTAGTGCCTAGAAAAAGCAATGTAG 8313
 QY 8282 gtaagatctcagacattatattgagtttcttcaagatcttgaagtaactctaatc 8341
 |||||
 Db 8314 GTAGAGATCTCATGACATTAATTTAGATTCTTTCAGATTCATTTTAGTACTCTTAATC 8373
 QY 8342 tcaacttcaatcaacaataatttttgaagtgatgctgtaagctgaagaatgtaagtaac 8401
 |||||
 Db 8374 TCACCTTCATCAATCAATATATTTTTCAGTGTAGTGTAGTGAAGATGATAGTACTG 8433
 QY 8402 gtaataagcagagagataatgaatcagtaacactcctggtccatgtattcagctca 8461
 |||||
 Db 8434 GTATTAAGACTAGAGATATATTAAGTCTCAGTACCTTCTGTCCTGATTTATTCACCTCA 8493
 QY 8462 ctggtttacaacatagatgctgctgctggttgaagagccactgtaacaataatgagca 8521
 |||||
 Db 8494 CTGCTTACCAATATATGTTGTCTGTGTGTGTAAGAGCCCACTGTAAACATATTTGGGA 8553
 QY 8522 gaccttt 8581
 |||||
 Db 8554 GCGTTTTTTTTTTTTTTTAAATGCAAAATGCAAAAGCCAAAGATTAAGGTGCACA 8613
 QY 8582 agtttaacaagaatctcgaacagggaaacaagctagcttgaanaactgtcgaaanaac 8641
 |||||
 Db 8614 AGTTTAAACATGATTAATCTTCAACAGGGAAMACAGCTAGCTTGAATACTGTGAAATAAC 8673
 QY 8642 acaactgtgtttagcagatctgtaacactcgaataatgagcttgcagatctgagatc 8701
 |||||
 Db 8674 ACACTGTGTATATGCAATTTAGTACCTTCAATTAATTTGGCTTTGCAAGTATTTGGATAC 8733
 QY 8702 cccattaaatctgacagctcctcaaatcttcaatcctcctcaactagctcaagaanaatat 8761
 |||||
 Db 8734 CCGATTAAATCTGACAGTCCCAATTTTTCATCTCTTCAATCACTAGTCAAGAAAAATAT 8793
 QY 8762 aaaaaacaacaatactcatalatgagacatcttcaagagtttctcaaccagctcattc 8821
 |||||
 Db 8794 AAAAAACAACAATATCTCCATATGAGAGCATTTTTCAGAGTTTCTCAACCCAGCTCTAATTT 8853
 QY 8822 tttaagcagtaaacatttttaaaaactggttcaactaactaactgtaactgttcaacttct 8881
 |||||
 Db 8854 TTCTAGTCAGTAACATTTGTAATAATCTGTTTCACTAATCTTACTTGTAACTGTCTT 8913
 QY 8882 gagagaaagaanaataatgagagagactgttctgaggaagtcaagtgatcttcaata 8941
 |||||
 Db 8914 GAGAGAAAAAATAATGAGAGACATATTTGGGGAGAGTTCAAGTATCTTTTCAATA 8973

QY 8942 tcaattactaacttcttcactttttccaaaaattgaaatlattaaagcgttaaaagtgaagc 9001
 |||||
 Db 8974 TCATTTACTTAACCTTTTCCACTTTTCCAAAATTTGAATTAATTAAGCTTAAGGTGAAGC 9033
 QY 9002 ttcaagtttcaaatcttctcatalatttttaaatcttcaagaataatataataaccac 9061
 |||||
 Db 9034 TTCAAGATTTCAATTAATCTTTCTATATTTTAAATTTTACAGAAATTAATTAACCCAC 9093
 QY 9062 tgcctgaanaaagaanaaagtgttctttagaagttlaaagttcaatataatgtattcaatata 9121
 |||||
 Db 9094 TGCTGAAAAAGAAAAATGATTTGTTTGAAGTTTAAAGTCAATTAATGATTTTAAATATA 9153
 QY 9122 agtaatgaagcagatattccaataactagatgataatgcatcggttgaacttaagatactc 9181
 |||||
 Db 9154 AGTATGAGAGCATATTTCCATTAATAGTATGATGATGATGATGATGATGATGATGATGAT 9213
 QY 9182 tcaaaaatacagaattatagaataatctcctcatttaataattttcaaatcaaaagt 9241
 |||||
 Db 9214 TCAAAAAATACGAATTTTATTAATTAATTTTCCATTTTAAATTTTCAAAATCAAAAGT 9273
 QY 9242 taagtttccctacttactaataatcgtaattcattcctcattatagtaataatctatagag 9301
 |||||
 Db 9274 TATGTTTCCATTTTACTTAAATCGTATTTCTAATTTCTAATTAATGTAATTTATGAG 9333
 QY 9302 caactccttacttgcgttccctctgatttcaagagccataattttaaanaaacaagcact 9361
 |||||
 Db 9334 CAACCTCTTACTTGCTTCTCTGATTTTCAAGGCCATATTTTAAAAATCAAAAGGCACT 9393
 QY 9362 gtaactaatttgaagaanaacagacatcttcaacagatgaaagagacactctgaag 9421
 |||||
 Db 9394 GTGAACCTTTTGAAGAAACAGACATTTAATACAGATGGAAGAGACCTCTCTGAG 9453
 QY 9422 ctagaanaacactaagttataactcattcaataactggttcccttttaaaatagtaa 9481
 |||||
 Db 9454 CTAGAAACAACTAATTAATTAATCACTTCAATTAATGATGATGATGATGATGATGATGAT 9513
 QY 9482 ttttctacatttccctgtaaacactaattgtgtagaatcttcccaactcatalactc 9541
 |||||
 Db 9514 TTTTTCATATTTTCCGTGTAACCTAATTTGTGTAGAAATTTTACCAACTATATCTC 9573
 QY 9542 aatcaagaanaattctglatattccctgtaagatgaactatgtgagttcagaatctc 9601
 |||||
 Db 9574 AATCAAGCAAAATTTCTGTATTAATCCCTGTGAATGATGATGATGATGATGATGATGATG 9633
 QY 9602 tcaaatcagttgttaaaaattctcgcttcttgaactcttgggaacccctcagaanaactat 9661
 |||||
 Db 9634 TCAAAATACGTTTAAAAATTTCTGTTTGCATCTTTGGACACTCAACAAAATCTTAT 9693
 QY 9662 taacaacgttgataatgagaatatacagaanaaataataaagccctcatalataaatgccc 9721
 |||||
 Db 9694 TTAACAATCTGATTAATGAGAAATTAAGAAAGAAATTAATTAATTAATTAATTAATTAAT 9753
 QY 9722 cagcaaatcttctgtaaaaaacaacaacactcacaactcattcattatctgta 9781
 |||||
 Db 9754 CAGCAAAATTAATGTTTAAAAAACCAACCAACCTCACTGATTAATTTCAATTTCTGTA 9813
 QY 9782 ctgaagaacaaatgcttctgtaacttaaatgtgtgacaactcattcattatctgta 9841
 |||||
 Db 9814 CTGAAGCAAAATGCTTGTGACTATTAATGTTGCAATCACTCTTCACTGATTAATTAAT 9873
 QY 9842 tcaattgactaaagcatttgcgtgttcttctctgtgtgtnatataatcaagtaaaaaa 9901
 |||||
 Db 9874 TCAATTAAGCAAAATTTGCTGTGTTTCTTCTGTGNTGNATATTAATTAATTAATTAATTA 9933
 QY 9902 ttttccaaagaacatgltgtaactgtaaaccttggatattgagacatatttgg 9961
 |||||
 Db 9934 TTTTCCAAAGAGCATGTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 9993
 QY 9962 gacctgtgtatataactaataaataatgtaataactgtnagaanaatatgtcttaattctt 10021
 |||||
 Db 9994 GACCCCTGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 10053
 QY 10022 caaatgtgtacatcccccataaangttcattcatalaagattagctgtatccc 10081

Db 10054 CAAATGTCATCCCCCTTAANAAGTTCATTTCCATAGATTAAGCTTGCTTATCCC 10113
QY 10082 ttttataccctaagaatgaagctgttttggctctttgtlcaatcattggcccatcc 10141
Db 10114 TTTCTATACCTTAAGATGAAGTGTGTTTGTGCTTTGTTCATGATGGCCCATTC 10173
QY 10142 aagcatttagctgtctgaatgagatclattttggcactgggaatatctgaattgca 10201
Db 10174 AAGCAGCTTATGCTGTCTGTATGATGATCTATTTTTCATGCAATATCTGAGAAATGCA 10233
QY 10202 aaactagacaaagtttccacaagaatcttaagtttaacatcttccatlaaagaanaa 10261
Db 10234 AAACCTAGACAAAGTTTCAACAAGATTTCTAAGTTAATTCATTTATTAAGAGAAA 10293
QY 10262 aagaaaaaaaatttgaatgcaataacttatatagaaglatnaaaycatattctat 10321
Db 10294 AAGAAAAAAATTTTGTATGTCATTAACCTTATATGATGATTAATTAATGATATTTCTAT 10353
QY 10322 gtgtataataatgagtcacaataaagctgtgacagttctgttaaaaaaataaaaaa 10381
Db 10354 GTTGTATATTAATGATGTCACAAATTAAGCTGTGACAGTTCTGTTAAAAAATAAAAAA 10413
QY 10382 aaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaa 10441
Db 10414 AA 10473
QY 10442 a 10442
Db 10474 A 10474

RESULT 5
AX060721 10474 bp DNA linear PAT 22-JAN-2001
LOCUS AX060721
DEFINITION Sequence 9 from Patent WO0078972.
ACCESSION AX060721
VERSION AX060721.1 GI:12406109
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Law, R.M., Wade, D. and Garvin, M.
TITLE Regulation with binding cassette transporter protein abcl
JOURNAL Patent: WO 0078972-A 9 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
source location/Qualifiers
1..10474
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 2907 a 2304 c 2415 g 2844 t 4 others
ORIGIN

Query Match 99.9%; Score 10429; DB 6; Length 10474;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10436; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 214 CAAAGTGGAAGAACGTTAATGACGACGAGGCGTCCCTGCTGATGCTGGCCGCT 273
QY 242 gcttcacaggtcccgagacacagctgagctgagctgagagaaatgctttg 301
Db 274 GCTTCCAGGGCTCCGAGCCACACGCTGGGCGTGTGCTGAGAGAAATGCTTTG 333
QY 302 gcttcagctgagctgctgtgtggaagaacctcaacttcaagaagaacacatgtca 361
Db 334 GCTCAGCTGAGGTGCTGCTGCTGAGAGAACCTCACTTCAAGAGAGAACAAATGTCA 393
QY 362 gctttactgaaatgagctgagctgagctatattatcttccatctgagcttctgtgct 421
Db 394 GCTGTATCTGGAAGTGGCTTGTGCTTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 453
QY 422 gactacccacccctataac 481
Db 454 GAGCTACCCACCTTATGACAAATGATGATGATGATGATGATGATGATGATGATGATGAT 513
QY 482 aggaacacttccctggttcaagggatatactgtatgcaacacacacacacacacacacac 541
Db 514 AGGAACACTTCCCTGGGCTTCAAGGGATTAATCTGAATGCCAACACCCCTGTTCCGTTA 573
QY 542 cccgactcctgagagagctcccgagttgttgaacattcaacacacacacacacacacacac 601
Db 574 CCGACATCTGTGGGAGGCTCCCGGAGTTGTGGAATTTTAACAAATCCATTTGCTGCTG 633
QY 602 cctgttctcagaatgctgagagcttcttatacagccagaaagacacacacacacacacac 661
Db 634 CCTGTTCAGATGCTCTGGAGGCTTTCTTTATACAGCCAGAAAGACACGATGAAAGA 693
QY 662 catgcacaaagttctgagacattacagacagatcaagaataatccagctcaacttgaagct 721
Db 694 CATGCGCAAGTTCTGAGAACATTACGACGATCAAGAAATCCAGCTCAACTTTGAAGCT 753
QY 722 tcaagattcctgtgtgacaatgaagacacttctctgtgttcttatalacacacactctct 781
Db 754 TCAAGATTTCTGCTGTGACAAATGAACCTTCTGAGGTTCTTATACCAACCTCTCTG 813
QY 782 cccaaagtctactgtgacaagaatgctgagagctgagctgagctgagctgagctgagctgag 841
Db 814 CCAAAAGCTTACCTGTGACAAAGATGCTGAGGCTGAGTGTATTTCTCCACAAAGATTTT 873
QY 842 gcaagctacagttacatttgaac 901
Db 874 GCAAGCTACAGATTTACATTTGACAAAGTGTGCAATGATGATCAAAATTCAGAAAGATGAT 933
QY 902 tcaacttggtagacaaagaatttctgagcttctgtgcttaccacaaagagagaactgtgtc 961
Db 934 TCAACTTGGTGAACCAAGAAAGTTTCTGAGCTTTGTGCTTCAACAAAGAGAACTGGCTGC 993
QY 962 agcagagcagttactcgttcccaacatgacatcctgaagcacaactcctgagacacataa 1021
Db 994 AGCAGAGCAGATTAATTTGCTTCCAAATGACATCTTCAACCAATCTCTGAGAACATTA 1053
QY 1022 ctctaatctcccttcccgacagagagctgtgctgaagccacaacaaatctgctcatag 1081
Db 1054 CTTTACATTTCTCCCTTCCCGAGCAAGAGCTGTGTAAGCCACAAACAAATCTTGCATAG 1113
QY 1082 tcttggagactctgcccagagagctgttcaacatgaaagctgaaagctgaaagctgaaag 1141
Db 1114 TCTTGGGACTCTGGCCCAAGAGCTGTTCAACATGAAAGCTGAGTGAATGAGACATGGAAGA 1173
QY 1142 ggtgatgttctgacaaatgtgaacagctcacaactcctccacacaaatctacacagctgt 1201
Db 1174 GGTGATGTTTCTGACCAATGTAAGACGCTCCAGCTCTCTCCACCAATATTCACAGGCTGT 1233
QY 1202 gtctcgtattgtctgagagacaccccgagagaggggctggaagataagctctcactgt 1261
Db 1234 GTCTCGATTTGTCTGCGGGATCTCCAGAGGAGGGGGCTGAAATCAAGTCTCTCAATG 1293
QY 1262 gtaagagacaac 1321

Db 1294 GATATGAGCAACAACACTACAAAGCCCTCTTGGAGCAATGACACTGAGAAAGATGCTGA 1353
OY 1322 aacctctatgacaactctacaaactctactgaaatgattgaaatgagatc 1381
|||||
Db 1354 AACCTTATGACAACTCTACAACTCTTACTGCAATGATTTGATGAAGATTTGGAGATC 1413
OY 1382 tagtctctctccgcatactgaaagctctgaagccctgctcgttggaaagatcct 1441
|||||
Db 1414 TAGCTCTCTTCCGCTATATCTGGAAAGCTCTGAAAGCCGCTCGTTGGGAAAGATCCT 1473
OY 1442 gtaacacctgacactccagccacaaggaagctgactgctgagtgaaacaaagacttcca 1501
|||||
Db 1474 GATATACCTGACACTCCAGCCACAAGGAGTGTGCTGAGTGGAACAAAGACTTCCA 1533
OY 1502 ggaactgctgtgtccatgatactgaaagcaatgtggaaagaaactcagccccaagatctg 1561
|||||
Db 1534 GGAATGTGCTGTGTTCATGATCTGGAAGGCTGTGGGAGGAACTCACCCCAATATGTG 1593
OY 1562 gacctcatggaagacaagcaagaaatgacctgtccgcatgctgttggacagagga 1621
|||||
Db 1594 GACCTTCATGGAGAAACGCAAGAAATGACCTTGTCCGATGCTGTTGGACAGAGGA 1653
OY 1622 caatgacacacttttggaaacagcaatgtgagtgcttagattggacagcccaagacatcgt 1681
|||||
Db 1654 CATGACCACTTTTGGAAACACAGCTTGGATGGCTTAGATTGGACAGCCAAAGACTCGT 1713
OY 1682 ggcgtttttggccaagcaccagagaatgtccagtcagtaatgttctgtgtacactg 1741
|||||
Db 1714 GCGGTTTTGGCCAAAGCACCCAGAGATGTCAGTCCAGTAAATGTTGTTGATCACTG 1773
OY 1742 ggaagaagcttccaaggaactcaacaggaacaaatccggaacataatcgtcttaagatg 1801
Db 1774 GAGAGAAAGCTTTCAACGAACTAACCAAGCAATCCGACCAATATCTCGCTTATGAGATG 1833
OY 1802 tctcaacctgaaacaagctlagaaacccaatagcaacaagaatctgtgctcaatcaaatgcat 1861
Db 1834 TGTCAACCTGAAACAACTGAAACCCATAGCAACAGAACTGGCTCATCAACAACTGCCAT 1893
OY 1862 ggaagctgctgagatgagaagaatcttgggctgtgtatgtgttcactggaattaccacag 1921
|||||
Db 1894 GGAAGCTGTGGATGAGAGAAAGTTCTGGGCTGTGATTTGTTGCTACGGAATTAATCTCAAG 1953
OY 1922 caacatgagctgagcccatcactgtaagtaagaatccgaatggaacatggaatgtgga 1981
Db 1954 CAGCATTTGAGCTGCCCATCATCTATCTCAAGTACAAAGATCCCAATGGACATTTGATGGA 2013
OY 1982 gaagacaataaatacaaggaatggtactggaacccctgttccctgagctgaccccttga 2041
|||||
Db 2014 GAGCAATGTAATAATCAAGATGGTACTGGAGCCCTGTCTCGAGCTGAGCCCTTTGA 2073
OY 2042 ggaacatgagtaagctctgggggggcttgcctacttgcaggaatgtgtgtgagcaagcaat 2101
|||||
Db 2074 GGCATATGTGTACTGCTGGGGGGCTTGCCTTACCTTGACAGATGTGTGAGAGGCAAT 2133
OY 2102 catcagagtgatcagcagcagcagagaagaacatgtgtctatcatcaacagatgccccta 2161
|||||
Db 2134 CATCAAGGTGTCTACCGGACCGCAAGAAAGAAATGTGTCTATATCAACAGATGTCCTTA 2193
OY 2162 tccctgttaagctgatacacttcttgcggtgtgataagccggltcaatgccccttcat 2221
|||||
Db 2194 TCCCTGTATGATGATGACATCTTTCTCGGGGATGATGAGCGGTCAATGCCCTCTTCAT 2253
OY 2222 gaagctgagctggaattactcagtggtgtgatacatcaaggaatggtgtatgaaagga 2281
|||||
Db 2254 GAGCGTGGCTGTGATTTACTCACTGTGCTGTGATCATCAAGGATGTGTATAGAAAGGA 2313
OY 2282 ggaacagctgaagagacacatgcaatgcaatgagcctggaacaagacatactctgtttag 2341
Db 2314 GGCACGGCTGAAGAGACATGCGGATCATGGGCTGTGANAACAGCATACTCTGTTTGG 2373
OY 2342 ctgttcaatagtagcctcaatccctctctctgtgagcgtgtgcctctagtgatcatcct 2401
|||||
Db 2374 CTGGTTATTAGTAGCTCATCTCTCTTCTTGTGAGGGCTGGCTGTCTAGTGTCTATCC 2433
OY 2402 gaagttagaagaacctctgcccctacagatgataccagcgtgtgttctctccctgcgt 2461
|||||
Db 2434 GAAGTTAGAAACCTGTGCTCTACATGATATCCACAGGTGTGTGTCTCTCTGTCGCT 2493
OY 2462 gttctgtgtgtgacaatccctgcaagtcttccctgataagacactctctccagagccaa 2521
Db 2494 GTTTGCTGTGTGACAAATCTCGAGTGTCTCTGATATGACACACTCTCTCCAGAGCCAA 2553
OY 2522 cctggacagcctgtgtggggaatcactactcaagctgttactctccctagctctgtg 2581
Db 2554 CTTGGACAGACCTGTGGGGGCATCATCTTACGCTGTACTGCTCCACTGCTCTG 2613
OY 2582 ttgtgcaatggcaagactacgttgggcttcaacactcaaatctctgtaagcctgtctctcc 2641
Db 2614 TGTGGCATGGCAGACACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2673
OY 2642 ttgtgcttgggt 2701
Db 2674 TGTGCTTTTGGGTTGGT 2733
OY 2702 gcaatgggacaacactgtttgagatcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2761
Db 2734 GCAATGGGACAACCTGTTTGAAGTCTGTGAGAGATGCTTCAATCTCACACTTC 2793
OY 2762 gatcccaatgt 2821
Db 2794 GATCTCCATGATGCTGT 2853
OY 2822 tgtcttccagcagactagcgaatctccagccctgtgtgtgtgtgtgtgtgtgtgtgtgt 2881
Db 2854 TGTCTTTCCAGCCAGTACGGAATTTCCAGGCCCTGTGTATTTCTTGGACCAAGTCTTA 2913
OY 2882 ctgtgttggcaggaagaatgataagaaagcaccctgtgtgtgtgtgtgtgtgtgtgtgtgt 2941
Db 2914 CTGTTTGGCCAGGAAGATGATGAAAGAGCCACCTGTTCCACCAAGAACATGTC 2973
OY 2942 agaatctgcaatggaaggaagcaaccacacttgaagctgtgtgtgtgtgtgtgtgtgtgtgt 3001
Db 2974 AGAATCTGCATGAGGAGGAGGAACCCACACTTGAAGTGTGGGCTGTGTGTGTGTGTGTGT 3033
OY 3002 ggtaaagcttaccagagatgagatgaaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3061
Db 3034 GGTAAAGTCTTACCGAGATGGGATGAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3093
OY 3062 tgaagggcagatccactctctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3121
Db 3094 TGAGGGCCAGATCACCTCTCTCTGTGGCCACAAATGAGCGGGAAAGACACCATGTC 3153
OY 3122 aatctgacggtgtgttcccccagacctcggtgacacgcttacttctgtgtgtgtgtgtgt 3181
Db 3154 AATCTGACCGGGTGTCTCCCGGACCTGGGACCGGCTTACATCTCGGGAAAAAGACAT 3213
OY 3182 tgcctctgagatgagacacatcccgagacactctgtgtgtgtgtgtgtgtgtgtgtgtgt 3241
Db 3214 TCGCTCTAGATGAGACACCATCCGACAACTGGGGCTGTGTGTGTGTGTGTGTGTGTGTGT 3273
OY 3242 gtttacaatgctgactgtcgaagaacacatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3301
Db 3274 GTTTACATGTGACTGTGAGAGACACATCTGTTCTATGCTCCGCTTGAAGGGCTCTC 3333
OY 3302 tagaagacagtgaaagcgaatgtgaagcaatgtgcccgtgtgtgtgtgtgtgtgtgtgt 3361
Db 3334 TGAGAGACACGTGAAGGGGAGATGAGACAGATGSCCTGTGATGTTGTGTGTGTGTGTGT 3393
OY 3362 caagctgaaagcaaaacaagcagctgtcaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3421
Db 3394 CAAGCTGAAGAAACAAACCAACCTGTGAGGTGAATGAGAAAGCTATCTGTGTG 3453
OY 3422 ctgtgacctgtcgggggatacgaagtgtcaatctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3481
Db 3454 CTTGGCTTTTGTGGGGGATCTTAAGTTGTCTATTTGTGATGAACCCACAGCTGGGTGTGA 3513

QY	3482	cccttactcccgaggggaataatgagagctgctgctgaataacgacaagccgacat	3541
Db	3514	cccttactcccgaggggaataatgagagctgctgctgaataacgacaagccgacat	3573
QY	3542	tattctctcaacacccacatgatatgaagcgagctccttgaggagcaagatgtgcatcat	3601
Db	3574	tattctctcaacacccacatgatatgaagcgagctccttgaggagcaagatgtgcatcat	3633
QY	3602	ctcccatggggaagctgtgctgtgtgggtcctccctgttcttgaaacccagcttggagac	3661
Db	3634	ctcccatggggaagctgtgctgtgtgggtcctccctgttcttgaaacccagcttggagac	3693
QY	3662	aggctactacccctgtgctgaagaaagatgttgaatccctccctcaattctctgcaaga	3721
Db	3694	aggctactacccctgtgctgaagaaagatgttgaatccctccctcaattctctgcaaga	3753
QY	3722	caagtaagtagcactgtgtcatatccctgaaaaagagagcaagtgcttctcgaagcaattcga	3781
Db	3754	caagtaagtagcactgtgtcatatccctgaaaaagagagcaagtgcttctcgaagcaattcga	3813
QY	3782	tgctgagctgggacgacacacatgagagtgacacgctgacacatgagctgtcctgtcatc	3841
Db	3814	tgctgagctgggacgacacacatgagagtgacacgctgacacatgagctgtcctgtcatc	3873
QY	3842	caactcatcaagaaagcatgtgtctgaagccggtgtgtggaagacataagggacatgaagct	3901
Db	3874	caactcatcaagaaagcatgtgtctgaagccggtgtgtggaagacataagggacatgaagct	3933
QY	3902	gaactatgtctgacatgaagctgtctlaagggagggagcccttggaaaccttctcga	3961
Db	3934	gaactatgtctgacatgaagctgtctlaagggagggagcccttggaaaccttctcga	3993
QY	3962	gattgtagaccggtctcgaacctgggacattctcagtaatgacatctcgaagacacct	4021
Db	3994	gattgtagaccggtctcgaacctgggacattctcagtaatgacatctcgaagacacct	4053
QY	4022	ggaagaataatctcccaaggtggccgaagagatggtggttgatgtctgaagcctaagtg	4081
Db	4054	ggaagaataatctcccaaggtggccgaagagatggtggttgatgtctgaagcctaagtg	4113
QY	4082	taccttgcagcaagacgaacagcgcggtccttgaggacaagcagagctgtcttcgccc	4141
Db	4114	taccttgcagcaagacgaacagcgcggtccttgaggacaagcagagctgtcttcgccc	4173
QY	4142	gttcaactgaagatgagctgtcgtatccaaatgatttgcacatagaccacaatctcaaga	4201
Db	4174	gttcaactgaagatgagctgtcgtatccaaatgatttgcacatagaccacaatctcaaga	4233
QY	4202	gacagactgtctcaagtggagatgagtgacaaaggtccctacacagtgtaagctgtgaact	4261
Db	4234	gacagactgtctcaagtggagatgagtgacaaaggtccctacacagtgtaagctgtgaact	4293
QY	4262	tacacagcaacagttgttggtcccttcttgagaaagagactctaattgcgaacggagctg	4321
Db	4294	tacacagcaacagttgttggtcccttcttgagaaagagactctaattgcgaacggagctg	4353
QY	4322	gaaaggaattttgtctcaagatgtcttgccaagctgtgtgtctgcaattcccttggtt	4381
Db	4354	gaaaggaattttgtctcaagatgtcttgccaagctgtgtgtctgcaattcccttggtt	4413
QY	4382	cagccctgacgtggtccaccccttggagaaagtaacccagcctgtgaactcgaagctgatat	4441
Db	4414	cagccctgacgtggtccaccccttggagaaagtaacccagcctgtgaactcgaagctgatat	4473
QY	4442	caacgaacagtaacatattgtgaagcaatgatgtccttgagacaaggagaaaccttgaact	4501
Db	4474	caacgaacagtaacatattgtgaagcaatgatgtccttgagacaaggagaaaccttgaact	4533
QY	4502	cttaaacgctctcaacaaagacccctgtgcttgcggacccgtatgtgaagaaacccaat	4561
Db	4534	cttaaacgctctcaacaaagacccctgtgcttgcggacccgtatgtgaagaaacccaat	4593
QY	4562	cccagaacgcccctgcaggtcaagggaggaagagatgtgaccacgtcccgaattccccaagc	4621

Db 5674 CAOCCTTGTGTCGAGACGTCTGTCCACGACAAATAGCTGAATATATCATATGATATCTCGAA 5733
Qy 5702 gtccgtgttcttgatcctccacatttctgctgggaagaggtccatcgacatggttaa 5761
Db 5734 GTCCGCTTCTTGATCTTCCACATTTTTTGTGCTGGAGAGGGCTCATCGAATGTTGAA 5793
Qy 5762 aaacagggaatgctgtagtgccttcgaaaggtttgggagaaatgcttctgtaccatt 5821
Db 5794 AAACCGAGCAATGCTGATGCTCCGAAAGTTTGGGAGAAATCCCTTTGTCTCACCAATT 5853
Qy 5822 atcttggaactgtgtgggaagaaacctcttcgcaatggcgtgggaaggggtgtgttctt 5881
Db 5854 ATCTTGGACCTTGTGGGAGCAACCTCTTCCCATGGCCGTGGAAGGGGTGTGTCTT 5913
Qy 5882 cctcatctgttcttgatccagtaacagatcttcacagcccaagcctgtataatgcaa 5941
Db 5914 CCMATTAATGTTCTGATCCACTACAGATTTCTTCATCAGGCCCAACCTGTAAATGCAAA 5973
Qy 5942 gctatcctctgaaatgaaatgaaatgtgagggcggaagaaagaaagaaatcttga 6001
Db 5974 GCTATCTCTGTGAATGATGAAGATGAAGATGAGGCGGGAAGACAGAAATTTCTTGA 6033
Qy 6002 tggtagaagccagaaatgacatcttaagaaatcaagagttgacgaagataatagaagaa 6061
Db 6034 TGSTGAGGCGCAAGATGACATCTTGAATCAAGGAGTTGACGAAGATATAGAAGAA 6093
Qy 6062 ggggaagcctgtgttgacagaattggtaggacatcctcctgtgtgagttgttggt 6121
Db 6094 GCGGAAGCCTGTGTGACAGATTTGCGTGGGCAATTCCTCTGTGAGTGTGTGGGCT 6153
Qy 6122 cctgggaagttaatggggtcggaataatcatcaacttcaagatgttaacagagagataccac 6181
Db 6154 CCGGGAATTAATGGGCTGGAATAATCATCACTTTCAAGATGTTAACAGAGATACCAAC 6213
Qy 6182 tgtaccagagagatgtcttcccttaacaaataglatcttaacaaatccatgaagt 6241
Db 6214 TGTACCAAGAGATGCTTCTTCTTAACAAATAGTATCTTATCAACATCCATGAAGT 6273
Qy 6242 acctggaacatgtgtactgcctcagtttgaagccatcaagagacgtttaagtgagag 6301
Db 6274 ACATCGAATGATGGCTACTGCTCCTCAGTTTGAATGCCATCACAGACTGTGTGGAG 6333
Qy 6302 agaaacgttgagttctcttgccttggagagagcccaagaaagttggcaaggt 6361
Db 6334 AGAAGACGTGATCTTCTTCCCTTTGAGAGAGATGCCAGAAAGAAAGTTGGCAAGGT 6393
Qy 6362 tggtagtgagagatccggaactgggctcgtgaaatgtagagaaataatgctgttaa 6421
Db 6394 TGGTAGTGGGCGATTCGGAACCTGGGCTCTGAAGTATGAGAAATAATGCTGTATA 6453
Qy 6422 ctatagtgagagaaagaaagcgtcttaccagcaatggtttgatcggggagctcc 6481
Db 6454 CTATAGTGGAGCAACAAAGCAAGCTCTTACAGCCATGGCTTTATCGCGGGCTTC 6513
Qy 6482 tgtgtgttcttgatgaacccacacagagcatgtaaccacaaagccgggtgttctgt 6541
Db 6514 TGTGCTTCTTCTGATGAACCAACACAGGATGATCCCAAAAGCCGGGCTTCTTGTG 6573
Qy 6542 gaattgtgccatagtggttcaagagagagagatcaatgagtgcttaccatctcatat 6601
Db 6574 GAATTTGGCCCTAAGTGTCTCAAGGAGGAGATAGTATGCTTACATCTTATAGTAT 6633
Qy 6602 ggaagaatgtgaagcctcttgacactagaatggaatcatgtaatgaaaggttcagtg 6661
Db 6634 GGAAGATGTGAAGCTTCTTGCACCTAGATGGCAATCATGTCATGGAAGGTTCAAGTG 6693
Qy 6662 ccttgagagtgccagcatctaaataataggttggagatgttataaataagttgtag 6721
Db 6694 CCTTGGCAGTGTCCAGCATTAATAAATAAGTTGGAGATGTTATATCAATAGTTGAGC 6753
Qy 6722 aatgagaggttcaaccggagcctgtccagagtttcttgagttcatcttc 6781
Db 6754 AATAGCAGGGTCCAAACCGGACCTGAAGCCTGTCCAGGATTTCTTGTGACTGTGCTTC 6813

Qy 6782 tgaagtgcttcaaaagagaacaccggaacatgctacaataccagcttccatcttcaat 6841
Db 6814 TGGAAAGTCTTAAAGAGAAACCGGAACATGCTCATATACAGCTTCTCATTT 6873
Qy 6842 atctctctggccagatlatcaagcatctctccagagacaaagcagctccacataga 6901
Db 6874 ATCTTCTGTGSCAGATATTCAGCATCTCTCCCAAGGCAAAAAGCGACTCCACATAGA 6933
Qy 6902 agactactctgttctcagaacaaacttgaagcaagatattgtgaactttgcaagacca 6961
Db 6934 AGACTACTCTGTCTCAGACACACTTGACCAAGTATTTGTGAATTTGCCAAGHACA 6993
Qy 6962 aagtgatgaacacttaagaacccctcctacatcaacaaacagacagtagtgcagct 7021
Db 6994 AAGTGATATATACCACTTAAAGACCTCTCATTTACAAAAAACGACAGATGAGGAGT 7053
Qy 7022 tgcagttctcacatcttcttaccagatgagaagtgaaagaaagctatgataagaat 7081
Db 7054 TGCACTTCTCAGATCTTCTTACAGATGAGAAGTGAAGAAAGCTATGTATGAAGAT 7113
Qy 7082 cctgttcaacaggtgtgtgtaaaagtaagagaaactagacttctccttgacacatga 7141
Db 7114 CCGTTTCATAGGGGTGCTGAAAGTAAAGGAGACTAGACTTTCCTTGTGACCATGTGA 7173
Qy 7142 agtgtgtggaagaaagccagagagttgagtgtggaagaaatgaactgatactact 7201
Db 7174 AGTGTGTGGAGAAAGAGCCAGAAAGTTGATGTGGGAAGAAAGTAACTGGATGTGACT 7233
Qy 7202 galactatcaatgcaatgcaatccaatgcaatgcaatgcaatgcaatgcaatgcaatgcaat 7261
Db 7234 GATACTATTAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 7293
Qy 7262 tgccttgtagcttaagcttgtagtgcctcagtgaaagaaacttgatattgatttla 7321
Db 7294 TGCCCTTGTAGCTATGCTGTGTATGCTCTCAAGTGAAGAACTTGAATTTAGTTTAA 7353
Qy 7322 cctatacctatgtaaacctatataatggaacccaatgacatagatggttgaactcaac 7381
Db 7354 CCTATACCTATGTAACCTATATATGAGAACCAATGAGCATATGAGGTTGAACTCACAC 7413
Qy 7382 ttt 7441
Db 7414 TT 7473
Qy 7442 aatcagccagcagatattatgaacaaatgaagatgaacatccatccatcaatgaag 7501
Db 7474 AATCATGGCCAGCATTTATGATCAAAATCAAAAGGTAAATGCACATCCTCATTCAGTAAG 7533
Qy 7502 ccatgcataatgccaagagagagtttcccggtgacacatccatgtgcaagtgagtg 7561
Db 7534 CCATGCAATGCCAGAGAGACTGTGTTCCGGGAGACATCATGCTGCAATAGTGTG 7593
Qy 7562 ccaagatattatgagcagaatttccagaagattggaagcccatggtgtgcatgtcca 7621
Db 7594 CCAGAGTTATTTGTGCCAAAGTTTTCAGAAAGTTTGAAGCCACATGAGTGTGATGCTCA 7653
Qy 7622 ctttgtagaagctgtcgtcagagatctacaacatlgaaatlaacatgttgacagaatg 7681
Db 7654 CTTTGTGAACACTGCTGCTGCTACAGATCTATCAACATTTGATATACATGACAGAAAGG 7713
Qy 7682 tgcagtgagtgtaacatcctgtcttgatctccctcgtataagctgtctgtgtgagta 7741
Db 7714 TGCCATGCTGTGCTTAACATCTGCTTGTGATTCCTCTATAGAGCTGTCTGTGAGCACTA 7773
Qy 7742 acatgcaacaaatgtgtgtgtctcctagagcaggaagcctgtgttcatctgttatactg 7801
Db 7774 ACATGCAAAAAAATGTGGGTGCTCTACAGCAGGGAACCTTGTGTATGTTATATG 7833
Qy 7802 tccatagcttcagagccatgagtgctacaggttccatccatagagactcttaataactta 7861
Db 7834 TCTTATGCTTGCAGCATGTGGTCTACAGGTCATCTTATGAGACTCTTAATATATCTTA 7893

Db 10054 CAAATGTCATCCCTTAATAANGTCTATTTCATAGAGATTAGTCTTATCC 10113
Qy 10082 ttcttataccctaagaatgaagctgttttgyctcttltgtlcatcatgagccctatcc 10141
Db 10114 TTCTTATACCTTAAGATGAAGCTGTTTGTGCTCTTTGTTCATCATATGGCCCTCATCC 10173
Qy 10142 aagcaacttaagctgtctgtatgtgatactatltttgcactgtgaatatctgtgaattga 10201
Db 10174 AAGCATTATACCTGCTCTGTATGTGATCTATTTTGGCATCTGAATATCTGAAATTTGCA 10233
Qy 10202 aaactgacaaaagtctcaacaagaattctaaatcaatcttcatlaaagaagaa 10261
Db 10234 AACTTGACAAAGTTTCAACAGTTTCTAGTTAATCATTTTCAATTAAGGAAA 10293
Qy 10262 aagaaaaaaatttltatgtcaataacttatatgaaglatlaaattgcatattctat 10321
Db 10294 AAGCAAAAAAATTTTGTATGTCAATTAATTAATGAATTAATTAATCAATTTCTAT 10353
Qy 10322 gtgtataataatgaatcaataaataaagctgtgacagctctgttaaaaaa 10381
Db 10354 GTGTATATTAATGAATCAATAAATTAATGAATGTGACAGTTCTGTAAATAAAAAA 10413
Qy 10382 aaaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaa 10441
Db 10414 AA 10473
Qy 10442 a 10442
Db 10474 A 10474

RESULT 6
AX060898 10474 bp DNA linear PAT 22-JAN-2001
LOCUS AX060898 7 from Patent WO0078971.
DEFINITION Sequence
ACCESSION AX060898
VERSION AX060898.1 GI:12406275
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Law, R.M., Wade, D., Oram, J.F. and Garvin, M.
TITLE Atp binding cassette transporter protein abci1 polypeptides
JOURNAL Patent: WO 0078971-A 7 28-DEC-2000;
CY THERAPEUTICS, INC. (US)
FEATURES
source location/Qualifiers
1..10474
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2906 a 2305 c 2416 g 2843 t 4 others
ORIGIN

Query Match 99.9%; Score 10429; DB 6; Length 10474;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10436; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 214 CAAAGTGAACAAAGTAAATGACCAAGGCGTCCCTGCTGAGCTGTGGCGCT 273
Qy 242 gcttccagggctcccgagccacacgctgagcggtgctgctgagggagacatggtgttg 301
Db 274 GCTTCCAGGGCTCCCGAGCCACAGCTGGGCGTGGGCTGAGGGAACATGGCTTTTG 333
Qy 302 gcccaagctgaggtgtgctgctgtgaaagaacctcaacttcagaagaagaacatgtca 361
Db 334 GCCTCAGCTGAGGTTGCTGCTGTGGAAAGAACCTCATTTCAGAAAGAACAACTGTCA 393
Qy 362 gctgttactggaatgagcgtgagccttattatcttccctgactgtatctgtgct 421
Db 394 GCTGTACTGGAAGGCGCTGCTTATTTATCTTCCTGATCTCGATCTCTGTGCTG 453
Qy 422 gagctaccaccatcatgaacaacatgtaatgcatcttccaaataaagccatgcccctgc 481
Db 454 GAGTACCCACCTCATGTAACAAATGAATGACATTTTCCAAATTAAGCCATGCCCTTGC 513
Qy 482 aggaacacttctgtgtgtcagggatattctgtaatgtccacaacccctgttccgtta 541
Db 514 AGGAACACTTCTTGTGGTTCAAGGGATTAATGTAATGCCAAACCCCTGTTCCGTTA 573
Qy 542 ccgagctccctggggagctcccgaggtgtgtgaaacttcaacaatccatgtgctgc 601
Db 574 CCCGACTCCTGGGGAGCTCCCGGAGTTGTGAATCTTAAACAAATTCATTTGTGCTCG 633
Qy 602 cctgtctcagaatgtcggagcttcttatacagccagaagaacacacagatgaaga 661
Db 634 CTTGTTTCAGATGCTCGGAGGCTTCTTTATACGCCAGAAACACACACATGAAGA 693
Qy 662 catgcaaaagttctgaaacattacagacagatcaagaatccagctcaaaactgaagct 721
Db 694 CATGGCAAAAGTTTGAGAACATTAACAGACATCAAGAAATCCAGCTCAAACTGAAGCT 753
Qy 722 tcaaatcttctgtgtgagaaatgaacttctgtgttctatatatacaacccctctct 781
Db 754 TCAAGATTTCTGTGGCAATGAATGAATCTCTGTGGTTCTATATACAACTCTCTCT 813
Qy 782 cccaagctactgtgcaagaatgtcagagctgtatgtcatcttccacaagaatttt 841
Db 814 CCCAAAGTACTGTGGAACAAATGCTGAGGCTGATGTCATTTCCCAAGGATTTT 873
Qy 842 gcaaggtcacagttacatttgaacagatctgtgcaatgtgataaatacaagaagatgat 901
Db 874 GCAAGGCTACCGATTACATTTGACAAAGCTGTGCAATGATCAAAATGAGAAAGATAT 933
Qy 902 tcaactgtgtgcaagaagatgtcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 961
Db 934 TCAACTTGTGTACCAAGAGATTTGTGAGCTTTGTGGCTTACCAAGGAGAAATGCTGC 993
Qy 962 agcagagcagtaactgttcccaaatgtgacatccctgaagcccaatccctgagaacataa 1021
Db 994 AGGAGAGCGAGTACTGTTCTGCAACATGAGATCTCTGAAGCCCAATCTGAGAACCTAAA 1053
Qy 1022 ctctacatctccctcccgagcaagagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1081
Db 1054 CTTCAATCTCTCTTCCAGCAAGAGCTGTGCTAAGCCACAAATAATTTGCTCATAG 1113
Qy 1082 tcttggagctctgtgcccagagatgtgtgacatgtgaagctgtgagatgtgacatgtgac 1141
Db 1114 TCTTGGGACTGTGGCCAGAGACTGTTCAGCATGAAGAACTGTGAGCATGCGACAGGA 1173
Qy 1142 gttgatttcttgaacatgtgaacagctccagcttccaccacaatctacagagctgt 1201
Db 1174 GTGATGTTTGTGACCAAGTGAACAGCTCCAGCTCTCTCCACCAATCTTACAGGCTGT 1233
Qy 1202 gtctgtattgtgtgtgagcattccgagagagagagagagagagagagagagagagag 1261
Db 1234 GTTCTGATTTGTGTGGGCAATCCGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1293
Qy 1262 gttgaggaacaacataaagcccttltgaggaatgtgaggaatgtgaggaatgtgag 1321
Db 1294 GTATGAGCAACAACTACAAAGCCCTTTTGGAGCAATGACACTGAGAGAGATGCTGA 1353

OY 5702 gtccgtgtcttcttgatcttccacatcttctgctggaacgaggtcatcagatgttga 5761
DB 5734 gtccgtgtcttcttgatcttccacatcttctgctggaacgaggtcatcagatgttga 5793
OY 5762 aaaccgagcaatgctgagatgctcctggaaggttgggaggaatcgcttctgacacatt 5821
DB 5794 aaaccgagcaatgctgagatgctcctggaaggttgggaggaatcgcttctgacacatt 5853
OY 5822 atcttgggaacttggtggaacgaacctcttgcacatgagcgctggaaggggtgtgttctt 5881
DB 5854 atcttgggaacttggtggaacgaacctcttgcacatgagcgctggaaggggtgtgttctt 5913
OY 5882 ccccatctatgcttctgataccagatcttcatcagagcccaagcctgttaattgcaaa 5941
DB 5914 cctcatattactgttctgataccagatcttcatcagagcccaagcctgttgaattgcaaa 5973
OY 5942 gctatctcctctgataagataagatgtgagcggaaggaagcaagaaattcttga 6001
DB 5974 gctatctcctctgataagataagatgtgagcggaaggaagcaagaaattcttga 6033
OY 6002 tggtagaagcccaagatgatactctagaacatcaagagttgagcaagatataagaagaa 6061
DB 6034 tggtagaagcccaagatgatactctagaacatcaagagttgagcaagatataagaagaa 6093
OY 6062 ggcgaagcctgctgttgtaagagattgctgaggtatcctcctgtgtgagcttctgagct 6121
DB 6094 ggcgaagcctgctgttgtaagagattgctgaggtatcctcctgtgtgagcttctgagct 6153
OY 6122 ccttgagagtaataagggcgtggaacatcaactctcaagatgtaacagagatataccac 6181
DB 6154 ccttgagagtaataagggcgtggaacatcaactctcaagatgtaacagagatataccac 6213
OY 6182 tcttaccagaagagatgcttcttcttaacaaataagatcttatacaacatcagatga 6241
DB 6214 tcttaccagaagagatgcttcttcttaacaaataagatcttatacaacatcagatga 6273
OY 6242 acatcagaacatgaggtactgctcctcagtttgaatgacatcagagcgtgttaacaggag 6301
DB 6274 acatcagaacatgaggtactgctcctcagtttgaatgacatcagagcgtgttaacaggag 6333
OY 6302 aaaaaacgtgaggttcttcttcttgaagaggtcccaagaaagaagtgtgcaaggt 6361
DB 6334 aaaaaacgtgaggttcttcttcttgaagaggtcccaagaaagaagtgtgcaaggt 6393
OY 6362 tggtagtggagcgtatcggaacatgagcgtcgtgaagatagagaataatgtcgtgtaa 6421
DB 6394 tggtagtggagcgtatcggaacatgagcgtcgtgaagatagagaataatgtcgtgtaa 6453
OY 6422 ctatagtgaggaacaaacgaagcctctcaagacatgagcgttgaatcgagcgtcc 6481
DB 6454 ctatagtgaggaacaaacgaagcctctcaagacatgagcgttgaatcgagcgtcc 6513
OY 6482 tggtagtggagcgtatcggaacatgagcgtcgtgaagatagagaataatgtcgtgtaa 6541
DB 6514 tggtagtggagcgtatcggaacatgagcgtcgtgaagatagagaataatgtcgtgtaa 6573
OY 6542 gaattgtgcctaaagtgtgttgaagaggaagatcagatagtgcttatacatcagat 6601
DB 6574 gaattgtgcctaaagtgtgttgaagaggaagatcagatagtgcttatacatcagat 6633
OY 6602 ggaagaatgtaagcttctgacatgagatgagcaatctgttcaatgtaaggttcaagtg 6661
DB 6634 ggaagaatgtaagcttctgacatgagatgagcaatctgttcaatgtaaggttcaagtg 6693
OY 6662 ccttggcagtgatcagcaatctaaataataggttggagatggtatacaatagtgtaag 6721
DB 6694 ccttggcagtgatcagcaatctaaataataggttggagatggtatacaatagtgtaag 6753
OY 6722 aatgagaggtgcaaaccccgagacctggaagcctgctcagagattcttggacttgatctcc 6781
DB 6754 aatgagaggtgcaaaccccgagacctggaagcctgctcagagattcttggacttgatctcc 6813

OY 6782 tggaaagtgtctaaagaagaacccggagacatgatacaatcagatcttcatcttcaatt 6841
DB 6814 tggaaagtgtctaaagaagaacccggagacatgatacaatcagatcttcatcttcaatt 6873
OY 6842 atcttctggccaggaatattcaagatccttcccaagagcaaaaagcagatccacataga 6901
DB 6874 atcttctggccaggaatattcaagatccttcccaagagcaaaaagcagatccacataga 6933
OY 6902 agactactctgttctcagacaacaacatgacaaagtatttggacttggcagaagca 6961
DB 6934 agactactctgttctcagacaacaacatgacaaagtatttggacttggcagaagca 6993
OY 6962 aagtgatgataccacttaagaacccctcattcaacaaaacagcaagtaagtgagct 7021
DB 6994 aagtgatgataccacttaagaacccctcattcaacaaaacagcaagtaagtgagct 7053
OY 7022 tgcagttctcaatccttcttcaagatgagaagtgaaagaaagctatgataagaat 7081
DB 7054 tgcagttctcaatccttcttcaagatgagaagtgaaagaaagctatgataagaat 7113
OY 7082 cctgttcaatgaggttggtgaaagtaagaagagatgagcttcttccacatgta 7141
DB 7114 cctgttcaatgaggttggtgaaagtaagaagagatgagcttcttccacatgta 7173
OY 7142 agtgltgtagaagaagcgaagtgatgagtgtaggaagaagtaaacgtgatacttact 7201
DB 7174 agtgltgtagaagaagcgaagtgatgagtgtaggaagaagtaaacgtgatacttact 7233
OY 7202 galactatcaatgaaatgaaatcaatgaaatgaaatgaaatgaaatgaaatgaaatgaaat 7261
DB 7234 galactatcaatgaaatgaaatcaatgaaatgaaatgaaatgaaatgaaatgaaatgaaat 7293
OY 7262 tgccttgaagcctatgcttctgataaggtcctcaagtgaaagactgaaattgatttla 7321
DB 7294 tgccttgaagcctatgcttctgataaggtcctcaagtgaaagactgaaattgatttla 7353
OY 7322 cctatcactatgaaatcctatattatgaaacccaatgaaatgaaatgaaatgaaatgaaatgaaat 7381
DB 7354 cctatcactatgaaatcctatattatgaaacccaatgaaatgaaatgaaatgaaatgaaatgaaat 7413
OY 7382 ttt 7441
DB 7414 ttt 7473
OY 7442 aatcatgagcgaagatattatgatacaaatcaaaagttaatgacatccatcactaag 7501
DB 7474 aatcatgagcgaagatattatgatacaaatcaaaagttaatgacatccatcactaag 7533
OY 7502 ccatgcatgcccagagagactgttcccggtgacacatccatgctggaatgagtg 7561
DB 7534 ccatgcatgcccagagagactgttcccggtgacacatccatgctggaatgagtg 7593
OY 7562 ccagagttatagtgccaagtcttccagaagtttgaagaagttgaagcacaagtggtgtcatgctca 7621
DB 7594 ccagagttatagtgccaagtcttccagaagtttgaagaagtttgaagcacaagtggtgtcatgctca 7653
OY 7622 ctttggaaagctgtcctgctcagagctatcaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaat 7681
DB 7654 ctttggaaagctgtcctgctcagagctatcaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaat 7713
OY 7682 tgcacatgctgcttcaagacaacatgacaaagtatttggacttggcagaagca 7741
DB 7714 tgcacatgctgcttcaagacaacatgacaaagtatttggacttggcagaagca 7773
OY 7742 acatgcaacaaaatgtgggtgtctctgaagcagcgggaacgtgtgtcatcttattatg 7801
DB 7774 acatgcaacaaaatgtgggtgtctctgaagcagcgggaacgtgtgtcatcttattatg 7833
OY 7802 tccatgcttgcagccatgaggtctatagaggtatcccttataagaaatgaaatgaaatgaaatgaaatgaaat 7861
DB 7834 tccatgcttgcagccatgaggtctatagaggtatcccttataagaaatgaaatgaaatgaaatgaaatgaaat 7893
OY 7862 gatccgtgtaagaagcaagaatcaacagccaactgtcggggtcgcaagctgtcgagac 7921

```
|||||
Db 7894 GATTCGTGAAGGCAAGAAATCAACAGCCAACTGCTGGGCGTCAAGCTGCTGAAGC 7953
QY 7922 caggccatggagatlaaagagatlgcgcgtlcaaacctlagggagagcgtlgcccatltgctc 7981
|||||
Db 7954 CAGGGCATGGGATTAAGAGATTTGCGTCAACCTAGGGGAAGCGCTGGCCATTTGTC 8013
QY 7982 ctgaactgctgaacatggtacactgcactcaagaagtgcttactgacacaaagtctatc 8041
|||||
Db 8014 CTGACGTGCTGCTAATGTAACACTGCACTCAAGATGTTATCTGACACAAAGTGTAT 8073
QY 8042 atttcgagcttttgaatcaatctgaagaatgaaagatlgagatggttcttctgaacaaa 8101
|||||
Db 8074 ATTTCGGCTTTTGAATTAATCTGAAGAAATGAAAAGATGGATGTTGATTTGACAAAAA 8133
QY 8102 tglttgacttcttaagtgtatlttggaatttaagttcctaactgaactctgaactcctc 8161
|||||
Db 8134 TGTGTGACTTTTAAATGTTATTTGGAATTTTAACTTCTATCAGTACTTCTGAATCTCT 8193
QY 8162 agaatggcctcttctgaagacccttggtatagagagatlgcgaactggcccaactattt 8221
|||||
Db 8194 AGAATGGCTCTTTGTGAAGACCTGTGGTATAGAGAGATGGCACTGGCCACTATTT 8253
QY 8222 ttaattcttaagtaagtttgatcatcaagtaagtaagtaagtaagtaagtaagtaag 8281
|||||
Db 8254 TTAATTTCTATGTAAGTTTGATATCACTATGACTATGCTGCTGAAGAAATGATGATG 8313
QY 8282 gtcaagatctcatgacatatatlttgagtttcttccaagtaacttaagtaacttaac 8341
|||||
Db 8314 GTCAGATCTCATGACATTAATTTGAGTTTCTTCAGATCAATTAAGATTAATCTTAAAC 8373
QY 8342 tcaactcatcaatcaaatlttttgaagtgtatgctgtagcgaagaagatgtagctac 8401
|||||
Db 8374 TCCTTCATCAACCAATATTTTGTGAGTATGCTGATAGCTGAAGAAAGATATGTACGTAC 8433
QY 8402 gtaagaaatgaagagataatlaagctcagtaactcctgtgccaactgtatctacgtca 8461
|||||
Db 8434 GTATAAGACTAGAGAGATTAATTAAGTCTCAGTACACTTCTGTGCCATGTTATTAACCTCA 8493
QY 8462 ctggttcaacaataatagttgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 8521
|||||
Db 8494 CTGTGTACAAATATATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8553
QY 8522 ggccttttttttttttttttttttttttttttttttttttttttttttttttttttttt 8581
|||||
Db 8554 GCGTTTTTTTTTTTTTTTTTATTTGCAACATGCAAAAGCCAAAGAAAGCTTAAGGGTCAAA 8613
QY 8582 agttaacaatgaatctctcaacagggaagaacagctagcttgaagaactgtctgaagaac 8641
|||||
Db 8614 AGTTTAAACAATGAATTTCTCAACAGGGAAGAACAGCTAGCTGAATACTGTGAATAAC 8673
QY 8642 acaactgtgttctatgagctttagtaccttcaataatagtgcttgcagatattgtagt 8701
|||||
Db 8674 ACAACTGTGTGTATGGCATTTATGTACCTTCAATTAATTTGGCTTGTGTGTGTGTGTGT 8733
QY 8702 cccattaaactcagacgtctcaaatlttcatctcttcaactcagtaagtaagaataat 8761
|||||
Db 8734 CCCATTAAATCTGACAGTCTCAAAATTTTTCATCTTTCATCACTAGTCAAGAAAAATAT 8793
QY 8762 aaaaaacaataactcocalatgagagcatlttcagagtttctcaaccagttctattt 8821
|||||
Db 8794 AAAAAACAATAATCTCCATATGAGACATTTTTCAGAGTTTCTTAACCCAGTCTTAATTT 8853
QY 8822 ttctagcagtaaacatttgaataaactggttcaacttaacttacttcttcttcttcttct 8881
|||||
Db 8854 TTTCTAGTCAGTAACATTTTGAATAATCTGTTTCACTAATTAATTAATTAATTAATTAAT 8913
QY 8882 gagagaaagaaaaataatgagagaaactatgttctgggaagtccaagtgtacttccaata 8941
|||||
Db 8914 GAGGAAAGAAAAAATATGAGAACTATTTGTTGGGAAGTTCAAGTGAATTTTCAATA 8973
QY 8942 tcaatctaactctccaacttttccaataattgaataataagctcaaaaggtgtagagc 9001
|||||

Db 8974 TCATTACTAATCTTCTCCTACTTTTCCAAATTTGAATATTAACGCTAAAGGTATAGAC 9033
QY 9002 ttcaagattccaataacttcttctataatltttaaattcaagaatataataataaccac 9061
|||||
Db 9034 TTTCAATTTTCAAAATTAATCTTTCTATATTTTAAATTTACAGAAATTAATTAATTAAT 9093
QY 9062 tgcgtaaaagaaaaaatatgttctttagaagltlaaagtaacatattgattttaaata 9121
|||||
Db 9094 TGCAGAAAAAAGAAAAATATGATTTGTTTACAGTTAAAGTAAAGTAAATTAATTAATTA 9153
QY 9122 agtaagagagcatattccaataactagtgatagatggcactgtgtgcaatttcaagatct 9181
|||||
Db 9154 AGTATGAGGCAATATTTCCAAATTAATTAATTTGATATGACATGCTGTAATTAAGTATCT 9213
QY 9182 tcaaaatacagaatttataagaataatlttcccaacttaataatlttccaataaagat 9241
|||||
Db 9214 TCAAAATTAACGAATTTATAGAAATATTTCTCCCATTTATATTTTCAAAATCAAAAGT 9273
QY 9242 tatgtttccctcatlttactaanaatcgtatcttaacttcaatlaagtaaatctatgag 9301
|||||
Db 9274 TATGTTTCCATTTACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 9333
QY 9302 caactcctactcgtgtccctcgtatlttcaagagcatattttaaataaagaagcact 9361
|||||
Db 9334 CAACCTCTTACTTGTGTTCTGTGATTTCAAGGCCATATTTTAAATAATCAAAAGGCACT 9393
QY 9362 gtgaactatttgaagaagaacagacatltttaaataagatgaaagagcctctcgaag 9421
|||||
Db 9394 GTGAACCTATTTTGAAGAAACACGACATTTTAATACAGATTTGAAGAGACCTTCTGAAG 9453
QY 9422 ctgaagaacatctatagtaacatctcaatlaaactgaactgttcaacttlaaagatlaa 9481
|||||
Db 9454 CTAGAAACAACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 9513
QY 9482 tttttacatttccctcgtgtataactaaatltgtgtgtgtgtgtgtgtgtgtgtgtgtgt 9541
|||||
Db 9514 TTTTTCATATTTTCTGTGTAACTTAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9573
QY 9542 aatcaagaacaaattctgtatattccctcgtgtgaatgtcaatgtgaatttcaagaatctc 9601
|||||
Db 9574 AATCAAGCAAAATTTCTGTATATTTCCCTGTGGAATGTATGCTATGTGAATTTCAAAAATTC 9633
QY 9602 tcaaaatcgttcaaaaatlttctgtccttltgcaactlttggaacccctcagaacattat 9661
|||||
Db 9634 TCAAAATAGCTGTCAAAAATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9693
QY 9662 taacaactgtgataatgagaataatagaagaataatagaacccctctataataatagcc 9721
|||||
Db 9694 TTAACAACGTGTGAATTTGAGAAATTAAGAAATTAATTAATTAATTAATTAATTAATTAAT 9733
QY 9722 cagcaaatctatgtttaaanaaacaacacccctcacactactglatlctatctgtga 9781
|||||
Db 9754 CAGCACAANTTCATTTTAAAAAACAACCAACCTCACACTACTGTATATCTGTAT 9813
QY 9782 ctgaagaacaaatgtctgtgactatlaaagtgtgcaatcaatctcaactgtatagtaa 9841
|||||
Db 9814 CTGAAGAAGCAAAATGCTTGTGACTATTAATATGTGACATCTTCAATTCAGTAAAGTAA 9873
QY 9842 tcaattgactaaagcaattgtcgtgttcttctcgtgtgtgtgtgtgtgtgtgtgtgtgtgt 9901
|||||
Db 9874 TCAATTTGACTTAAGCCATTTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9933
QY 9902 ttctccaagagccatgtgtcaatglaaactgaaccccttgatatttgaacataatttg 9961
|||||
Db 9934 TTTTTCAAAGAGCCATGCTCATGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 9993
QY 9962 gacctgtgtatctactactaagaataaagtaactgtaagaaataatgtcttaattctt 10021
|||||
Db 9994 GACCCCTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10053
QY 10022 caaatgtgtcatccccccttaanaangtctatlttccaataagatlttagcttatccc 10081
|||||
Db 10054 CAAAATGTCATCCCTTAAANAGTCTATTTCCATTAAGATTTACTGTGCTATCC 10113
```

QY	10082	ttcattaccctaaagltgaagctgltttagtgcctttgttcaatcttgccctaatcc	10141
Db	10114	ttctttatfacccttaagatgaagctggttttggctcttttttcaatcattggccctcaftcc	10173
QY	10142	aagcactttagctgctgctgtaatggatctatcttggcactggaatctcgagaattgca	10201
Db	10174	aagcacttttagcctgctgctgttaattggagatctatttttggcactggaaatattctgacaatttgc	10233
QY	10202	aaactagacaaagtttccacaacagatttctaagttaaattcatcttcatlaaaggaaaa	10261
Db	10234	aaactagacaaagtttccacaacagatttctaagttaaattcatcttcatlaaaggaaaa	10293
QY	10262	aagaaaaaaatttggtaagtcaataactttatagaagtattaaatgcatatttctat	10321
Db	10294	aagaaaaaaatttggtaagtcaataactttatagaagtattaaatgcatatttctat	10353
QY	10322	gtctgaatcaatgagtcacaataaagctgtgaacgtctgttcaaaaaaaataaaaa	10381
Db	10354	gttctgaatcaatgagtcacaataaagctgtgaacgtctgttcaaaaaaaataaaaa	10413
QY	10382	aaaaaataaaaaaaataaaaaaaataaaaaaaataaaaaaaataaaaaaaataaaaa	10441
Db	10414	aaaaaataaaaaaaataaaaaaaataaaaaaaataaaaaaaataaaaaaaataaaaa	10473
QY	10442	a 10442	
Db	10474	A 10474	

LOCUS	AX060900	10474 bp	DNA	linear	PAT 22-JAN-2001
DEFINITION	Sequence	9 from Patent WO0078971.			
ACCESSION	AX060900				
VERSION	AX060900.1	GI:12406276			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 10474)				
AUTHORS	Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.				
TITLE	ATP binding cassette transporter protein abci1 polypeptides				
JOURNAL	Patent: WO 0078971-A 9 28-DEC-2000;				

Source	Location/variables
BASE COUNT	2907 a 2304 c 2415 g 2844 t 4 others
ORIGIN	1. 10474 /organism="Homo sapiens" /db_xref="taxon:9606"

Query Match	99.9%	Score 10429;	DB 6;	Length 10474;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 10436;	Conservative	0;	Mismatches 5;	Indels 0;
			Gaps	0

QY	2	gcccggaccacccgacagacccgacgacaccccttctccggagtgtagcagagcgagcgcg	61
	1		
Db	34	GGCACGAGACCCCAAGACCCGAGCCACCTTTCTCCGGGCTCGCGCAGGGCGAGGGCGGG	93
QY	62	gagctccgcgcagcaacaacagacgacgcttctcaaggcgctttagctccctgtatttttccccc	121
	1		
Db	94	GAGCTCCGCGCGCACCAACAGACCGGTTCTCAGGGCGGCTTCTCTCTTTTTCGCCGG	153
QY	122	ttctggtttttctccctctctccgcgaagccttgtaaggaggttagsgaagaagacgcaaca	181
	1		
Db	154	TTCTGTTTTCTCCCTCTCTCCGAAAGGCTTGTCAAGGGGTAGGAGAAAGACGCAACA	213
QY	182	caaaagtcggaaaacagttaatgacacgaacgaaggcgctccctgcgtgtagctcttgccgct	241
	1		
Db	214	CAAAAGTCGAAACAGTTTAATGACCAACGAGGCGTCTCCGTGCTGTAGCTCTGTGCGCCT	273

QY	242	gcttcacaaagctctcccgagacacaaagctcggagcgtgcgtgcgtgagggaaatctgctgttg	301
Db	274	gcccttcacaaagctctcccgagacacaaagctcggagcgtgcgtgcgtgagggaaatctgctgttg	333
QY	302	gacctaaagctgaagttctgctgtctgtgtgaagaacactcaacttcagagaagaacaaacatgtca	361
Db	334	gccctaaagctgaagttctgctgtctgtgtgaagaacactcaacttcagagaagaacaaacatgtca	393
QY	362	gctgttactggaagtagagcgtctgctctatattcttcctgatactctgatactctgtctgct	421
Db	394	gctgttactggaagtagagcgtctgctctatattcttcctgatactctgatactctgtctgct	453
QY	422	gaagtaaccacaccttaatgaacacaaatgaaatgcatttccaaataaagccaatgcccctctgc	481
Db	454	gaagtaaccacaccttaatgaacacaaatgaaatgcatttccaaataaagccaatgcccctctgc	513
QY	482	aggaacactctctctgtgtgtctcaggagatatactgtaatgcccacaacaccctggttccgtta	541
Db	514	aggaacactctctctgtgtgtctcaggagatatactgtaatgcccacaacaccctggttccgtta	573
QY	542	cccgaactccttgaggagctcccggaatgtgtgtgaacatttaacaataatctgtgtctgc	601
Db	574	cccgaactccttgaggagctcccggaatgtgtgtgaacatttaacaataatctgtgtctgc	633
QY	602	cctgttctcgaatgtctggaagcttctttatcacagccagaagaacccagaatgaaga	661
Db	634	cctgttctcgaatgtctggaagcttctttatcacagccagaagaacccagaatgaaga	693
QY	662	catgtgcaaaagtctcgaagaacattacagacagatcaagaanaatcacagctcaaacattgaagt	721
Db	694	catgtgcaaaagtctcgaagaacattacagacagatcaagaanaatcacagctcaaacattgaagt	753
QY	722	tcaagaattcctgtgtgacaaatgaaacctctctctggttccctatatacaacacctctct	781
Db	754	tcaagaattcctgtgtgacaaatgaaacctctctggttccctatatacaacacctctct	813
QY	782	cccaaaagctactcttgacaaagatctgcagagagctgatactctccacaagttatctt	841
Db	814	cccaaaagctactcttgacaaagatctgcagagagctgatactctccacaagttatctt	873
QY	842	gcaaggtaccacagttacaatttgaacaaatctctgtgcaatgataccaataatcgaagaagatgat	901
Db	874	gcaaggtaccacagttacaatttgaacaaatctctgtgcaatgataccaataatcgaagaagatgat	933
QY	902	tcaacttggtagccaaagaagtcttctgtgaccttctgtgctcctccaaaggagaactgtgctgc	961
Db	934	tcaacttggtagccaaagaagtcttctgtgaccttctgtgctcctccaaaggagaactgtgctgc	993
QY	962	agcagaagcagtaactcgttccacaatcagacatccctgaagccaatccttagaacaactaa	1021
Db	994	agcagaagcagtaactcgttccacaatcagacatccctgaagccaatccttagaacaactaa	1053
QY	1022	ctctacatctccctctcccgagcaagaagctgtgcttgaagcccaaaaaacatctgtctgataag	1081
Db	1054	ctctacatctccctctcccgagcaagaagctgtgcttgaagcccaaaaaacatctgtctgataag	1113
QY	1082	tcttggaaactctgcccgaagaagctgttccagcatgaaagaactgtagtgaatctgcagaa	1141
Db	1114	tcttggaaactctgcccgaagaagctgttccagcatgaaagaactgtagtgaatctgcagaa	1173
QY	1142	ggtatgttcttcagcaaatgtgaacagctccacatcctctccacccaatatctacagagctgt	1201
Db	1174	ggtatgttcttcagcaaatgtgaacagctccacatcctctccacccaatatctacagagctgt	1233
QY	1202	gtctcgtatattgtctgtcggtgcatcccggaaggaggggggtgaaagatcaagttcttcaacty	1261
Db	1234	gtctcgtatattgtctgtcggtgcatcccggaaggaggggggtgaaagatcaagttcttcaacty	1293
QY	1262	gtatagaagaaacaaactaaacaaacccctcttttggaggcaatctgacatctggaggaaatgctga	1321
Db	1294	gtatagaagaaacaaactaaacaaacccctcttttggaggcaatctgacatctggaggaaatgctga	1353

Qy	1322	aacttctatagaaactcaaaccttactgcaatgatttggtaaagaatttggagtc	1381
Db	1354	aaaccttatgaaacacttcaaacctcttactgcgaatgatttggtaaagaatttggagtc	1413
Qy	1382	tagtccctcttcccgattatcttggaaagctctctgaagccgtctgcgttttggaaagctc	1441
Db	1414	taagtcctcttcccgattatcttggaaagctctctgaagccgtctgcgttttggaaagctc	1473
Qy	1442	gtataaccttgacatctccagccaagaagcagttcatgtgaggttgaaacaagaccttcca	1501
Db	1474	gtatataccctgacacacacccagccaagaagcagttcatgtgaggttgaaacaagaccttcca	1533
Qy	1502	ggaactgacgtgttctccatgacttgaagcctgtggaaggaagaaactccagcccaagatctc	1561
Db	1534	ggaaactgacgtgttctccatgacttgaagcagctgtggaaggaagaaactccagcccaagatctc	1593
Qy	1562	gaccttcatgagaaacagccaagaatggaacctgtgccgtaigtctgttggacagcagga	1621
Db	1594	gaccttcatgagaaacagccaagaatggaacctgtgccgtaigtctgttggacacagga	1653
Qy	1622	caatgaccacttlttgggaacagcagttgattgacttaattggagcagcccaagacatcgt	1681
Db	1654	caatgaccacttlttgggaacagcagttgattgacttaattggagcagcccaagacatcgt	1713
Qy	1682	ggcgcttlttggccaagcaccagagatctccagtcceagtaatgttctgtgtgacactg	1741
Db	1714	ggcgcttlttggccaagcaccagagatctccagtcceagtaatgttctgtgtgacactg	1773
Qy	1742	gagagaagcttccaagagacttaaccaggaactccgagaccatactcgtctcatgtagtg	1801
Db	1774	gagagaagcttccaagagacttaaccaggaactccgagaccatactcgtctcatgtagtg	1833
Qy	1802	tgtaaccttaacacagctaaacccaatgacaacagaagctcgtgctcatcaacaagtcac	1861
Db	1834	tgtaaccttaacacagctaaacccaatgacaacagaagctcgtgctcatcaacaagtcac	1893
Qy	1862	ggagctgcgtgattgagagaagaagtcctggcctggtatgtgttctactggaattactcagg	1921
Db	1894	ggagctgcgtgattgagagaagaagtcctggcctggtatgtgttctactcgaattactcagg	1953
Qy	1922	cagatttgagctggcccaatgataatgaagaagaatccgaatgagacatttggacaattgtgga	1981
Db	1954	cagatttgagctggcccaatgataatgaagaagaatccgaatgagacatttggacaattgtgga	2013
Qy	1982	gaggacaataaataccaaggaatggatcatctgggaacctgtgctcctgagctgagcccttga	2041
Db	2014	gaggacaataaataccaaggaatggatcatctgggaacctgtgctcctgagctgagcccttga	2073
Qy	2042	ggaactgcgtagcgtctggggggagcttgcctacttggcagagatgtgtgtggggagagcaat	2101
Db	2074	ggaactgcgtagcgtctggggggagcttgcctacttggcagagatgtgtgtggggagagcaat	2133
Qy	2102	catcagggctgtgcacgggacccgagagaagaanaacttggtgtctatatlgaacaacgatgtcccta	2161
Db	2134	catcagggctgtgcacgggacccgagagaagaanaacttggtgtctatatlgaacaacgatgtcccta	2193
Qy	2162	tcctctgttaagtgtgaataatcttctctggggtgtgatagacccgttcaatagccccccttcat	2221
Db	2194	tcctctgttaagtgtgaataatcttctctggggtgtgatagacccccgttcaatagccccccttcat	2253
Qy	2222	gaacgtgcgcctggaatttaccagtgagctgtgatcatcaagaggacatcgttatgaaaga	2281
Db	2254	gaacgtgcgcctggaatttaccagtgagctgtgatcatcaagaggacatcgttatgaaaga	2313
Qy	2282	ggcagcgtctgaagaagacatgtgagatcatgtggcttggacaacagcatactctgtgttag	2341
Db	2314	ggcagcgtctgaagaagacatgtgagatcatgtggcttggacaacagcatactctgtgttag	2373
Qy	2342	ctggtctaatgttagcctcatctctctctctgtggaagcctgcgcctgtatgtatcatcct	2401
Db	2374	ctggtctaatgttagcctcatctctctctctgtggaagcctgcgcctgtatgtatcatcct	2433
Qy	2402	gaagtttagaaacbcgtgccttaacagtgatcccaagcgtgtgtgttcttctcgtcgcgt	2461

Db	2434	GAATTTAGAAACCTGGTGGCTTACAGTAGATCCAGCGGGTGTGTGCTTCGTCCGT	2493
OY	2462	gtttgtctgtgtgacaaatcctctgaagtgtcttcttgattagcaacctctcttcagaagcaa	2521
Db	2494	GTTTGCTGTGTGTGACAACTCTGACAGGCTTCCGTATTACACACCTTCTCCAGAGCCAA	2533
OY	2522	ccctggcaagcaacccgtgtgggggacaaatcactcaactcaagcgtatccctggcctaaagctctgtg	2581
Db	2554	CTTGCCACAGACACCTGTGGGGGCACTACTTCACTTACAGCGTGTACGTGCCCTAGTCTGTG	2613
OY	2582	tgtagcagtgcaagaaactagtggtgtctcaactcaagaatcttcgtatgctgtgtctcc	2641
Db	2614	TGTGGCAATGGCAGAGACTACCTGGGCTTCACTACCAAGACTTTCGCTACCTGTCTCC	2673
OY	2642	tgttgacttttggttttgctgtgaagtaactttgcccctttttggagagcaaggaattgagat	2701
Db	2674	TGTGGCTTTTGGTTGGCTGTGTGATGATCTTGGCCCTTTTGTGAGAGACAGGGCATTTGAGT	2733
OY	2702	gcagtgagacaacactgtttttagagtcctgtgtgagagaatggcttcaactlctcaacactc	2761
Db	2734	GCAGTGGGACAACTGTTTGTAGAGTCCCTGTGGAGAAATGGCTTCAATCTCACCACTTC	2793
OY	2762	gactcctaagtatgctgttttgaacactctctctatbggtgtgtagactgtgtatattgagc	2821
Db	2794	GATCTCCATGTATGTCTTTGACACCTTCCCTGTGGGGTGTATGACTGGTATATTGAGGC	2853
OY	2822	tgctcttcagaagcagtaagaaatctcccaagccctgtatcttctcttgacaagtctcta	2881
Db	2854	TGTCTTTCCAGGCCAGTACCGAATTCACAGGCCCTGTATTTTCCGTGCACCAATCCTA	2913
OY	2882	ctgtgtttggcgaagaaatgtagaagagccacccgtgtctcaacagaagaagatct	2941
Db	2914	CTGTGTTTGGCCAGAGAAAGTGTATGAGAGACCCACCTGTTTCCAAACAGAAAGATGTC	2973
OY	2942	agaaatctgcagttagagagaagaaaccccaacttgaagcctggggcgtgtccattcaaacct	3001
Db	2974	MAAATCTGCAATGGAGAGAGAACCCACCACCTTGAAAGCTGGGGTGTCCATTCAACAACCT	3033
OY	3002	ggtlaaaagtctacccgagatggatgaaagtgtgctgtcgatgagccttgagcaatcttcta	3061
Db	3034	GGTAAAGTCTACCGAGATGGGATGGAAGTGCGTGTGATGGCTTCGCACTGAATTTTTA	3093
OY	3062	tgaggcagaagtaactcctctctcctggggccaaatbtgagcggggaaagaagacaacatctc	3121
Db	3094	TGAGGGCCAGATCACCTCTTCTCTGGGCCACAATGAGCGGGGAACACACCACTATGTC	3155
OY	3122	aatctctgacccgggttgttctcccccgaactcgtgggacacgcctatactcttggaaagaat	3181
Db	3154	AATCTGTGACCGGGTGTTCCTCCCGACCTGTGGGCACTATCATCTGTGGGAAAGACAT	3213
OY	3182	tcgctctgtgagatgagacacatccggcagaagaccctgggggtgtctgtcccccaataaagtgct	3241
Db	3214	TGCGCTCTAGATGAGACACCACTCCGGCGAAGCTGTGGGGTGTGTGCCAGATTAAGTGCT	3273
OY	3242	gtttacatgtgcagctgtgcgaagaacacatcgtgtlctatgtcccgcgttlaaagggctctc	3301
Db	3274	GTTTGACATGCTGCACTGTCCAAAGAACATCTGGTTTATGCCGCTTGAAGAGGCTTTC	3333
OY	3302	tgagaagcagtgaaagcggagatgtgagcaagatggtccctgtgattgtgtttgtccatcaag	3361
Db	3334	TGAGAGACACGTGAAGGCGGAGATGTGAGCAAGATGGCTCTGAGTGTGGTTGTGCATCAAG	3393
OY	3362	caagctgaaanaaacaacaagcagcgtgtcaaggtgtgaaatgcagagaagaactatctgtgc	3421
Db	3394	CAGACTGAAAAGCAAAACAAACCACTGTCTAGGTGGGAATCAAGAAAGCTATCTGTGGC	3455
OY	3422	cttgagcctttgtctcggggagatctaagttgttcatctctgtgataaaccacagcctgtgtgtga	3481
Db	3454	CTTGGCCTTTGTCTGGGGGATCTAAGGTGTTCATTTCTGTGATGAACCAACAGCTGTGTGGA	3513
OY	3482	ccctactctccgcaagggaaataatgtgagctgtcctctaatactcgaagaagccgaacat	3541

QY 5702 gtccgltgtcttgatcttccacatttttgccttggagcgaaggctcatcgaatgtgaa 5761
|||||
Db 5734 gttccgtgttcttgatcttccacatttttgccttggagcgaaggctcatcgaatgtgaa 5793
QY 5762 aaaccaggaatgtcgtatgccccgtgaaagtttggggagaatcgtcttctgacacatt 5821
|||||
Db 5794 aaaccaggaatgtcgtatgccccgtgaaagtttggggagaatcgtcttctgacacatt 5853
QY 5822 atcttggagactgtgtggaagaaacctcttcgcctatgcccgttgaaggggtgtgtctt 5881
Db 5854 atcttggagactgtgtggaagaaacctcttcgcctatgcccgttgaaggggtgtgtctt 5913
QY 5882 cctcatcgtcttcttgatccagtaacagatttctcatcgaagccagaccctgttaattgcaa 5941
|||||
Db 5914 cctcatcgtcttcttgatccagtaacagatttctcatcgaagccagaccctgttaattgcaa 5973
QY 5942 gttatctctctcgaatgtatgaatgtgaagatgtgaaggcgggaaagaaagaaatcttga 6001
|||||
Db 5974 gttatctctctcgaatgtatgaatgtgaagatgtgaaggcgggaaagaaagaaatcttga 6033
QY 6002 tgggtgaagccagaatgacatctcttagaatacaaggaagtgtgacgaagatatagaaggaa 6061
|||||
Db 6034 tgggtgaagccagaatgacatctcttagaatacaaggaagtgtgacgaagatatagaaggaa 6093
QY 6062 gcggaagcctgctgttgacaggaattgcgtgaggcaatccctccgtgtgaagtgttgggt 6121
|||||
Db 6094 gcggaagcctgctgttgacaggaattgcgtgaggcaatccctccgtgtgaagtgttgggt 6153
QY 6122 ccttggagatgtatggggtctggaataatcaacttcaagaatgttacaagagataccac 6181
|||||
Db 6154 ccttggagatgtatggggtctggaataatcaacttcaagaatgttacaagagataccac 6213
QY 6182 tgttaccagaaggagatgtcttcttcaacaaaatagiatcttcatcaaacatcgaatg 6241
|||||
Db 6214 tgttaccagaaggagatgtcttcttcaacaaaatagiatcttcatcaaacatcgaatg 6273
QY 6242 aaatcagaacatgtggtctactgcccctcaatttgaatgacatcaagaagcgttgaatggaag 6301
|||||
Db 6274 aaatcagaacatgtggtctactgcccctcaatttgaatgacatcaagaagcgttgaatggaag 6333
QY 6302 agaacagctgagatgtcttcttgccttcttgaaggagatcccaagaaagaaagtttggcaagt 6361
|||||
Db 6334 agaacagctgagatgtcttcttgccttcttgaaggagatcccaagaaagaaagtttggcaagt 6393
QY 6362 tgggtgagtggtgagatcgcgaataatggtgctcgttgaagtatggaagaaatgtgtcgtgaa 6421
|||||
Db 6394 tgggtgagtggtgagatcgcgaataatggtgctcgttgaagtatggaagaaatgtgtcgtgaa 6453
QY 6422 ctatagtgagagcaacaacgcgaagctctctacagccatggtcttgcgcgcgcctcc 6481
|||||
Db 6454 ctatagtgagagcaacaacgcgaagctctctacagccatggtcttgcgcgcgcctcc 6513
QY 6482 tgtgtgttcttcttgatgaaaccaacgaagcatgtatcccaagaccgcgcgccttctgtg 6541
|||||
Db 6514 tgtgtgttcttcttgatgaaaccaacgaagcatgtatcccaagaccgcgcgccttctgtg 6573
QY 6542 gaatttgccttaagtgttgaagaaggagagatcaagtagtcttaactcatcaatg 6601
|||||
Db 6574 gaatttgccttaagtgttgaagaaggagagatcaagtagtcttaactcatcaatg 6633
QY 6602 ggaagaatgtgaagcctcttgcactagatggaatcatcgttcaatgtgaaggttcaagtg 6661
|||||
Db 6634 ggaagaatgtgaagcctcttgcactagatggaatcatcgttcaatgtgaaggttcaagtg 6693
QY 6662 ccttggagatgtccagcatcctaaataatgtgttgaagatgtgttatcaatgtgtgag 6721
|||||
Db 6694 ccttggagatgtccagcatcctaaataatgtgttgaagatgtgttatcaatgtgtgag 6753
QY 6722 aatagcaggtgtcaaacccgaagccttgaagcctgtcgaagatcttcttggacgttgcattcc 6781
|||||
Db 6754 aatagcaggtgtcaaacccgaagccttgaagcctgtcgaagatcttcttggacgttgcattcc 6813
QY 6782 tgaagatgttcttaaaagagaacaccggaacatgtctacaataccagcttccatcttcaat 6841
|||||

Db 6814 tgaagttgttcttaaaagagaacaccggaacatcttaccacgttccatcttcaat 6873
QY 6842 atcttctctggccaggaatcatcgaatcctctccagagcaaaaagcactccacataga 6901
|||||
Db 6874 atcttctctggccaggaatcatcgaatcctctccagagcaaaaagcactccacataga 6933
QY 6902 agactactcgttctctcagaacaacatttgcacaaagtatttggtaacttggcgaagaca 6961
|||||
Db 6934 agactactcgttctctcagaacaacatttgcacaaagtatttggtaacttggcgaagaca 6993
QY 7022 tgcagttctcactcttcttctacagatgagaagtgaaagaagcctatgtatgaagat 7081
|||||
Db 7054 tgcagttctcactcttcttctacagatgagaagtgaaagaagcctatgtatgaagat 7113
QY 7082 ccttcttcaaggggtgtgtgaagaaaggaaggaacttcttcttccacatgta 7141
|||||
Db 7114 ccttcttcaaggggtgtgtgaagaaaggaaggaacttcttcttccacatgta 7173
QY 7142 agtgtgtgtgaagaaaggaaggaagtgatgtgtgaagaaaggaagtgatgtgt 7201
|||||
Db 7174 agtgtgtgtgaagaaaggaaggaagtgatgtgtgaagaaaggaagtgatgtgt 7233
QY 7202 gatactatcatcgaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaat 7261
|||||
Db 7234 gatactatcatcgaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaat 7293
QY 7262 tgccttcttgaagccttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 7321
|||||
Db 7294 tgccttcttgaagccttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 7353
QY 7322 cctatacctatgtgaacatctatatagaacccaatggaatggaatggaatggaatggaatggaat 7381
|||||
Db 7354 cctatacctatgtgaacatctatatagaacccaatggaatggaatggaatggaatggaatggaat 7413
QY 7382 ttt 7441
|||||
Db 7414 ttt 7473
QY 7442 aatcatgcccagcagatctatgatacaaaatgaagaaatgaagaaatgaagaaatgaagaaatgaag 7501
|||||
Db 7474 aatcatgcccagcagatctatgatacaaaatgaagaaatgaagaaatgaagaaatgaagaaatgaag 7533
QY 7502 coactgcaatgcccagcagatctatgatacaaaatgaagaaatgaagaaatgaagaaatgaagaaatgaag 7561
|||||
Db 7534 coactgcaatgcccagcagatctatgatacaaaatgaagaaatgaagaaatgaagaaatgaagaaatgaag 7593
QY 7562 coactgcaatgcccagcagatctatgatacaaaatgaagaaatgaagaaatgaagaaatgaagaaatgaag 7621
|||||
Db 7594 coactgcaatgcccagcagatctatgatacaaaatgaagaaatgaagaaatgaagaaatgaagaaatgaag 7653
QY 7622 ctttcttgaagcctgtcttgcctgaagatctatcaaatgtgaatcagtgacagaatg 7681
|||||
Db 7654 ctttcttgaagcctgtcttgcctgaagatctatcaaatgtgaatcagtgacagaatg 7713
QY 7682 tgcacatgctgtgatacactcctgttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 7741
|||||
Db 7714 tgcacatgctgtgatacactcctgttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 7773
QY 7742 acatgcaacaataatgttgggtgtcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 7801
|||||
Db 7774 acatgcaacaataatgttgggtgtcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 7833
QY 7802 tccatagcttgcagcaatggtgtcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 7861
|||||
Db 7834 tccatagcttgcagcaatggtgtcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 7893
QY 7862 gatcctgttgaagggcaagaatcaacagccaaactgtcgtgggcgtcgaagcgtcgtgaagc 7921
|||||

Db 7894 GATCTGTGTAAGAGCAAAATCAACAGCAAACTGCTGGGCTGCACTGCTGAAGC 7953
Qy 7922 CAGGCACTGGATTAAGAAATGTCGTCCTCAAACTAGGAAAGCTGTGCTCCTTCTC 7981
Db 7954 CAGGCACTGGATTAAGAAATGTCGTCCTCAAACTAGGAAAGCTGTGCTCCTTCTC 8013
Qy 7982 CTGACTCTGCTAACAAGTACACCTGCACTGCAAGTGTCTTCTGCAACAAGTGTCTT 8041
Db 8014 CTGACCTGTGCTAACAAGTACACCTGCACTGCAAGTGTCTTCTGCAACAAGTGTCTT 8073
Qy 8042 ATTCTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8101
Db 8074 ATTCTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8133
Qy 8102 TGTCTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8161
Db 8134 TGTCTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8193
Qy 8162 AGAATGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8221
Db 8194 AGAATGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8253
Qy 8222 TGTCTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8281
Db 8254 TGTCTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8313
Qy 8282 GTCAAGATCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8341
Db 8314 GTCAAGATCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8373
Qy 8342 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8401
Db 8374 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8433
Qy 8402 GTCAAGATCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8461
Db 8434 GTCAAGATCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8493
Qy 8462 CTGCTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8521
Db 8494 CTGCTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8553
Qy 8522 TGTCTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8581
Db 8554 TGTCTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8613
Qy 8582 GTCAAGATCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8641
Db 8614 GTCAAGATCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8673
Qy 8642 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8701
Db 8674 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8733
Qy 8702 GTCAAGATCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8761
Db 8734 GTCAAGATCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8793
Qy 8762 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8821
Db 8794 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8853
Qy 8822 GTCAAGATCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8891
Db 8854 GTCAAGATCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8913
Qy 8882 GTCAAGATCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8941
Db 8914 GTCAAGATCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 8973
Qy 8942 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9001
Db 8974 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9033
Qy 9002 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9061
Db 9034 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9093
Qy 9062 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9121
Db 9094 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9153
Qy 9122 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9181
Db 9154 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9213
Qy 9182 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9241
Db 9214 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9273
Qy 9242 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9301
Db 9274 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9333
Qy 9302 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9361
Db 9334 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9393
Qy 9362 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9421
Db 9394 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9453
Qy 9422 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9481
Db 9454 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9513
Qy 9482 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9541
Db 9514 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9573
Qy 9542 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9601
Db 9574 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9633
Qy 9602 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9661
Db 9634 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9693
Qy 9662 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9721
Db 9694 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9753
Qy 9722 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9781
Db 9754 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9813
Qy 9782 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9841
Db 9814 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9873
Qy 9842 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9901
Db 9874 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9933
Qy 9902 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9961
Db 9934 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 9993
Qy 9962 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 10021
Db 9994 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 10053
Qy 10022 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 10081
Db 10054 TCACTGCTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTTCTGCAACAAGTGTCTT 10113

QY	10082	ttcttaaaccttaagaatgaagctgcttttggcctcttgcacatcattggccctatcc	10141
Db	10114	TTCTTATATACCTTAAGATTAAGCTGTTTGGCTCTTTGTTTCATCATATGGCCCTATGCC	10173
QY	10142	aagcactttagcgtcgtctgtataatggagatcatalttttgacatggaatcaltctagaattgca	10201
Db	10174	AAGCAGCTTTAGCGCTGTCTGTATGGAGATCTATTGTCAGATGAAATATCTGAGATTGCA	10233
QY	10202	aaactagagcaaaagctttcaccaacagatcttccaagtttaatacatctttcatttaaaggaana	10261
Db	10234	AAACTAGACAAAAAGTTTACACAACAGATTTTCGTAAGCTTAATCATTTTCATTTAAAGCAAAA	10293
QY	10262	aagaaaaaaaatttgtatgtcgaacttcatatgatgaagatltaaatgcatattctcat	10331
Db	10294	AAGAAAAAAATTTTGTATGTGTCATTAACCTTTTATATGAAGATATTAAATGCAATATTTCTAT	10353
QY	10322	gttgtatataatgaatgcacaaaataaagcgtgtgaacgtctcgtttaaaaaaa	10381
Db	10354	GTTGTAAATATATATGAGTCACAAAATTAAGCTGTGACAGTCTGTTAAAAA	10413
QY	10382	aaa	10441
Db	10414	AAA	10473
QY	10442	a 10442	
Db	10474	A 10474	

RESULT	8		
AX127831			
LOCUS	AX127831	9854 bp	DNA
DEFINITION	Sequence 70 from Patent WO0130848.		linear
ACCSSION	AX127831		PAT 15-MAY-2001

ACCESSION	AX127831
VERSION	AX127831.1
GI	GI:14134478

KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens

REFERENCE
1 (bases 1 to 9854)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS
Denefle, P., Rosier-Montus, M.F., Arnould-Reguinne, I., Prides, C.,
Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searios, G.H.,
Remaley, A., Brewer, H.B. and Dean, M.

TITLE Nucleic acids of the human abcl1 gene and their therapeutic and diagnostic application
Patent: WO 0130848-A 70 03-MAY-2001:
JOURNAL

FEATURES	source
Aventis Pharma S.A. (FR)	
Location/Qualifiers	1. 9854

BASE COUNT	
2665	/organism="Homo sapiens"
2319	/db_xref="taxon:9606"
2374	
2635	+
1	others

[illegible]

Query Match	93.68;	Score 9777.8;	DB 6;	Length 9854;
Best Local Similarity	99.88;	Pred. No. 0;		
Matches 9810; Conservative	0;	Mismatches	18;	Indels 2;
				Caps 2

QY 1 ggcgcgagaccgcagagagccgagccacctctctcccggtctcggcagggcagggcg 60
|||||

Db 9 GGCCTGGACCCGCGAGCCGAGCCCTTCTCTCCCGGGCTGCGCAGGGCAGGGCGG 68
QY 61 GGAgtctcgcgacacnaagaagccggtctctcagagcgctcttgctctgtlcttcccg 120

Db 69 GGAGCTCCGGCGCACCCAGAGCGGTTCTCAGGGCGTTGCTTCCTTGTTTTCCCGC 128

Qy 121 gtcctgtttctcccccctctccggaaagctgtgtaaggagtgagagaagacgcacaac 180
Dh 129 gttctgtttttctccctctccggaaagccttgctcaaggcgttagagacaaagcgaac 188

181 acaaaagtcgaaacagttaatgaccagccacggcgctccctgtgtgagcttggcgc 240

Db 189 ACAAAGTGAACACAGTTAATGACCAGCCAC -GGCGTCCCTGCTGTGAGCTCTGGCCGC 247

QY

241 tgcctccagggcctccgagcacacagctggcgctgtgcctgaaggaaacatgacttgc 300
|||||
|||

Db 248 TGGCTTCCAGGGCTCCCGAGCCACACACGCTGGGGGTGCTGGCTGAGGGAACTGGCTTGT 307

QY 301 ggccctcagctgagttgtctgtctgtgagaaacctcacttcacagagaagacaaatgtc 360

Db 308 GGCCTGAGCTTGCTGCTGTGAGAGAACCTTACCTTCAGAGAGAGCAACATGTC 367

```
.QY      361 agctgttactggaagtgcgcgcgcctcattatcccgataccgatcctcgttcggc 420
        ||||| |-----|-----|-----|-----|-----|-----|
Db       368 AGCTGCTGCTGGAGTGGCGCCCTCAATTATCTTCGTATCCTGAATCCTGTTCGCC 427
```

QY 421 ttgagctaccacccctatgacacacatgaatgcccatttccaataaagcgcctcctg 480

Db 428 TGAGCTACCCACCCCTATGACACACATGATGCCATTTCCAAATAAAGCCATGCCCTCTG 487

Db 488 CAGGAACACTTCCTTGGGTTACAGGGGATTATCTGTAATGCCAACACCCCTGTTCGGTT 547

QY 541 acccgactcttgaggagctcccgagttgttgaaacttaacaalccattgtgctc 600

601 gccctgttctcagatgctcgagagctcttttataacagccagaagaacacaccagcatgaag 660

Db 608 GCCTGTTCTCAGATGCTCGGAGSCTTCTTTATACGACGCAAGAACACCGCATGAAGG 667

668 ACATGCGAAAGTTCTGAGAACATTACACGATCATCAGAAATCCAGCTCAACTTGAAGC 727

Qy 721 ttcagattctctgtggaacatgaacctctctgggtccctatatacaacctctc 780
|||||

Db 728 TTCAAGATTTCCTGCTGGACACAGAAACCTTCTCTGGGTTCCGTATACACAACTCTCTC / 67

Db 788 TCCCAAGTCTACTGTGGACAGATGCTGAGGGCTGATGTCAATTCTCCACAGGTAATTTT 847

QY 841 tgcgaagctaccagcttaccattgcacaagctctgtgcattgcatgaatcagaagacatga 900

D8 848 tgcgaagctaccagcttaccattgcacaagctctgtgcattgcatgaatcagaagacatga 907

901 ttcaactgttgaccaagaagtttctgagcttgtgacctaccaaggaagaactgctg 960

Dc 908 TTCACCTTGGTGACCAGAAGTTTCTGAGCTTTGTGGCTACCAAGGGAGAACTGGCTG 961

Ov 961 CATTGAAGCAGATTAATTCCTTCCAACATAGACATCTGAAGCCCAATCGTAGAACACTAA 1020

668 CAGCAGAGCCAGTACTTCGTTCCACATGGACATCCGAGGCAATCCCTGAGACACTAA 102

QY 1021 actctacatctcccttcgccgagcaaggagctgctggaagccacaaacacattgctgcata 108
|||||

1081	gtcttggaactctggcccagagctgttcagcatgaaagctgagtgacatgacacagg	114
D5	1028 ACCTACATCTCCCTTCCGAGCAGAGACCTGGCCGAGCCACCAACACATGCTGACAT	108
D6	1028 ACCTACATCTCCCTTCCGAGCAGAGACCTGGCCGAGCCACCAACACATGCTGACAT	108
QY	1081	

Db 1088 GCTTGGACACTGCCCCAGAGCTGTTCAACATGAGAAAGCTGGAGTGACATGCCGACAGG 114

Db 1148 AGGAGATGTTTCGACCAATGTGAACAGCTCCAGCTCTCCACCCAAATCTACCAAGGCTG 12

Qy 1201 tgtctgtattgtctctgcggcatcccgaggaggggctgaatcatcaagttctcctaact 1206
|||||

Db 1208 TGTCTCGATTMTGCTCGGGGCATCCGAGGAGGGGGCTGAAGATCAAGTCTCTCAACT 1209
0v 1361 gqatagagacaacaactacaaagccclctttgaagcaatgqcactgaagaaagtctg 1362

[illegible]

Db 1268 GGTATGAGCAACACTACAAAGCCCTTTGGAGGCAATGGCACTGAGAGAAATGCTG 1327
QY 1321 aaacctctatgacaactctacactctactactgcaatgtaattgataagaatcttgagat 1380
Db 1328 AAACCTTCTATGACAACACTACAACTCTTACGCAATGATTTGATGAGAAATTTGGAGT 1387
QY 1381 ctgactctcttccgcattatctgaaagctctgaaagccgctgcctgtctgttggaagatcc 1440
Db 1388 CTATGCTCTTTTCCCGCATTTATCTGAAACCTCTGAAAGCGCTGCTGTTGGGAAATGCC 1447
QY 1441 tgaatacactggaactccagccacaagagagatcagtgatgagtgatgagtgaaagaactctcc 1500
Db 1448 TGATATACCTGACACTCCAGCCACAAGAGAGTCAATGGCTGAGTGAGAACAACTTCCTCC 1507
QY 1501 aggaactgctgtgttccatgatactgaaagcaatgtaagaagaaactcaagccccaagatct 1560
Db 1508 AGGAACCTGCTGTGTTCCATGATCTGGAAGGCATGTGGGAGGAACACAGCCCAAGATCT 1567
QY 1561 ggaaccttcataggaagcaagccaaagaatggaacttgctcggaatgctgtgttgacaagaag 1620
Db 1568 GGACCTTCATGAGAACAGCCAAAGAAATGACCTTGTCCGGATGCTGTTGACAGCAGG 1627
QY 1621 acaatgaccacttttgggaacagcagtgatgagtgatgagtgagtgagtgagtgagtgagtgag 1680
Db 1628 ACAATGACCACTTTTGGGAACAGCAGTGGATGGCTTACATTTGACAGCCCAAGACATCG 1687
QY 1681 tggcgttttttggccaagcaagcccaagagatgctcagtgcaatgagtgatgagtgagtgag 1740
Db 1688 TGGCGTTTGGGCAAGCAAGCCAGAGATGTCCAGTCAGTAATGCTTGTGTACACT 1747
QY 1741 ggaagaagaacttcacaaggaactcaagcaaatccggaacatcttgcttcacatgagtgagtg 1800
Db 1748 GGAGAGAGAGTTTCAACGAGACATAACCGACATCCGGACATATCTCCCTTCATGAGAT 1807
QY 1801 gttcaactctgaacaaagctagaagcccaatgcaacagaagtgctgctcatalcaacaagtcca 1860
Db 1808 GTGTCAACCTGAAACAAGCTAGAAACCCATGCAACAAGATCTGGCTCATCAACAAGTCCA 1867
QY 1861 tggagtgctggaatggaagaagtgctgagtgatgagtgatgagtgatgagtgatgagtgatgag 1920
Db 1868 TGGAGCTGCTGATGAGAGAACTTGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1927
QY 1921 gcaagcttgagtgcccaatcatalgtaagaatgtaagaatccgaatggaatggaatggaatggaat 1980
Db 1928 GCGACCTTATGAGTCCCTCATATGTCATACAGTACAGATCCGAATGAGCATTTGCAATGTGG 1987
QY 1981 agaggaacaataaatacaagagatgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2040
Db 1988 AGAGGCAATATAAATCAAGAGATGGTACTGGGACCTGTGCTGTGAGCTGACCCCTTTTG 2047
QY 2041 aggaactgcggtatgctgaggggggcttcgactacttgagaatgagtgagtgagtgagtgag 2100
Db 2048 AGGACATGCGGTACCTGTGGGGGGGCTTGCCTACTTGCAGAGATGTGGGAGAGCA 2107
QY 2101 tcaatgagtgctgaagggcaccgagaagaactggtgtatctatgtaacaagatgagtgagtgag 2160
Db 2108 TCAATGAGGTGCTGACGGGACCCGAAAGAAACTGAGTCTATATGCAACAGATGCCCT 2167
QY 2161 atccctgtatgagtgatgacatcttctgagggatgagtgagtgagtgagtgagtgagtgagtgag 2220
Db 2168 ATCCCTGTAGCTGATGATCTTCTGCGGGTATGAGCGCGGTCANTGCCCTCTTCA 2227
QY 2221 tgaagtgctgagtgatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2280
Db 2228 TGAAGCTGCGCTGATTTAATCAGTGGCTGTGATCATCAAGGCGCATGCTGTATGAGAGG 2287
QY 2281 aggaagcagtgagaagagagacatcgagatcagtgagtgagtgagtgagtgagtgagtgagtgag 2340
Db 2288 AGGACAGGCTGAAAGAGACATGCGGATCATGAGGCTTGACAAACAGCATCTCTGCTTTA 2347
QY 2341 gctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2400
Db 2348 GCTGCTTATATGATGCTCATCTCTTCTGTGAGCGGTGGCTGCTAGTGTGATCC 2407

QY 2401 tgaagtgagaacactgctgcctctacagtgatcccaagtgagtgagtgagtgagtgagtgagtgag 2460
Db 2408 TGAAGTTAGAAACCTGCTGCCCTTACAGTGAATCCAGCGTGATGTGTGTGTGTGTGTGTGTGTGTGT 2467
QY 2461 tgttgcctgagtgagaacatccctgcaagtgctctctgattgaacacactctctcagaagcca 2520
Db 2468 TGTGTGCTGTGATGACATCTGAGTCTCTGATGATGAGACACTCTTCCAGAGCA 2527
QY 2521 aactggcagagcctgtagggagcatcactactcaactcaagctgtagctgagtgagtgagtgagtgag 2580
Db 2528 ACTGGCAGACCTGTGGGACATCATCTTACGCTGTACTCTCCCTACGCTCTGT 2587
QY 2581 gtaggcaatggcagagctacagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2640
Db 2588 GTGTGATGAGAGAGTACAGTGGGCTTCAACATCAAGATTTGCTGAGCTGTCTC 2647
QY 2641 ctgagtgcttgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2700
Db 2648 CTGTGGCTTTTGGGTGTGGCTGTGATGATCTTGTGCTTTTGAAGAGAGAGGCAATGGAG 2707
QY 2701 tgcagtggaacactgcttgagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2760
Db 2708 TGCACTGGGACAACTGTTTGAAGTCTCTGTGAGAGAGATGCTTCAATCTCAACTT 2767
QY 2761 cgaatccatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2820
Db 2768 CGGTCTCATGATGCTGTGTGACACTTCCCTCTGTGAGGAGATGACCTGTGATGAGG 2827
QY 2821 ctgctcttcagagcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2880
Db 2828 CTGTCTTTCAGAGCAGTACGGAATTCAGAGCCCTGTGTGATTTCTTGTGCAACAAGTCT 2887
QY 2881 actggttgaggaagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2940
Db 2888 ACTGTTTGGGAGAAAGTATGAGAAAGCCACCTGTGTGATGATGATGATGATGATGATGATGATGATGAT 2947
QY 2941 cagaatctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3000
Db 2948 CAGAAATCTGATGAGAGAGAGAACCCACCTTGAAGCGGGGTGTGCTCATTCAGAAC 3007
QY 3001 tggtaaaagtgtaacagagatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3060
Db 3008 TGTGAAAAAGTACCGAGATGGATGAAAGGTGCTGTGATGAGCTGTGAGCTGAGCTGATTTT 3067
QY 3061 atgagggcagagatcact 3120
Db 3068 ATGAGGGCCAGATACCTCTCTCTGAGCCACATGAGAGCGGGAGAGACGACACCATGT 3127
QY 3121 caatcctgaacgggtgtgttcccccagacactcgagcaacgagcctacatcctctggaagaaagaca 3180
Db 3128 CAATCTGACCGGGTGTGTCCTCCCGGACCTGCGGACCGCTGACATCTGTGGAAGAGAC 3187
QY 3181 ttgcctctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3240
Db 3188 TTGCTCTGAGATGAGCACCATCCGCGCAACCTGGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3247
QY 3241 tgttgaacatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3300
Db 3248 TGTGTTGACATGCTGATGCTGTGAGAGACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3307
QY 3301 ctgagaagcagtgagaagcgagagatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3360
Db 3308 CTGAGAGCAGCTGAGAGGCGAGATGAGAGATGAGGCTGTGATGTTGGTTTCCATCA 3367
QY 3361 gcaagctgaaagaagaagaagcagctgtcagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3420
Db 3368 GCAAGCTGAAAGAGAAAGCAAGCCAGCTGTCAAGTGTGAGAGAGAGAAAGATATCTGTGTG 3427
QY 3421 ccttgagccttgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3480
Db 3428 CTTTGGCTTTGTGCGGGGATCTTAAGTTGTCTGTGATGAGACCCACAGCTGTGTGTG 3487

Db 5648 CCACCTTTGCTGAGAGCTTACCCGACAAATAGCTGAATTAATATCATGATATCCCTGA 5707
QY 5701 agtcgctgttccttgatctcccaacatttctccttggaagagagcctcaatcgaatgta 5760
Db 5708 AGTCGGTCTTGTGATCTTCCACATATTTTGGCTGGGACAGAGGCTCATGACATGTTGA 5767
QY 5761 aaaaacggcaatgagcctgagcttggaagaggttgaggagaaatcgcttctgacacat 5820
Db 5768 AAAACCGAGCAATGGCTGAGAGCCCTGGAAAGTTGGGAGAAATCCCTTTGTCACCAAT 5827
QY 5821 tatcttggaacttggttgagagcaaacctctcgcacatgagcgttggaaggggtggtct 5880
Db 5828 TATCTTGGAGCTTGGTGGAGCAAACTCTTCCGCAATGGCCGTGGAAGGGGTGTTCT 5887
QY 5881 tcccatctactgttcttgatccagtlacagatcttctcaatcagcccaagcctgttaatgca 5940
Db 5888 TCCCATTAATCTGTTGATCCATGACAGATTTTCATCAAGCCCAACCTGTAAATGCA 5947
QY 5941 agctatctcctctgaatgtaagatgaagatgagcgttgagcggagagagagatctctg 6000
Db 5948 AGCATCTCTCTGAATGATGAAATGAAATGATGAGGCGGAGAAAGACAGATTTCTTG 6007
QY 6001 atggttgagagcagcaatgacatcttaagaaatcaagaggttgacgaatataagaaga 6060
Db 6008 ATGGTGAGGCCCAAGAAATGACATCTTAGAAATCAAGAGATTGACGAAGATATAGAA 6067
QY 6061 agcgaagagcctgctgttgacagagattgagtgagcaltctcctgtggtggttgagc 6120
Db 6068 AGCGGAAGCTGCTGTTGACAGATTTGCTGGGACATCTCTGCTGAGTGGCTTTGGG 6127
QY 6121 tccctggagatlaaagtgagcctggaataatcaacttcaagatcttaacagagagatca 6180
Db 6128 TCTCGGAGATTAAATGGGGCTGGAAATCATCACTTTCAAGATTTAAACAGAGATACCA 6187
QY 6181 ctgttccagagagagatgcttcttcaacaaataglatctatacaaatcagag 6240
Db 6188 CTGTATACCAAGAGAGATGCTTCTTACAGAAATAGTATCTTATCAACATCCATGAAG 6247
QY 6241 tacatcagaacatgagcctactgctcctcaatcttatgcatcagagagcgttgagagga 6300
Db 6248 TATCATGAAACATGGGCTACTGCTCATGTTGATGCCATCAAGAGCTGTGACGGGA 6307
QY 6301 gaaacacgctgagagcttcttgccttgaagagagctcccaagaaagagttgagag 6360
Db 6308 GAAACACGCTGAGATCTTGTGCTTTGAGAGAGTCCCAAGAAAGATGGGCAAG 6367
QY 6361 ttgttgagtgagcagatcgaacatgagcctgagcctgagatgagagaaatagctgta 6420
Db 6368 TTGTTGATGGGCGATTCGAAACTGGGCTGCTGAAGTATGAGAAATATGCTGTA 6427
QY 6421 actatagtgagagcaacaaacgaagcctctacagcatalgcttgatcgagcgtc 6480
Db 6428 ACTATATGTGAGGCAACAAACGACATCTCTACAGCCATGAGCTTGATGGGCGGCTC 6487
QY 6481 ctgttgatgttctgagatgaacccacacagagatgaatcccaagccgagcttctgt 6540
Db 6488 CTGTGATGTTCTGATGAAACCAACACAGGCTGATCCCAAGGCGGCGTCTTCT 6547
QY 6541 ggaattgtccctaaagtgttgaagagagagagatcaatgagcttctgacatcagta 6600
Db 6548 GGAATTTGTGCCCTAATGTTGTCAGAGAGGAGATCAATAGTGTCTTACATCTCATAGTA 6607
QY 6601 tggagaatgtgaagctcttgaactaggatgagcaatcagtgatcaatggaagagttcaggt 6660
Db 6608 TGGAAATATGTGAAGCTTTTGGACTAGAGATGCAATGATGCAATGAAAGTTAGGT 6667
QY 6661 gacttgagcagttccagcatctaaataaagtttgagagatggttatatacagttgac 6720
Db 6668 GCGTTGGCAGTGTCCAGCATTAATAAATAGGTTGGAGATGTTAATACAAATAGTTGAC 6727
QY 6721 gaatacagagttccaaacccgagacatgaagcgttcagagattcttggacttgatc 6780
Db 6728 GAATACAGGGTCCAAACCCGACCTGAAGCTGTCCAGGATTTCTTTGAGCTTGCAATTC 6787

QY 6781 ctggaagtgcttaaaagagaacacccgaaacatgctcaaatcagcttccatctcat 6840
Db 6788 CTGGAAGTGTCCAAAGAAAGAAACCGGAACATGCTCAATACAGGTTCCATCTTCAT 6847
QY 6841 tatcttctctgccaagatatcagatcctctcccaagcaaaaagcactccacatag 6900
Db 6848 TATCTTCTTGCCAGAGATTTACATCTCTCCCAAGCAAAAAGGCACTCCACATAG 6907
QY 6901 aagactactgcttctcagaacaacacttgaaagagatggtgaacttgcgaagacc 6960
Db 6908 AAGACTACTGCTTCTCTAGACACACCTTGACCAAGTATTTGTCACTTTCACAGAAC 6967
QY 6961 aagatgatgagacacttaaaagacctctcaatcacacaaaacagagtagtgagc 7020
Db 6968 AAAGATGATGATCACCTTAAAGACCTCTATTACAAAAACAGACAGATAGTGAGC 7027
QY 7021 ttgagcttccatcattcttctacagagtgaggaagtgaagaagctatgtatgaaga 7080
Db 7028 TTGCAATCTCATCTTTCTTACAGATGAGAAAGTAAAGAAAGCTATATGAAAGAA 7087
QY 7081 tccgttcaataggggtgagcctgaagaaagaaagagactagacttctccttgacacatg 7140
Db 7088 TCTGTATACAGGGGTGCTGAAAGTAAAGAGNACTAGACTTCTTCCACCATGTG 7147
QY 7141 aagtgcttgagaaagagcagagatgagtgtgaggaagagtaaatgatactgtac 7200
Db 7148 AAGTGTGTGGAGAAAGCCAGAAAGTTGATGTGGAGAAAGTAACTGATCTGTAC 7207
QY 7201 tgatactatcaatgcaatgcaatcaatgcaatgaacaaatccatcagagagga 7260
Db 7208 TGATCTATTCATGCAATGCAATTCATGCAATGCAATGCAATGCAATGCAATGCAATG 7267
QY 7261 gtgccttgtgagcctatgcttctgagagcctcgaatgaagagctgaattagttt 7320
Db 7268 GTGCTTTGTGAGCCATGCTTGTGATGCTCTCAAGTAAAGACCTTAAATTAATTTT 7327
QY 7321 accataccatgtaaacctcatatgaagcccaatgagacataggttgaactaca 7380
Db 7328 AACTATACCTATGTAACACTTATTAATGAAACCAATGCAATGAGGTTGAACCTACA 7387
QY 7381 ctcttcttcttcttctgctcgtgcatctcattgggggttgcaacaatcaatcaag 7440
Db 7388 CTTTTTTTTTTTTTTTGTCTCTGTATCTCATTTGGGGGTGCAACAAATTAATCATAG 7447
QY 7441 taatcatgccaagcattatgatacaaaaatgaagaaatgaagacatcccatcactaa 7500
Db 7448 TATATATGCGCAAGCATTTATGATCAAAATGAAAGTATGACATCTCATCTAA 7507
QY 7501 gccatgcaatgccagagagactggttcccggtgacacatccatctgctgcaatgagt 7560
Db 7508 GCATGCGCATGCCAGAGAGACTGTTCCCGGTGACACATCCATGCTGGCAATGATGT 7567
QY 7561 gccagagttatagtgcaagatlltccagaagattgaagacacatggtgtgcatgctc 7620
Db 7568 GCCAGAGTTATTAAGTGCACAAATTTTTCAGAAAGTTTAAGCACCATGATGTCATCTC 7627
QY 7621 acttttgaaagcgtcgtcctcagagctcatcaaatgaaatgaatgaatgagagag 7680
Db 7628 ACTTTTGAAAGCTGCTGCTCTCAGAGCTATTAACATTTGAATATAGTTGACAGATG 7687
QY 7681 gtgcagatgctggttcaacatccttctgattccctctgataagcgttctggtgagc 7740
Db 7688 GTGCAATGCGGCGCTTAACATCTCTTGAATCCCTTGATTAAGCTGTGTGGAGGAGT 7747
QY 7741 aacatgcaacaaaatggtggtgtctcctaggaacaggaacatggttcaatgtatatt 7800
Db 7748 AACATGCAACAAAATGTTGGGTGTCTCTAGGCAAGGGAACCTTGTTCAATTTGTTAT 7807
QY 7801 gtccatagcttcagagcagatggtctacagagtaacctttagagacttaataact 7860
Db 7808 GTCTTATGCTTGAGCAATGAGGTCTACAGGCTCATCTTATGAGACTCTTAATATACCT 7867

OY	7861	aagccctgynaagaggcaaaagaatacaaacgcacaaactcctcgggcttcgaagctgcgtgaag	7920
Db	7868	AGATCCCTGGTAAAGGCCAAGAATCAACAGCCAAACTGCTGGGCTCGAAGCTGCTGAAG	7927
OY	7921	ccaagggcatggattcctaagaatcttgctgttcaaaccttaagggaagccctggtgccatttgt	7980
Db	7928	CCAGGGCATGGATTAAAGATTTGTGGCTTCMAACTTAAGGAAGCCTGTGCCATTGT	7987
OY	7981	ccctgacctgtcgttaaacaatggtfacaccgtcalctcaagaigtlttatctgnaacaagtglat	8040
Db	7988	CCMGACTGTCGTCACTACATGATGACACTGCATCTCAAGATGTTTTATCTGACACAAGTGSTAT	8047
OY	8041	tattcttgacctttgtaattaatctcagaanaatgaaaagaatggagtgttattttgacaanaa	8100
Db	8048	TATTTCTGGCTTTTAAATTAATCTBAGAAAAAGAAAAGATGGAGCTGTATTTTTCACAAA	8107
OY	8101	atctttgtaacctttaatgttatcttggaatttaagttcctaagttgaacttcgaactcctc	8160
Db	8108	ATGTTGTACTTTTAAATGTATTTTGGAATTTTAAAGTTCTATCACTGACTTCTGAATCCT	8167
OY	8161	tagaatgcccctcttgtaaacocctgtggtatagaggagla tggccactgccccactat	8220
Db	8168	TAGAATGGCCCTTTGTTAGAACOCCTGTGTATAGAGGAGTATGGCCACTGCCCACTAT	8227
OY	8221	ttatattctctatgtaagttgcatatcacgtca gtaactagtgacctagaagaactgtgat	8280
Db	8228	TTTTATTTCTTAAATGTAAGTTTGTGATATCACTAGTCATACAGTCCCTAGMAACAATGTGAT	8287
OY	8281	gttcagagatctcagacatatatattggaattcttcagacatcatttaagataactcctaat	8340
Db	8288	GGTGAGGATCTCAAGACATTAATAATTGAACTTCTTCAGATCATTTTAGGATACCTTTAAT	8347
OY	8341	cctcaactlcaaccaatcaaatatttttgtagtga tgcgtgaactgaaagatglatagcla	8400
Db	8348	CTCACTTCATCAATCAAAATATTTTTTGAATGTATCTGTAGCTGAAAGATATGTACGTA	8407
OY	8401	cgataaagcatagagsagataataagtcctcagtaacactccctgtgcacatgltattcaagctc	8460
Db	8408	CGRATAAGCATAGAGAGATTAATTAAGTCTCACAGTCACTTCCTGTGCCAATGTTATTCAGCTC	8467
OY	8461	actggtttacaagaataggtgtgcctgtggttgtagggagcccaactgtaaaaaatcttgggc	8520
Db	8468	ACTGTTTACAAATATAGGTGTCTTGTTGTGTGTAAGAACCCACTGTACAAATCTGGGC	8527
OY	8521	agccctttttttttttttttaaattgcaacaatgcaaaagccaagaagtataaaggtctaac	8580
Db	8528	AGCC-TTTTTTTTTTTTTTAAATTCGAACAATGCCAAAAGCCAGAAAGATATAAGGCTAC	8586
OY	8581	aagtttaacaatgaatctctcaacaggaaaacsqctagcttligaanaactgtctgaanaa	8640
Db	8587	AAGCTTAAACAAATGAATTTCTTCMACGGGGAACAGCTPAGCTTGAAAACTGCTGCAAAA	8646
OY	8641	caaacactgtgttataggcaatttagraccttcaaaataatcttgcttggaaatlgtgata	8700
Db	8647	CACAACTGTGTTATTTAGGCAATTTAGTACCTTCCTCAAAATATGGCTTTGCAAGATTTGGATA	8706
OY	8701	ccccattaaatctgcaagctcacaattttcatalctcttcaactcaacatgltcaagaanaata	8760
Db	8707	CCCCATTAAATCTGACAGCTCCAATTTTTTCAATCTCTTCAATCACTAGTCAAGAAAAATA	8766
OY	8761	taaaacaacaabaactcocalatagagacatttccagaagtttcttaaccagacttcatt	8820
Db	8767	TAAAAACAAACAATACTCTCCATPTGAGAGCAATTTTTCAGAGTTTCTTAACCCACAGCTTAT	8826
OY	8821	ttcttagtcagtaaacattgtgtaaaaaactcttccactcaactactactgtttaaactgct	8880
Db	8827	TTTTCTAGTCAGTAAACATTTTGTA AAAATCTGTTTTACTTAATACTTACTGTTAACTGTCT	8886
OY	8881	tgagagaaagaaaaaataatgagaaactatgtgttggygaattcaagtgactcttcaat	8940
Db	8887	TGAGAGAAAAGAAAATATATAGAGAACTATPTGTTTGGGAAGTTCCAAAGATCTTTCAAT	8946
OY	8941	atcataactaaacttctcacaacttlttccaanaattgaaatataataacgctaaagtgtaaga	9000

Db	8947	ATCATTTACTACTTCTTCCACTTTTTCOCAAAATTGGAATATTAAACGGCTAAAGGTGTAGA	9006
Qy	9001	ctcagatltcaaatlaatccttctctatactttttaaattcagagaatatataaacc	9060
Db	9007	CTTCGATTTCOCAAAATTATCTTTCATATTTTTTAAATTTACAGAAATATATATACCCA	9066
Qy	9061	ctgcgtgaaaaaagaaaatgatgtgtttaaggttaaagtcgaatltgatltttaa	9120
Db	9067	CTGCGGAAAAAGAAAAAATGATGTGTTTAAACAGTTAAAGTCAAATATGATTTTAAATAT	9126
Qy	9121	aagtaatgaagcatatttccaataacagtcgatctgcatcgttgcgaattacga	9180
Db	9127	ANGTATATAGGOCATATTTCCATATACAGTATATGSCATCGTTGCATTTACAGTATC	9186
Qy	9181	ttcaaaaaatacagaattatagaatlaatttccatcattataatlttcaaatcaa	9240
Db	9187	TTCAAAAATPACAGATTTATAGAAATATTTCCCTCATTTATATTTTCAAAAATCAAG	9246
Qy	9241	ttatggttctcctaatttctaataatcgtatattctaatttctcatatatagtata	9300
Db	9247	TTATGCTTTCCCATATTTACATAAAATCCATATCTTAATCTTCATATTAATGTAATCTTA	9306
Qy	9301	gcaactcccttacttgcgttcctcgtatcttcaagtcgaactattttaaataa	9360
Db	9307	GCAACTCCCTTACTTCTTGCGTTCCTGATTTTCANAGCCATATTTTAAAAATCAAAAGCAC	9366
Qy	9361	tctgacatttcttgaagaaacagacatttlaatacagattgaaagagcctctt	9420
Db	9367	TGTGAACATATTTTGAAGAAACACACAACTTTTAATACAGATTTGAAGAGACCTCTCTGA	9426
Qy	9421	gctagaacaacatcatagtalacatcttcaatlaactggttaccctttaa	9480
Db	9427	GCTAGAAAACAACTCTATGATTATATACATCTTCATTAATACCTGTGTTAACTTTAAATTA	9486
Qy	9481	atttttccatttctcgttgaaccctaatttggtagaaatttaccaccta	9540
Db	9487	ATTTTTTACATTTTCTGTGTAAACCTAATGTGTAGAAATTTTACCAACTCTATACT	9546
Qy	9541	caatcaagaacaaattctgtatataccctgttgaatgtacatgttgaattcaga	9600
Db	9547	CAATCAGAGAAATTTCTGTATATTTCCCGTGGATGATACCATGTGATTCAGAAATT	9606
Qy	9601	ctcaaatatcgttctcaaaaattctcgttlttgcacttgggacactcaga	9660
Db	9607	CTCAAAATPACGTGTCCAAAATTTCTGCTTTTGCACTTTTGGACACCTCAGAAAACCTTA	9666
Qy	9661	ttaacaactgtgaatataigagaataacagaagaaataaagccctcatacata	9720
Db	9667	TTTACCAACTGTAAATATGTGAATACAGAGAGAAATTAATACCCCTCTATATCATTAATGC	9726
Qy	9721	ccagacaaatcattgtttaaanaaaccaaacctccacactcigtlatlca	9780
Db	9727	CCAGCACAATTTATTTGTATAAAAAACCAACCAACCTCACACTCTGTATTTCAATATCTGT	9786
Qy	9781	actgaagcaaatgcttgttgactataaagtgtgcacatcatcatca	9830
Db	9787	ACTGAAGCAAAATGCTTTGTGTGACTTTTAATTTTGCACATCATTCATTTCA	9836
RESULT	9		
LOCUS	AX139818	9854 bp	DNA
DEFINITION	Sequence 70 from Patent EPI096012.		linear
ACCESSION	AX139818		
VERSION	AX139818.1	GI:14275400	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 9854)		
AUTHORS	Deneffe,P., Rosier-Montus,M.F., Arnold-Reguigne,I., Prades,C.,		

Naudin, L., Lemoine, C., Duverger, N., Jaje, M., searfoos III, G.H.,
Remaley, A., Brewer, H.B., and Dean, M.
Nucleic acids of the human abcl gene and their therapeutic and
diagnostic application
Patent: EP 1096012-A 70 02-MAY-2001;

JOURNAL
Aventis Pharma S.A. (FR)
Location/Qualifiers

FEATURES

1. 9854
/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 2665 a 2219 c 2334 g 2635 t 1 others

ORIGIN

Query Match 93.6%; Score 9777.8; DB 6; Length 9854;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 9810; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

QY 1 ggcggagaccgagagagcagaccctctctccggggtcggcagagagagcg 60
DB 9 ggcggagaccgagagagcagaccctctctccggggtcggcagagagcg 68
QY 61 ggaagtcgcgcacacacagagcggtctcaaggcgcttgctctgttttcccg 120
DB 69 ggaagtcgcgcgcacacacagagcggtctcaaggcgcttgctctgttttcccg 128
QY 121 gtctgtttctccctctccggagagcttgcaagggttagaagaagaagcgcaac 180
DB 129 gtctgtttctccctctccggagagcttgcaagggttagaagaagaagcgcaac 188
QY 181 acaaaagtggaaaaagatlaataacacagcgcgctcgtctgttgagctatgcgcg 240
DB 189 ACAAAAGTGAAGAAACAGTTATGACAGCCAC - GCGCTGCCCTGCTGAGCTGTGCGCCG 247
QY 241 tgccttcagagctcccgagcacaacgcgtgagcgctgctgagaggaacatgcttct 300
DB 248 TGCCTTCAGAGGCTCCCGAGCCACACGCTGGGGGTCTGAGGGAACATGGCTTGT 307
QY 301 ggcctcagctgaggtctgctgttggaagaacctcacttcaagaagaacaacatgctc 360
DB 308 GGCCTCAGCTGAGGTTGCTGCTGTGGAAGACCTCACTTTCAGAAACAAACATGTC 367
QY 361 agctgttaactggaagtggcctgctctatattctctcgtatcctcgtatctgttgcgc 420
DB 368 AGCTGTGCTGGAAGTGGCTGCTCTATTATTCTTCGATCCGATCTCGTTGCGCG 427
QY 421 tgaagtcacacacctgaacaacatgaatgcatcttcaacaataagaacatgctctg 480
DB 428 TGAGCTAACCAACCTATGAACAACATGAATGCCATTTCCTCAATTAAGCCATGCCCTCTG 487
QY 481 cagaagaacctctgtggtcagaggatlatctgtaatgcacaacacctgttccgt 540
DB 488 CAGGAACACTCTCTGGGTTCAAGGATTTATGTAATGCCAAACAAACCCCTGTTCCGTT 547
QY 541 acccgactcctgggagagctcccgaggtgttggaactttaacaatccattgtgctc 600
DB 548 ACCCGACTCCTGGGAGGCTCCCGAGTGTGGAACCTTTAAACAATTCATTGTCGCTC 607
QY 601 gctgttctcaagatgctggagagctcttatacagcagaagaagaacacacatgagag 660
DB 608 GCGTGTTCAGATGCTCGAGGCTCTTTTATACAGCCAGAAAGACACACATGAAGAG 667
QY 661 acatgcgaagatcttgagaacattacagacagatcaagaatccagctcaacttgaagc 720
DB 668 ACATGGCGAAAGTTCTGAGAACAATTACAGCATCAAGAAATCCAGCTCAAACTTGAAGC 727
QY 721 ttaagaattctcgtggagacatgaactctctcgtgggttctctatatacaacctctc 780
DB 728 TTCAAATTTCTCGGTGGCAATGAACCTTCTGGGTTCTGTATCAACAACCTCTCTC 787
QY 781 tcccaagctactgtggaagaatgctgaaggtctgatatctctcccaagctattt 840
DB 788 TCCCAAGCTCTACTGTGGCAAGATGCTGAGGCTGATGTCTCTCCCAAGATATT 847

QY 841 tgaaggtctaccagttacatttgacaagctctgtgaatgatacaaatcagaagatga 900
DB 848 TCCAAAGGCTACAGTTACATTTGACAACTGTGTGAATGATCAAAATCACAAGATGA 907
QY 901 ttaacattgggagacagaagttcttgagcttctgtgctatccaaagagaactgctg 960
DB 908 TTCAACTTGTTGTAACAAAGTTCTGTGAGCTTGTGGCTTCCCAAGGCAAACTGGCTG 967
QY 961 cagaagagagatctctgttccaaactgagacatccctaaagcaatccctgagacactaa 1020
DB 968 CAGCAGAGAGATCTTGTGTTCAACATGACATCTTAACCAATCTGTGAACACTAA 1027
QY 1021 actatcatctccctcccgagcagaagcgctgctgaagccacaanaacatgtgtcata 1080
DB 1028 ACTTCACATCTTCCCTCCCGAGCAGGCTGTGGCGGAGCCACAAAACATTTGCTGATA 1087
QY 1081 gctctggagacttgcccgagagctgttcaagatgaagaagcttgagatgagacag 1140
DB 1088 GTCTTGGGACTGTGCGCAGAGCTGTTCAGCATGAGAGCTGAGATGACATGCGACAG 1147
QY 1141 aggtgatgtttctgaccaaagtgaacagctccacgtccctccacccaactatcaggctg 1200
DB 1148 AGGTGATGTTCTGTGACCAATGGAACAGCTCCAGCTCTCCACCAAACTATACAGGCTG 1207
QY 1201 tctctgcatattgtcggcgacatcccgagagggagggctgaaagatcaagctctcaact 1260
DB 1208 TCTCTCGATTGTCTGCGGCGATCCCGAGGAGGGGGCTTAAMATCAAGCTTCAACT 1267
QY 1261 gtaagagaacaacaacatacaaacacctcttggaggaatgagacatgagaagaatgctg 1320
DB 1268 GSTATGAGAGACACACATCAAAAGCCCTTTTGGAGGAATGACATGAGGAAGATCTG 1327
QY 1321 aaaccttatagaacaactctacaactccttaactgcaatgatttgaagaatttgaat 1380
DB 1328 AAACCTTCTATGACAACTCAACTCTCTACTCAATGATTTGATGAAGATTTGGAGT 1387
QY 1381 ctgaactccttcccgacatctcgaagaagctcgaagacgctcgttgggagaagctc 1440
DB 1388 CTAGTCCCTTTCCCGCTATTATCTGGAAGCTCTGMAAGCCCTCTGTTGGAGATCC 1447
QY 1441 tgaatacccttgacactcgaacacacagcagatgcatgagctgaagtgaagaagaccttc 1500
DB 1448 TGTATACACTGAGACACTCCAGCCACAAGCGATGATGGCTGAGGTGAACAAGCTTCC 1507
QY 1501 aggaactgctgtgttccatgatactggaagcattgtggaggaactgaagcccaagatct 1560
DB 1508 AGGAACGTGGCTGTTCATGATCTGGAAGCATGTGGAGGAACCTCAGCCCAAGATCT 1567
QY 1561 ggaactcattgagaagaacagcaagaatggaactctgtccgagatctgttgacagcagg 1620
DB 1568 GGACTTATGAGAGACAGCAAGCAAAATGACCTTTGTCGGATCTGTTGGACAGCGAGG 1627
QY 1621 acaatgacaccttgggaacagcagttgagtggtttagatttgagacacccaagaatcg 1680
DB 1628 ACAATGACCACTTTTGGGAACAGCAGTTGATGATGATGAGTGGACAGCCCAAGCATCG 1687
QY 1681 tggcggttttggccaagcaccgaagagatgtccagctcagtaatggttctgttacaact 1740
DB 1688 TGGCGTTTGTGGCCAAAGCACCAAGAGATGTCACGTCCAGTAATGAGTTCTGTGTACACT 1747
QY 1741 ggaagaagacttcaagcagactaacaacagcaatcccgagacatatctcgtctcaagagt 1800
DB 1748 GGAAGAGAAGCTTTCAACGAGACTAACAGGAATCCCGACCATATCTCCGCTTATGAGAGT 1807
QY 1801 gttctcaacttgaaacaagctgaacccaatgaacaagaagctctgtctcatcaacaagtcea 1860
DB 1808 GTGTCAACCTGGAACAACCTGTGAACCCATGACACAGAAAGTCTGGCTATCAACAAGTCCA 1867
QY 1861 tggagctgctgagatgagaagagctctgagctgtatgttctcactcgtgaattactccag 1920
DB 1868 TGAAGCTGTGATGAGAGAGATTTGGGCTGGTATTGTCTACTGGGAATTAATCTCCAG 1927

QY	1921	gcacgaattgagctgcgcccaatcattgctcaagtaacagaatccgaatgacaattgacaaatg	1980
Db	1928	GCAGCAATGAGCTGCGCCCATCTCATGTCAAGTAAAGATCCGAATGGCAATTGACAAATTGG	1987
QY	1981	agagagcaaatataatccaagatagtgtaactggaacccgagcccgacccgagatgaccccttg	2040
Db	1988	AGAGAGCAAAATTAAATTCAAAGATGGGTACTGGAGACCCCTGAGTCTCGAGCTGACCCCTTGG	2047
QY	2041	agagacatgcgtacgtctcgtgggggggcttcgcctacttgcaagatgtggtgagcaagcaaa	2100
Db	2048	AGGACATAGCGGTACGTCCTGGGGGGGCTTCGCCCTACTTTCACAGAAATGGTGTGAGAGGCAA	2107
QY	2101	tcctcaagatgagctgcagacggccaccggagaagaacacgagtgctatataitcaaaagtgcct	2160
Db	2108	TCATCAAGGGTGCTGACAGGGGACCGGAAMAAACTGGTGATATATATGACACAGATGCCCT	2167
QY	2161	atccctgttaactgtgaacatcttctctgcgggtgatgtagccggttcaatgccccttca	2220
Db	2168	ATCCCTGTACGTGATGACATCTTTCTCGGGGTATGACCCGGGCAATGCCCTCTTTC	2227
QY	2221	tgaagctgcgccttgatttctactaagtgagctgtgatacaaggatlogtgaatgagaag	2280
Db	2228	TGAGCGCTGCGCTTGATTTACTAGTGGCTGTATATCAAGGGCACTGTATGAGAGG	2287
QY	2281	aggcacgctgcgaagaagacacatgagcatcatcagtcctgtgacaacagcaactcgtgtta	2340
Db	2288	AGGCAGCGCTGAAAGAGACCATAGCGGATATAGGGCTGAGACACGATCCTTGHTTA	2347
QY	2341	gcgtggtcattagtagcctcaatctctctctctgtgaagcgtgcgcctgtagtgtaatc	2400
Db	2348	GCTGTGTTCAATTATATACCTCATATCTCTTCTGTGAGCGCTGGCTGCTGATGGTCAATCC	2407
QY	2401	tgaagttaggaacacctgcgcgccttaagatcagatcccaagcagtggtgttcttccgtcgcg	2460
Db	2408	TGAAGTTAGGAACCTGCTGCCCTACAGATGCCAGGCTGGTGTGTGTCTCTGTCGCG	2467
QY	2461	tggttgctgtgtgtgaacaatcctgcagtgcttccctgattagaacactcttctccagaagca	2520
Db	2468	TGTTGTGCTGTGTGACAAATCTGCAATCGCTTCCTGATTAAGCACTCTTCTCCAGAGCCA	2527
QY	2521	acctggagaagagcctgtggggggacatactacttaacgctgtaacctgcacagctcctgt	2580
Db	2528	ACCTGGAGAGACCTGTGGGGGACATATCTACTTCAACGCTGATACCTGCCCTACGTCCTGT	2587
QY	2581	gtgtgcgcatgycagagactacgttgggcttcaacatacaatcttcgctagcgtcgtctc	2640
Db	2588	GTTGTGCATGTGGCAGAGACTAGTGGGCTTCACATCAAGATCTTCCCTAGCTGGTGTCTC	2647
QY	2641	cttggagcttttggttggtgtgtaatttgcctttttagagaagaagcattgag	2700
Db	2648	CTTGGGCTTTTGGGTTTGGCTGTGAGTACTTTCCTTTTAAAGAGCAAGGGCATTTGAG	2707
QY	2701	tgcaagtgcgaacaactgtttgaagatcctgtgtgaggaagaatgcttcaatctcaacact	2760
Db	2708	TGCAGTGGGACAACCTGTTTGAAGATGCTGTGAGGAAGATGGCTTCAATCTCACACACTT	2767
QY	2761	cgatctccatgatagtcgttttgaacaacttctctataggggtgtagccgtgataattgag	2820
Db	2768	CGGTCCTCATATGCTCTTTTGAACACTTCTCTATGSGGTATGACCTGTGTACATTGAGG	2827
QY	2821	ctgtcttctccagagcagtaagaaatcccaagcgcctgagatcttctctgcacaagtcct	2880
Db	2828	CTGTCTTCCAGGCGCATAGGGAATTCACAGGCGCTGATTTTCTCTTGACACAAAGTCTT	2887
QY	2881	actggtttgctgaggaagaatgatatgagaagaagccaccctggttccaaacgaagaagaatgt	2940
Db	2888	ACTGGTTTGGCGAGAAAGTATGAGAGAGCCACCTGTTTCCAAACAGAAAGAAATAT	2947
QY	2941	cagaaatctgataaggaaggaagaaacccaacacttgaagcttgggcgtgtccattcagaac	3000
Db	2948	CAGAAATCTGCATGAGAGAGGAACCCACCTTGAAGCTGGGGCTGTGTCAATTTCAGAAC	3007
QY	3001	tggtataaagcttaccagatatggaatgaaggtggcgtgtcgtgaatgaaattttt	3060

D	3008	TGCTAAAGTCTACCCAGATGGGATTAAGTGGCTGTGATGAGGCTGGCACTGAATTTT	3067
Q	3061	atgagggcagaatcaacctctctccggaacatgagcggggaagaagcaaccaat	3120
D	3068	ATGAGGGCCAGATACCTCTCTCTGGGGCACAAATGAGCGGGGAAGCGACCCATGT	3127
Q	3121	caatctgagccgggtgtttcccccgaacttgggaacccgcttaactctgggaagaca	3180
D	3128	CAATCTCACCGGGATTTCTCCCCCACTCGAGCACCGCCTACATCTGGGAAAAGCA	3187
Q	3181	ttcgctctgagatbtagcaaccatccggcagaacctgggggtctgttcccagaatacgtc	3240
D	3188	TTCCGCTGAGATGAGCAACCATCCGGCAGACCTGGGGGTGTGTCCAGCATAACTGC	3247
Q	3241	tgtttgacatgctcagctgttgaagaacacatctggtttcatgtccgccttgaaaggctc	3300
D	3248	TGTTTGACATGCTACCTGTGAAAGAACACTGGTGTTCATCCCGCTTGAAAGGGCT	3307
Q	3301	ctgaaagaacagctgaagaacggagatbtagagcagatgccccgtgatgttgtttgcataa	3360
D	3308	CTGAAACACAGCTGAAGCGGAGATGGAGCAATGGCCCTGGATTTGTTGCCATCAA	3367
Q	3361	gcaagctgaaaaacaaaaaagccagctgttcaagtgaaatgcagaagaactactgttg	3420
D	3368	GCAGACCTGAAAAAGCAAAACAGCCAGCTGTCACTGGAATCCAGAAAGCATCTGTGG	3427
Q	3421	ccgtgacctgtgtcgggggagcttaaggtgtcaatctgtagtaaccaacagctgtgtg	3480
D	3428	CCTTGGCTTTGTGGGGGATCTAAGTTGTCTATTGTGATGAACCCAGCTGGTGG	3487
Q	3481	accttactccgcgaagggaatatbtagagctgtcgtctgaataaccgaaggccgacaa	3540
D	3488	ACCCTTACTCCCGCAGGGGAATATGGAGCTGCTGTGAATAACGACAAGGCCACACA	3547
Q	3541	ttaatctctcaagcaacaaatgatabtaagcgaagctctctggggagacagattgcata	3600
D	3548	TTATTCTCTTACACACCACTGATGAACGGAGCTCTGGGGGACAGATTCGATCA	3607
Q	3601	tctccacatggaagaactgtgtctgtgttggtctctccctgttctgaagaacagactgga	3660
D	3608	TCCTCCATGGGAGAGTGCTGTGTGGCTCCCTCTTGTGAAACACAGCTGGGA	3667
Q	3661	caggctactactgaacctgtgtcaagaanaatgtgaatccctccctagttcctgcagaa	3720
D	3668	CAGGCTACTACTGACCTGTGTCAAGAAATGTGAATCTCTCCTCAATTCTCTCAAA	3727
Q	3721	acaagtagtagcaactgtgtcattacacttgaanaaaggagacagtttctccagagcaattc	3780
D	3728	ACAGTAGTAGCACTGTGTCTACTACTGAAAAAGGAGCAGTGTGTCTCAGACACTTCTG	3787
Q	3781	atgtctgacctgggagcagcaatgaagaatgaacagcttgacactcgatgtctctgtact	3840
D	3788	ATGCTGGCTGGGGCAGCACCATAGAGTACACGCTGACATCATGATCTTGCTATCT	3847
Q	3841	ccaacctcaatgaagaagatgtgtcctaagcccgagctgtgtgaagaacataggaatgagc	3900
D	3848	CCAACTCTCATGAGAGCATGTGTCTAACCCTGGGTGGTGAAGCATAGGCGATAGGC	3907
Q	3901	tgaactatgtctgcacatagaagaatgtctaaaggaaggagccttgttgaactcttcatg	3960
D	3908	TGACCTATGTGCTGCGCATATAAACCTCTTAAGAGGGAGCGCTTTGTGAACCTTTCAATG	3967
Q	3961	agaattgataacccggtctcagaaccttgggaattctatgtaatgtcactcaagagcagcc	4020
D	3968	AGATTGATGACCGGCTCTCAAACTGGGCATTTCTAATTATGSCATCTAAGAGAGACC	4027
Q	4021	tggaaagaataatctctcaagtggtgcgaagaagatggggatgtgaatgtctgagacctcaatg	4080
D	4028	TGGAATAAATATTCTCTCAAGGTGGCCAAAGAGATGGGGTGGATGCTGTGACCTCAGATG	4087
Q	4081	gtaccttgccagcaagaacaggggaccttggggagcaagcagagcttctctgc	4140

Db 4088 GTACCTTGCCAGCAAGACGAAACGCGGCGCTTCGGGAGACAGACGCTGCTTGGCC 4147
QY 4141 cgttcaactgaagaagatgctgctatccaaatgaltctgacatagaccagaatccagag 4200
Db 4148 CGTTTACAGGAAGATGATCTCTGATCCAAATGATTCGACATGAGACCAGCAATCCAGAG 4207
QY 4201 agacagactgctcaagtgaatgagtcgaagaagctctaccagaagtgaagagctggaac 4260
Db 4208 AGACAGACTTCTGCTAGTGGGATGGAATGGCAAGGGTCTTACAGAGTGAAGGGCTGGAAC 4267
QY 4261 ttacaagaacaagcttgctgagccctttgtgaaagaagactgctaactgccaagagagtc 4320
Db 4268 TTACACAGCAACAGATTGTGTGCGCTTTGTGGAAGAGAGCTGATATTGCCAGAGAGAGTC 4327
QY 4321 ggaagaagattttgtctcaagattgtctgccaagctgctgtgtgtgtgtgtgtgtgtgt 4380
Db 4328 GGAAGGATTTTGTGCTCAGATGTCTGTGCGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 4387
QY 4381 tcaagcctgactgctgcaacccctttgcaagatgacccagcctggaaactcagccctgagatg 4440
Db 4388 TCAGCTGATGCTGCCACCCCTTGGCAAGTACCCAGCTGGAATCTTACGCTTGATGT 4447
QY 4441 acaacgaagatcacatctgtcagcaatgagctcctgagagacagagacccctgagac 4500
Db 4448 ACAACGAAACATGACATTTGTGAGCAATGATGCTCTGAGGACACGGAACCCCTGGAAC 4507
QY 4501 tcttaaacgcccctaccagaagcccttgcttcgagaccgctgtatgaaagaagaccga 4560
Db 4508 TCTTAAAGCCCTCACCAGAACCCCTGCTGCGGACCCCTGTATGGAAGGAACCCAA 4567
QY 4561 tcccaagaacgcccctgcaag 4620
Db 4568 TCCAGAGACGCCCCCTGGCAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4627
QY 4621 ccaatcaagagaccccttccagaagagagagagagagagagagagagagagagagagagag 4680
Db 4628 CCATTCATGAGACTCTTCCAAATGGAACATGGAACATGGAACCCCTTACCTGATGCTATGCC 4687
QY 4681 agtgaagcagcgaacaatcaagaagatgctgctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4740
Db 4688 AGTGTACAGAGCAAAATCAAGAAAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4747
QY 4741 tgcctctccacaagaacaacaacaacatgacagatccctcagagacctgacagagagagag 4800
Db 4748 TGCTCTCTCCCAAGAAACAAACACTGACATATCTTACGAGACCTGACAGAGAAAGAA 4807
QY 4801 acatttcgagatctgctgaagaactatgtgagatcagatcagccaaagcttaagaaga 4860
Db 4808 ACATTTGGGATTATCTGTGAAGAGATGTGAGATCAGATCAGCAAAAGCTTAAAGAGCA 4867
QY 4861 agatctggagtgaaatgagttaggtatgagcgcttccctgggtgtcagtaataactcaag 4920
Db 4868 AGATCTGGGTGAATGAGTTAGGTATGGCGGCTTTTCCCGGGTGTGAGTAATACCTCAAG 4927
QY 4921 caattctccgagatcagaaggttaatgagagcacaacaatgaaagaacacactaaagc 4980
Db 4928 CACTTCTCTCGAGTCAAGAAAGTTAATGATGCCAACAAACAAATGAGAAACAACTTAAAGC 4987
QY 4981 tggccaagagacgtctgcaagatcgatllctccaagcgttggaaagattatgagagagagc 5040
Db 4988 TGCCCAAGGACACTTCTGCGAGATCGATTTCTCAACAGCTTTGGGAACATTTATGACAGGAC 5047
QY 5041 tggacaacagaataatgtaagaagtgtgtgtcaatlaacaagagctgagcaatgcaatcagct 5100
Db 5048 TGAGACACCGAATAATGTCAAGGTGTGTTCAATAACAAGGGCTGCGATGCAATCAGCT 5107
QY 5101 cttctcgaatgtcatcaacaatgcatcttcocgggccaactgcaaaagagagagagac 5160
Db 5108 CTTTCTGATGTATCAACAAATGCAATTCCTCGGGCCAAACCTGCAAAAAGGAGAGAAAC 5167
QY 5161 ctgagcatataggaatctgcttcaatcattccctgagatcccaagagagagagct 5220
Db 5168 CTAGCCATTATGGAATTACGCTTCAATCATCCCTGTGATCTCACAGACGACGCTCT 5227

QY 5221 cagaagtgctctgatgaccacaatcagttgagtgctctgtgtccatctgtgtcatcttg 5280
Db 5228 CAGAGTGCTGCTCGATGACCAATCATGATGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 5287
QY 5281 caatgtccttgctccagcagcttgctgtcatcttctgtatccagaagaggggtcagcaag 5340
Db 5288 CAATGTCTTCTGCTCCAGCCAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5347
QY 5341 caaaacacctgcaatgcatcagtgagatgaagccctgtcaactcagctgtcttaatttg 5400
Db 5348 CAANAACCTGCAATGATGATGAGAGTGAACCTGTATCTACTGCTCTTAATTTTG 5407
QY 5401 tctggagatbtgcaaatcagttgtccctgccaactggtcatatcatctcatctgtct 5460
Db 5408 TCTGGGATGTGTGCAATGTACGTTGTGCCGACACTGGTATATCATCTCATCTGCT 5467
QY 5461 tccagagaagtccttatgtgtctccacaactctccgtgtgtgtgtgtgtgtgtgtgtgtgt 5520
Db 5468 TCAGCAGAAATCTATGT 5527
QY 5521 tglatgtgtgtcaatcacaactctcatgttaccagccctctgtgtgtgtgtgtgtgtgtgt 5580
Db 5528 TGTATGGTGTGTGATCATACACCTCTCATGTATACCAAGCTCTTGTGTGTGTGTGTGTGTGT 5587
QY 5581 gcaacagcctatgt 5640
Db 5588 GCACAGCCATGT 5647
QY 5641 ccacacttgctgtgagctgt 5700
Db 5648 CCACCTTTGT 5707
QY 5701 agtcggt 5760
Db 5708 AGTCCGT 5767
QY 5761 aaaaacagcaatgctgt 5820
Db 5768 AAAAAAGCAATGT 5827
QY 5821 tatctgtgagcttgctgt 5880
Db 5828 TATCTTGGGACTGT 5887
QY 5881 tccatcaatcagttctgtatcagaatcagatcttctcaatcagaagccagacgtgttaatgcaa 5940
Db 5888 TCTCATTTACGT 5947
QY 5941 agctatccctctgaaatgataagaatgaaatgtgaaagcggaaagaaagaaatctgtg 6000
Db 5948 AGCTATCTCTCTGATATGATGAATGAATGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6007
QY 6001 atgtgtgagcgcgaatgacatcttaagaatcagaagagttgacgaagatatalagaaga 6060
Db 6008 ATGGTGGAGGCGCAGATGACATCTTGAATAACAAGAGTTGACGAATATATGAAAGGA 6067
QY 6061 agcggaagcctgctgtgtgacagagattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6120
Db 6068 AGCGGAAGCCTGT 6127
QY 6121 tcttgagagttaaatgagcgtgaaatcaatcaactctcaagatcttaacagagagatcca 6180
Db 6128 TCTGGGAGTTAATGGGCTTGAAATATCATCACTTTCAAGATTTTAAAGAGATTCGA 6187
QY 6181 ctgttaccagaagagatgcttctcttaacaaaataglatcatctatcaaacatcatgaag 6240
Db 6188 CTGTTACAGAGAGAGATGCTTCTTAAACAGAAATATATCTTAAACATCATCAAG 6247
QY 6241 tacatcagaacatgagctgactgacctgaatttgaatgcatcaagaagctgttgaagagga 6300
Db 6248 TACATCAGAAATAGGCTACTGCTCCTCAGTTGTGATGCATACAGAGAGCTGTGATGAGGA 6307

QY	466	aagccaatgcctctgacaggaacattcccttgggttcaagggaattatctgtaattgccaca	525
Db	360	AAGCATGCCCCCTCTCAGAGAACACTTCTTGCGTTCCAGGGGATTTATCTGTAATGCCAAC	419
QY	526	accctgttccgttaaccgactctctggggaagctcccggaatttcttgaaactttaaca	585
Db	420	ACCCTGTTTCCGTTACCAGACTCCTGGGGAGGCTCCCGAATTGTGGAAACTTTTAA	479
QY	586	aatccattgtgtctgcgctgttctcagaatgtctcggaggcttctttatcacgcgaaag	645
Db	480	AATCATGTGTGCTGGCCTGTTCTCAGATGCTCGGAGGCTCTTTTATACACCCAGAAAG	539
QY	646	acacagagatgaagaaacttgccaaagtcttgagaaccttaacagagatcaagaatcca	705
Db	540	ACACAGCATGAGAGACATGCCAAGTTCTGAGACATTTACAGCAGATCAAGAAATCCA	599
QY	706	gtccaacttgaagcttcaagaatttctcgttggtagacaatgaacctctctctgtgttctat	765
Db	600	GCTCAAACTTGAAGTTCAAGATTTCTTGTTGAGACAAATGAACCTTCTCGGGTCTGT	659
QY	766	atcaaacctctctctcccaagttctactgtggacaagaatgtctgaaggtctgaattatc	825
Db	660	ATCACAACCTCTCTCCCAAGTCTACTGTGACAAAGTGTGAGGGCTGATGTATTC	719
QY	826	tccacaagattatttgaaggctacaaattacatttgacaagctgttgcgaatgata	885
Db	720	TCCACAGGATATTTTGGCAAGGCTACCAATTACATTTGACAAAGTCTGTGCAATGATTC	779
QY	886	aatcagaagaagatgaltcaactgtgtgaccaaagaattcttcgaagtttgtgcctaca	945
Db	780	AATCAGAAAGATGATTCAACTTGTTGACCAAGAAAGTCTTGAGCTTTGTGGCTTACCA	839
QY	946	aagagaactctgtcgaagagacgaagtacttctgtccacaatgagcatctctgaaccaa	1005
Db	840	GGAAGAACTGGCTGCAGCAGACGAGCTACTTGTTCCAATGACATCTTAAGCCAA	899
QY	1006	tccctggaacactaaactacatctcccttcccgaacgaagagctgtgtgaaagccaa	1065
Db	900	TCCTGAGAACACTAACTCACTACATCTCCCTCCCGAAGCAAGAGCTGGCCGAGCCACA	959
QY	1066	aaacattgtctgaatgttcttgggaactctggcccagaagctgttcagatagaagctgga	1125
Db	960	AAACATTTGTGCTACTACTTGTGGACTCTGGCTCCAGGAGCTGTTACGATAGAAGCTGGA	1019
QY	1126	gtgacatgcaagaggtgaaatgttctcgaaccaatgaaacagctccagcttctccacc	1185
Db	1020	GTACACTGCCACAGGAGGTATTTTCTGACAAATGTGAACAGCTCCAGCTCCGCCACC	1079
QY	1186	aaactaccagactgtctcgtatgtctgtcgtgagcaatcccgagggaaggggagctgaaga	1245
Db	1080	AAATCTACACGGCTGTGTCTGATTGTCTGCGGGCATCCCGAGGGAGGGGGCTGAGA	1139
QY	1246	tcaagctctcaacttgatgaagacaacaactacaagaagccctcttggaggcaatgca	1305
Db	1140	TCAAGTCTCTCAACTGTTATGAGSACAAACAACATAAGGCCCTCTTTGGAGGCCAATGG	1199
QY	1306	ctgaggagaagtgtctgaaccttctatgacaaactacactccttactgaatgaattga	1365
Db	1200	CTGAGGAAGATGCTGAACCTTCTATGACAACCTTCACTCACTCTTACTGCAATATTTTGA	1259
QY	1366	tgaagaattggagctcagccctcttcccgcaatlatcttgaaagctctgaagccgtgc	1425
Db	1260	TGAGGAATTTTGGAGTCTAGTCTCTTCCGCAATTAATGTGAAAGCTCTGAGGCCGCTGC	1319
QY	1426	tcatgtggaagaatctctglatacacctgacactccagccaagaagcaggtcattgtag	1485
Db	1320	TCTGTGGAGGATCCTGTATACACTGACACTCCAGCCACAAGCAGAGTATGCTGAGG	1379
QY	1486	tgaacaagaccttccagaagactgtgtgttccatgtaatcttggaagatgtggaggaaac	1545
Db	1380	TGAACAAGACCTTCCAGAACTGGCTGTGTTCCATGATCTGGAAGGCAATGGGAGGAGAC	1439
QY	1546	tcaaccccaagatctgagacctcatgtgagaacagccagaagaattgacctgttccgagatc	1605

Db 2520 CTAGCCTGCTGCTCTGCTGCTGCTTTTGGCTTGGCTGTGAGTACTTGGCCCTTTTGGAG 2579
QY 2686 agcaggagcattgagtgagtgaggaacacgtgttgaagctctgtgaggaagatgagc 2745
Db 2580 AGCAGGCACTTGGAGTGCATGAGTGCACACCTGTTGAGAGTCTGTTGAGAGGATGGCT 2639
QY 2746 tcaatcaccacacttgatctcgaatgatctgttgaacacttccctctatgagtgatga 2805
Db 2640 TCATCTCACCACCTTGGTGTCTCATGATGCTGTGTGACACCTTCTCTATGAGGATGA 2699
QY 2806 cctgtgatactgagtgctgtcttccagccagtagcgaattccagagccctgtatctc 2865
Db 2700 CTTGAGTACATTTGAGCTGCTTCTCCAGGCCAGTACGAAATTCACAGCCCTGGTATTTC 2759
QY 2866 ctgtgacacagctcctactgtgttgaggaagatgatagaagagagccactgtatcca 2925
Db 2760 CTTGACACAGTCTCTACTGTTGGCGAGAAAGTATGAGAACCCACCTGTGTTCCA 2819
QY 2926 accagaagaagatgtaagaatctgcatgaggaaggaagccacccacttgaagctggagc 2985
Db 2820 ACCAGAAGAGAAATATCAGAAATCTGCATGAGAGAGAACCCACCTTGAAGCTGGCG 2879
QY 2986 tctcactgaagaacacctgttaaaagtctaccagagatgagatgagatgagctgtcgatgac 3045
Db 2880 TGTCCATTGAGAACCTGTGPAAGTCTTACCGAGATGGATGAAGGTGGCTGTGATGGCC 2939
QY 3046 tggacatgaatttlaagagggccagatcacctcctccttgggccaagatgagagggga 3105
Db 2940 TGGCACTGAAATTTTATGAGGGCCAGATACCTCCTTCTGGGCCCAATGATGAGGGGA 2999
QY 3106 agagagacacatgtaacatctgtaacgggtgtlcccccagaccctggagcagcctaca 3165
Db 3000 AGACGACCACTATGTAATCTGACCGGGTGTTCCTCCCGACCTCGGGCACCCGCTTACA 3059
QY 3166 tccctggaagaagacatctgctctgagatgagacacatcccgagagacactggaggtctgtc 3225
Db 3060 TCTCGGAAAGAACATTCCTCTGAGATGAGCAACATCCGCGAAGACCTGGGGCTGTGTC 3119
QY 3226 cccagcataagctgtcgttgaacatgctgtcgaagaaacatactgttctctatgccc 3285
Db 3120 CCCAGATTAACGTGCTGTGACATGCTGACGTGAGAACACATCTGTGTTCTATGCCCC 3179
QY 3286 gcttgaagaagctctctgagagcagctgaagcgagagatgagagatgagccctgagtg 3345
Db 3180 GCTTGAAGAGGCTCTCTGTGAGAGCACGTGAAGCGGAGATGAGAGATGGCCCTGAGTG 3239
QY 3346 ttgtttgccaatcaagcaagctgaaagcaaaacaaagcagctgtcgaagtgaatgcaga 3405
Db 3240 TTGTTTGGCATCAAGCAAGCTGAAGAAAGCAAAACAAAGCAGCTGTACAGTGAATGCAGA 3299
QY 3406 gaaagctatctgtgagccttgagccttctgcggggagatcaaggtgtcatctctgtgaac 3465
Db 3300 GAAACCTATCTGTGGCTTGGCTTGTGCGGGATCTTAAGTGTGTCAATTCGTGATGAAC 3359
QY 3466 ccacagctgtgtgagaccccttactcccgcaaggaagatgagagctgtgtgaataacc 3525
Db 3360 CCACAGCTGTGTGAGACCCCTTACTCCCGAGGGCAATTTGGAGTGTGCTGTAATATACC 3419
QY 3526 gacaaagccgaacataatctctctacacacacatgataagcagcagcttccgtggag 3585
Db 3420 GACAAGGCCGACCATTTATCTCTTACACACACATGATGAAGCGGAGCTCTGGGGGG 3479
QY 3586 acaagattgccaatctcctccatgggaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3645
Db 3480 ACAGATTGGCATCTCTCCATGGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGA 3539
QY 3646 agaaccagctggaagaagcactactacactgagcctgtgtcaagaagaagatgtaaccctccc 3705
Db 3540 AGAACCAGCTGGGAAGAGCTACTACTGACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3599
QY 3706 tcaagctcctgagaagaagtagtagcactgtgtcatcactgtaaaagagagagagtgctt 3765
Db 3600 TCAGTCTCTGCAAGAACGTAGTAGCACTGTGTATACCTGAAAGAGAGAGACGTGTCTT 3659

QY 3766 ctcaagacattctgatactgtgacctggcgcaagcagacatgaagatgacacgtgacacacg 3825
Db 3660 CTCAGAGCAATTTGATGATCTGCTGGCTGGCCACGACATGAGATGACACCTGACCTTCG 3719
QY 3826 atgtctctgatactccaactcatcaaggaagcaltgtctgaagcccgctgtgtgaag 3885
Db 3720 ATGTCCTGTATCTCCAACTCATCAGGAAGCATGTGTGTGAAGCCCGCTGTGTGAAG 3779
QY 3886 acatagggcagatgagcactatgtctgccaatagaagctgcaagaagagagagcccttg 3945
Db 3780 ACATAGGCAATGAGCTGACCTATGTGCTGCATATGAAGCTGCTAAGAGAGAGACCTTTG 3839
QY 3946 tgaactcttcatatgatatgataagcagctctcaagacccctggagatctcatatgca 4005
Db 3840 TGAACCTCTTATCATGATGATGATGACCGGCTCTCAGACCTGGGCAATTTAGTTATGCA 3899
QY 4006 tctcagaagaagacccctggaagaatattcctcaaggtgtgcccgaagagatgagtgatg 4065
Db 3900 TCTCAGAGACCACTCTGAGAAATATTTCTCAAGGTGCGGAGAGAGATGGGGTGATG 3959
QY 4066 ctgagacctcagatgtaaccttgccagcaagacgaacgaagcggtcctcgggagacaagc 4125
Db 3960 CTGAGACCTCAGATGATGATCTTCCAGCAAGACGAAGACGGCGGCTTCGGGAGACAGC 4019
QY 4126 agagctgtcttgcccgcttaactgaagatgatactgtctgatacaatgatactgacatag 4185
Db 4020 AGACCTGTCTTCCCGCTTCACTGAAATGATGCTGTGTGATCCAAATGATTTGACATAG 4079
QY 4186 accagaatccagagagacagactgtctcagtgagatgagtgaggaaggtctctacag 4245
Db 4080 ACCAGATCCAGAGACAGACAGACTTGTCAGTGGATGGATGGCAAAAGGTCTTACCAAG 4139
QY 4246 tgaaggtctggaaccttaacacagcaacagtttgtgccccttltgtggaagaagctgtaa 4305
Db 4140 TGAAGGCTGGAACCTTACACAGCAACAGTTGTGGCCCTTTGTGGAAGAGACTCTAA 4199
QY 4306 ttgcagaagcagagtcggaagaagatttltgtcagatgtcttcgagcagctgtgtgtct 4365
Db 4200 TTGCGACACGAGAGTGGGAAGGATTTTTCCTCAGATGTCTTGCACAGCTGTGTGTCT 4259
QY 4366 gcaatgcccctgtgttcaagcctgatactgtccaccccttggcaagtaecccaagctgaaac 4425
Db 4260 GCATTTGCCCTTGTGTTCAGCTGATGCTGACCCCTTGTGGCAAGTACCCAGCCTGGAAC 4319
QY 4426 ttcaagccctgatactgaagaagaacagatgatacttltgaagcaatgtgtccgaagaa 4485
Db 4320 TTCAAGCCTTGATGTACACGAACAGTACATTTGTCAAGCAATGATGCTCTGAGAGACA 4379
QY 4486 cgggaacccctggaactctttaaagccctcaacaaagaccccttgctcggagaccgtgta 4545
Db 4380 CGGGAACCTTGGAACCTTTAAACGCCCTCACCAAGAACCCCTGTGGAGACCCGCTGTA 4439
QY 4546 tggaaaggaaccccaatcccaagacagccttccagagcagggggaagaagtgaaccatg 4605
Db 4440 TGAAGGAACCCCAATCCAGACACCCCTTGCAGGAGGGGAGGAAGTGTGACCATG 4499
QY 4606 ccccaagttcccagacatataatgagccttccagaaatgggaactggaatgagcgaac 4665
Db 4500 CCCCAAGTCCCGACAGCATATGAGACCTTCTCAGAAATGGAACTGGACAAAGCAAAACC 4559
QY 4666 cttaacctgatactgcaagtgtaagcagcaaaaatcaagaagatgtctgtctgtgtccc 4725
Db 4560 CTTACACCTGATCCAGTGTAGAGGAGCAAAATCAAGAAATGCTGTGTGTGTGTGTGTGTGT 4619
QY 4726 cagggcaggggggtgtgtctctcccaagaagaacaacaacactgcagatctcctcag 4785
Db 4620 CAGGGCAGGGGGGCTGCTCTCCCAAAAGAAACAAAACACTGCAGATATCTTCAAG 4679
QY 4786 acctgacaggaagaacattcgagatctcgtgtgaagcgtatgtgaatcatagaca 4845
Db 4680 ACCTGACAGGAAGAAACATTTGGGATTATCTGTGTGAAGAGTGTGTGAGATCATAGCA 4739

Dh 6900 AGACAGTGTGACCTTTCACATCTTTCTACAGATGAGAAAGTGAAGAAA 6959
Qy 7066 gcatatgaagaatccctgttcaacaggggtgctgaagaagtaagaagtaagctacgtc 7125
Dh 6960 GCTATGTATGAAGAACTCTGTTTCATACGGGCTGCTGAAGTAAAGAGNACTAGACTTT 7019
Qy 7126 cctttgacacacatgtaagaatgtgtgtgagaagaagccagaagctgtagtggaagaagta 7185
Dh 7020 CTTTTCACACCATGTGAAAGTGTGTGAGAAAGAGCAGAAAGTGAAGTGGGAGAAAGTA 7079
Qy 7186 aactgatactgtactgatactatccaatgcaatgcaatgcaatgcaatgcaatgcaat 7245
Dh 7080 AACGAGTACTGTACTGTACTATTCATGCAATGCAATTCATGCAATGCAATGCAATGCAAT 7139
Qy 7246 tccattcaag 7305
Dh 7140 TCCATTACAGGGGAGAGTGTGCTGTGACCTATGCTGTGATGCTGTGATGCTGTGATGCT 7199
Qy 7306 tgaattagtttttttactaactaactaactaactaactaactaactaactaactaacta 7365
Dh 7200 TGAATTTAGTTTTCCTTACTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 7259
Qy 7366 ggggttgaactcaacttt 7425
Dh 7260 GGGTTTGAACCTCACCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 7319
Qy 7426 caaatatcatcaatgaatcatgagagagagagagagagagagagagagagagagagag 7485
Dh 7320 CAATATTCATTCATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7379
Qy 7486 atctcatcaactaactaactaactaactaactaactaactaactaactaactaactaact 7545
Dh 7380 ATCTCATCTACTAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7439
Qy 7546 gcttgagaaatgaatgag 7605
Dh 7440 GCTTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7499
Qy 7606 tgggt 7665
Dh 7500 TGGT 7559
Qy 7666 tcaatgag 7725
Dh 7560 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7619
Qy 7726 tgggt 7785
Dh 7620 TGGT 7679
Qy 7786 ttcattgttataatttccctatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7845
Dh 7680 TTTCCATTTGTATTTGTCTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7739
Qy 7846 ctcttaataatactatgag 7905
Dh 7740 CTTTAAAT 7799
Qy 7906 tgaagaatgag 7965
Dh 7800 TGAAGCTGCTGAG 7859
Qy 7966 cctgt 8025
Dh 7860 CCGTGTGCTATTTGCTGT 7919
Qy 8026 ctgaagaatgag 8085
Dh 7920 CTGAGCAAGTGTAT 7979
Qy 8086 tgaatttgaagaagaatgt 8145
Dh 7980 TGTATTTTGTACAAAATGTTGTACTTTTATGTTATTTTGAATTTTGAATTTTGAATTTT 8039

Qy 8146 tgaatttgaagaagaatgt 8205
Dh 8040 TGAATTTGAT 8099
Qy 8206 cactgt 8265
Dh 8100 CACTGCCCAT 8159
Qy 8266 agaaagaatgag 8325
Dh 8160 AGAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 8219
Qy 8326 taggaatacttcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaat 8385
Dh 8220 TAGGATATCTTAACT 8279
Qy 8386 aagagatgt 8445
Dh 8280 AAGAGATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8339
Qy 8446 catgttatcaagctcaagctcaagctcaagctcaagctcaagctcaagctcaagctcaag 8505
Dh 8340 CATGTTATTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT 8399
Qy 8506 gtaacaataatgag 8565
Dh 8400 GTAAACAATGCTGGCAGGC - TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 8458
Qy 8566 aagtaagaag 8625
Dh 8459 AAGTATTAAGGCTACAAAGCTTAACAAATGATTTCTTCAACAGGAGAAACACACTGCTTGA 8518
Qy 8626 aaactgt 8685
Dh 8519 AAACCTGCTGAAAAACAACTGTTGTTATGAGCTTTAGTACTTCAATTAATTTGGCTT 8578
Qy 8686 tgcagatatgt 8745
Dh 8579 TGCAGATTTGTGATTTCCCATTAATTTGACAGTCAATTTTCAATTTCTTCAATTTCAAC 8638
Qy 8746 taatgaagaagaataataaacaacaataataataataataataataataataataataat 8805
Dh 8639 TAGTCAAGAAAAATATAAACAACAATACTTCCATATGAGAGATTTTCAAGATTTTC 8698
Qy 8806 taaccagcttatt 8865
Dh 8699 TAACCACTGTTATTTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 8758
Qy 8866 taatgaagaagaataataaacaacaataataataataataataataataataataataat 8925
Dh 8759 TACTGTATACGT 8818
Qy 8926 aagtgatcttcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatca 8985
Dh 8819 AAGTATCTTTCAAT 8878
Qy 8986 gctaaagtgtaagaacttcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatca 9045
Dh 8879 GCTAAAGGTGTAAGACTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTT 8938
Qy 9046 atattataaaccac 9105
Dh 8939 ATATTAT 8998
Qy 9106 atgatttataataataataataataataataataataataataataataataataataata 9165
Dh 8999 ATTGATTTTAAAT 9058
Qy 9166 gcaatttaagaatctcaaaataataagaataataagaataataagaataataagaataata 9225
Dh 9059 GCATTTTACAGTATCTTCAAAATACAGAAATTAAGAAATTTTCTCTCTTAAATATAT 9118

QY 9226 ttltcaaaatcaagttatggttccatatttactaaatcgtatctcaatttccatt 9285
|||||
Db 9119 TTTTCAAAATCAAGTTATGTTTCTCTCATTTTACTAAATCGTATTTCTTATTTCTTCAATT 9178
QY 9286 atagtaaatctatgagcaactcttacttccgttcccttgatatttcaaggacataatttaa 9345
|||||
Db 9179 ATAGTAAATCTATGAGCAACTCTTACTCTGCTTCTCTGATTTCAAGGCATATTTTAA 9238
QY 9346 aaatacaaaagcacttgaactattttgagaagaacacgcacattttatatacagattaa 9405
|||||
Db 9239 AAAATCAAAAGGCACTGTAAGTATTTTGAAGAAACACAACTTTTAAATACAGATTGAA 9298
QY 9406 aggaactcttctgaagcctagaacaacatctatagttatatacattcttcaacttctgta 9465
|||||
Db 9299 AGGACTCTTCTGAGCTAGAAACATCTATAGTTATACATCTTCTATTAATCTGTGTA 9358
QY 9466 cctttaaataagtaatttttcaatttccgttgaagaaacctaatttctgtagaataattt 9525
|||||
Db 9359 CTTTTAAATAGTATTTTACATTTTCCGTGTAACCAATTTGTTGTAAGAAATTTT 9418
QY 9526 taaccaacttactcaatcaatcaaaatttctgtatatttccctgttgaagttccattg 9585
|||||
Db 9419 TACCAACTTATACTCAATCAAGCAAAATTTCTGTATATTCCTGTGGAATGTACTATAG 9478
QY 9586 tgaatttcagaaattctcaaaatacgttctcaaaaatttctgcttcttctgacttctggac 9645
|||||
Db 9479 TCAGTTTGGAATTTCTCAAAATACGTGTCAAAATTTCTGCTTTTCTCATCTTTGGGAC 9538
QY 9646 accccaagaactcttcaaaactctgtaatatgagaatacagaagaataataagccc 9705
|||||
Db 9539 ACCCTAGAAATCTTTTAACTGTGATATGAGAAATACAGAAATTAATTAAGCCC 9598
QY 9706 tctatataaattgcccagacacattctgtttaaatacaaccaactcaacttactg 9765
|||||
Db 9599 TCTATACATTAATGCGCCAGCAATTCATGTTTAAAAACAACCACTCACACTACTG 9658
QY 9766 tattcatatctgtactgaagcaaatgcttctgtactatataatgttgcacatcttc 9825
|||||
Db 9659 TATTTATATCTGTACTGAAAGCAAAATGCTTTGTACTATTAATGTGACATCATTTG 9718
QY 9826 attca 9830
|||||
Db 9719 ATTCA 9723

RESULT 11
AX139817 9741 bp DNA linear PAT 30-MAY-2001
LOCUS AX139817
DEFINITION Sequence 69 from Patent EPI096012.
ACCESSION AX139817
VERSION AX139817.1 GI:14275399
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Deneffe, P., Rosier-Montcus, M.F., Arnold-Reguigne, I., Prades, C.,
Naudin, L., Lemoine, C., Duverger, N., Jaye, M., searloss Il, G.H.,
Renaley, A., Brewer, H.B. and Dean, M.
TITLE Nucleic acids of the human abcl gene and their therapeutic and
diagnostic application
JOURNAL Patent: EP 1096012-A 69 02-MAY-2001;
Aventis Pharma S.A. (FR)
FEATURES
source 1. 9741
Location/Qualifiers
1. 9741
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2650 a 2180 c 2290 g 2620 t 1 others
ORIGIN
Query Match 92.6%; Score 9672.8; DB 6; Length 9741;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 9705; Conservative 0; Mismatches 18; Indels 2; Gaps 2;
QY 106 ctgttttttcccggttctgttttctcccttcccggaagctgttcaaggtataga 165
|||||
Db 1 CTTGTTTTTCCCGGTTCTGTTTTTCTCCCTTCTCCGGAAGCTGTCAAGGGGTAGGA 60
QY 166 gaagagagcgaacacacaaatgtaaacagttatagaccacacacggtcgtccgtc 225
|||||
Db 61 GAAAGAGACGCAACACAAAAGTGAACAGTTAATGACACGAC-GGCGTCCCTGCT 119
QY 226 gtgagctctgcccgttcccttccagggctccgagcacacgctgtggtcgtcgtg 285
|||||
Db 120 GTGAGCTCTGGCGGCTGCTCTTCCAGGCTCCGAGCACAACGCTGGGGGTGCTGGGTGAG 179
QY 286 ggaacatggtctgttgcctcagctgtaggttctgtctgttgaagaacctacttaaga 345
|||||
Db 180 GGAACATGGCTTGTGTTGGCTCAGCTGAGTTGCTGCTGTGGAAGAACCTTCATTCAGAA 239
QY 346 gaagacaaacatgctcagcttcttactggaagtgtgctgtgctctatattcttctgac 405
|||||
Db 240 GAACACAAACATGTCACCTGCTGTGAAAGTGGCTTGCTTATTTATTTCTCTGATTC 299
QY 406 tgaatctgttgcgttgaagcttaccacccctatgaacacataatgacatttccaaata 465
|||||
Db 300 TGATCTCTGTTGGCTGAGCTACCCACCTATGAAACATGATGACATTTTCCAAATTA 359
QY 466 aagcctatgctctgcaagaaacttcttctgtgttcaaggtatctgtatagcaaca 525
|||||
Db 360 AAGCAATGCTCTGAGGAACATCTTCTTGGGTGAGGGGATTTATCTGTAAGCCAAACA 419
QY 526 accctgttctcgttaccacacacctctgtggaaggtcccggaagttgttgaactttaa 585
|||||
Db 420 ACCCTGTGTTCCGTACCCTGCTGCTGAGAGCTCCCGAAGTTGTTGAACTTTAAACA 479
QY 586 aatccattgtgctgcgttcttcaagatgctcggaggttcttatacagccagaag 645
|||||
Db 480 AATCATTTGGGCTGGCTGCTTCTGCAATGCTGGAAGCTCTTTTAAACGACCAAAAG 539
QY 646 acaccagatgaagagatctgcgaagttcttgaagaatacagaatcaagaataatcca 705
|||||
Db 540 ACACGACATGAAAGACATGCGCAAAATCTTGAAACATTTACGACATTAACAAATCCA 599
QY 706 gctcaaatctgaagcttcaagatttccctgtgtgacaataatgaacttctcgtgttccat 765
|||||
Db 600 GCTCAAACTTGAACCTTCAAGATTTCTGTTGGACATGAACCTTCTCGGGTTCTGTG 659
QY 766 atcaaaccttcttctcccaagttctactgttgaacaaagtctgaaggtctgtatctc 825
|||||
Db 660 ATCAACAACCTCTCTCTCCCAAAAGCTACTGTGCAAGATGCTGAGGGCTGATGATTC 719
QY 826 tccagaaggtatttttgaaggtcaccagttacttgaagaatctgttgaatgagatcaa 885
|||||
Db 720 TCCACAAAGTATTTTTCAGAGGCTACCAAGTTTACATTTGACAAAGTCTGTCAATGATCAA 779
QY 886 aatcagaagatgattcaacttgttgaacaaagaatttctgtgacttgtgtgcttacc 945
|||||
Db 780 AATCAGAAGAGATGATTCACTTGTGACCAAGAGTTTCTGTGAGCTTTGGGCTTACCAA 839
QY 946 agagaagaactgtgctgcaagcagagagagttacttgttccaaatgagaaatcttgaagcaa 1005
|||||
Db 840 GGGAGAAATCTGCTGAGCAGACAGAGGAGTACTTGTTCACATGAGATCTTCAAGCCAA 899
QY 1006 tctcgaagaacataacttcaacttcccttcccggaagagcgtgtgctgaagccaa 1065
|||||
Db 900 TCTGAGAACACTTAACCTTACATCTCCCTTCCGAGACAGAGCTGCGGAGCCACAA 959
QY 1066 aaacattgtcagatagttctgtggaacttggcccaagagactgttccaagtatagaagcttga 1125
|||||
Db 960 AAACATTGCTGCAATAGTCTTGGAGCTGCGCCAGAGAGCTGTTACAGATGAGAAGCTGGA 1019
QY 1126 gtgacatgcaagcagaggtatgttcttgaaccaatgtgaacacactcagcttccacc 1185
|||||

Db 1020 GTGACATGCAGAGAGATGATGTTCTGTGACCAATGTGAACAGCTCCAGCTCCGCCAACC 1079
QY 1186 aaatcaaccagcgtgtctcgtatctgtctcgggcaatcccgaggagggggtctgaaga 1245
Db 1080 AAATCTACAGAGCGGTGTCTGTCTATGTCTGCGGGCATCCCGAGGAGGGGGCTGAAAGA 1139
QY 1246 tcaagctctcaactagtgatagagaaacaactaagaagccctcttggaagcaatgga 1305
Db 1140 TCAAGTCTTCACTGATAGAGAGACAACTACAAAGCCCTCTTTGGAGGCAATGGCA 1199
QY 1306 ctgagagagatgtctgaacctctatagaaacttaactaactctactgaatgattga 1365
Db 1200 CTGAGGAAGATGCTGAACCTTCTATGACAACTTACAACTCCTTACTGCAATGATTGA 1259
QY 1366 tgaagaatttggaagctagctcctctcccgcaatlatctggaagcctctgaaagccgtgc 1425
Db 1260 TGAAGATTTGAGATGATGATGCTCTCTTCCGCAATATCTGGAAGCTCTGAAACCGCTGC 1319
QY 1426 tccgttggaagatccctgtatacaacttgaaactccagcccaagagcaatgtgaggaac 1485
Db 1320 TCGTTGGGAAGATCTCTATACACCTGACACTCCAGCCACAAAGGCAAGTCTATGGCTGAG 1379
QY 1486 tgaacaagacctcccaagaaactgctgtgtccatgatctggaagcaatgtggaagaaac 1545
Db 1380 TGAACAAGACTCTTCAGGAACCTGGCTGTGTTCATGATCTGGGAAGGCAATGGAGAGAAC 1439
QY 1546 tcaagcccaagatcttgaaactctcatggaagaaacagccaagaatgtgacctgtccgagatgc 1605
Db 1440 TCAGCCCCAAGATCTGAGACCTTCATGAGAACAGCCAAATGAGACCTTGTCCGATGC 1499
QY 1606 tttgttggaacaggaagaaatagcaactcttggaagaaagcaagcttgatgagctatgga 1665
Db 1500 TGTGTGACACAGAGCAAAATACCACTTTGGGAACAGCAAGTGTGAGATGCTTGTGATTGGA 1559
QY 1666 caagcccaagacatgtgtgcttcttgccaagcaagcaagagagatgtcccaatcaatg 1725
Db 1560 CAGGCCAAGACATGCTGCGCTTTTGGCCAAAGCAACCCAGAGATGTCCATCCAGTAATG 1619
QY 1726 gttctgtgtcaacctggaagaaagcttcaagagactaaacagcaatcccgaaatc 1785
Db 1620 GTTCTGTGTACACCTGAGAGAAAGCTTTCACAGACAGACTAACAGGCAATCCGAGCAATAT 1679
QY 1786 ctgccttcaatgagatgtgtcaaccttgaaagactagaacctatgaaacagaaagctgtgc 1845
Db 1680 CTCCTTCATGAGAGTGTGTCAACCTGACAAAGCTAGAACCCATAGCAACAGAAAGTGTGCG 1739
QY 1846 tcatcaacaagatcagatgagctgtgtgaatgagaagaaagctgtgagctgtatgtgtca 1905
Db 1740 TCATCAACAAGATCATGAGAGCTGTGTGATGAGAGAAAGTCTGGGCTGTGATTGTGTTC 1799
QY 1906 ctggaatctcaagagagattgagctggcccatcatgtcaagttaagaatccgaatg 1965
Db 1800 CTGGAATTTACTCCAGAGGAGATGAGCTGCCCATCATGTCAAGTACAAATGCGAATGG 1859
QY 1966 acattgacaatgtggaagagaaacaataaatacaagatgagatgactggaagcctgtgtc 2025
Db 1860 ACATTGACATGAGAGAGAGACAATAATCAAGATGGGTACTGGGACCTCGTGTCTC 1919
QY 2026 gagctgaaccccttggaagaaatgctgtgagctgtggaagagcttcgactactgtcaagatg 2085
Db 1920 GAGCTGACCCCTTTGAGAGATGCGTACGTCTGGGGGGGCTTCGGCTACTTTCAGAGATG 1979
QY 2086 tgggtgagagagcaatcatcaagagtgctgacgagccaggaagaaacactggtgtctata 2145
Db 1980 TGGTGGAGAGGCAATCATAGGGTCTGTGACGGGCAACCGAAGAAACCTGGTCTTATA 2039
QY 2146 tgcagagatgacctatccctgttactgtatgacatcttctgcggtgtatgagccggt 2205
Db 2040 TGAACAAGATGACCTTACCTGTTAGCTGATGACATCTTTCGCGGATGATGAGCCGG 2099
QY 2206 caatgccctctcatgagctgtgagctgtgattactcaagtgagctgtgatatcaagaagca 2265
Db 2100 CAATGCCCTCTTCTATGACGCTGCGCTGAGATTACTAGTGGCTGTGATCATCAAGGGCA 2159
QY 2266 tccgtgtatgagaagaggaacagctgtaagaagaaacatgctgagatcagctgtgacaaca 2325
Db 2160 TCGTGTATGAGAGAGGACAGGCTGAAGAAGACCATCGATCATGGGCTGTGACAAACA 2219
QY 2326 gcaatacctgtgtttagctgtgttcaatgaatccatcttccctctctgtgtgagcgtgc 2385
Db 2220 GCATCCTGTGTTTAGCTGATTAATGATGATGATGATGATGATGATGATGATGATGATG 2279
QY 2386 tgcagtgatcaatccctgaagatgaagaacccagctgtgagcaatgcatccagcgtgtgt 2445
Db 2280 TGTCTAGTGTCTCTCTGAAAGTGAAGAACTGTGCTCTCTCTCTCTCTCTCTCTCTCTCT 2339
QY 2446 tttgtctccctgtcgt 2505
Db 2340 TTTGTCT 2399
QY 2506 tcttctcagaagcaacctgtgagagagcctgtggaagagatcatctactgaagctgtgac 2565
Db 2400 TCTTCTCAGAGCAACCTGGCAGAGCTGTGGGGGATCATCTTCAAGCTGTGATCC 2459
QY 2566 tgccttaagctcgt 2625
Db 2460 TGCCTAGCTCTCTGT 2519
QY 2626 ctgagctgtgtctcctgt 2685
Db 2520 CTAGCCTGTGTCT 2579
QY 2686 agcaagagatgagatgagatgagagaaacccgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2745
Db 2580 AGCAGAGGCTGT 2639
QY 2746 tcaatcacaacctgt 2805
Db 2640 TCAATCTGACCACTCTGT 2699
QY 2806 cctgtgtatctgt 2865
Db 2700 CCGTGTATCTGAGGCTGT 2759
QY 2866 ctgtgacaagctcctactgt 2925
Db 2760 CTTGACCAAGTCTGT 2819
QY 2926 accagaagaagatgtcgaagaatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2985
Db 2820 ACCAGAGAGATATCAAGAAATCTGATGAGAGAGAACCCACACTTGAAGCTGTGGCG 2879
QY 2986 tgtccatcagaacctgt 3045
Db 2880 TGTCTATTCAGAGCTGT 2939
QY 3046 tggcactgaatttataagagagcaagatcaactccttctgtggtccacaatgtgagcgga 3105
Db 2940 TGGCACTGAATTTTATAGGGGCGAGATCACCTCTCTCTGGGCAATGTGAGCGGGGA 2999
QY 3106 agcagacacacatgtcaatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3165
Db 3000 ACACGACCACTGT 3059
QY 3166 tctctggaagaagacatctgt 3225
Db 3060 TCTCTGGAAGAGACTGT 3119
QY 3226 ccagacatacgt 3285
Db 3120 CCCACATATAGCTGT 3179
QY 3286 gcttgaagaagctctctgagaagacagctggaagagagagagagagagagagagagagatg 3345
Db 3180 GCTTGAAGGGCTCTCTGTAGAGACAGCTGAAGGCGGAGATGAGACAGATGAGCTGTGATG 3239

QY 3346 ttggttgcatacaagcagctgaaagcaaaacagccagctgtcaagttgaaatgcaga 3405
|||||
Db 3240 ttgtttggcattcaaacagctgaaacaaacagccagctgtcaagttgaaatgcaga 3299
QY 3406 gaagatactgtgagcttgagccttgttcgaggaatcaagttgcatcttgatgaac 3465
|||||
Db 3300 gaagatactgtgagccttgagccttgttcgaggaatcaagttgcatcttgatgaac 3359
QY 3466 ccaagctgtgtgagccttactcccgaggggaatctggaagctgtctgtgaatacc 3525
|||||
Db 3360 ccacacctgtgtgagccttactcccgaggggaatctggaagctgtctgtgaatacc 3419
QY 3526 gaagaagccgaccattattctctacacacacacatgatatgaagggagctccctggag 3585
|||||
Db 3420 gaagaagccgaccattattctctacacacacacatgatatgaagggagctccctggag 3479
QY 3586 acagagctgcatcatctccacatgaggaagctgtctgtgtgagctccctgtttctga 3645
|||||
Db 3480 acagagctgcatcatctccacatgaggaagctgtctgtgtgagctccctgtttctga 3539
QY 3646 agaaccagctggaagaaagctactactgaccttgatcaagaagatgtggaatccctcc 3705
|||||
Db 3540 agaaccagctggaagaaagctactactgaccttgatcaagaagatgtggaatccctcc 3599
QY 3706 tcaagttctgcagaaacagtagtagcactgtgtcataccatgaaagagagagacgtgtt 3765
|||||
Db 3600 tcaagttctgcagaaacagtagtagcactgtgtcataccatgaaagagagagacgtgtt 3659
QY 3766 ctcaagagcattctgatatgtctgtgagcagcagcatgagagtgacaagctgtacatcg 3825
|||||
Db 3660 ctcaagagcattctgatatgtctgtgagcagcagcatgagagtgacaagctgtacatcg 3719
QY 3826 atgtctctgtcatctccaacctatcaagaagatgtgtctgaagcccgctgtgtgaag 3885
|||||
Db 3720 atgtctctgtcatctccaacctatcaagaagatgtgtctgaagcccgctgtgtgaag 3779
QY 3886 acataagagcattgacatgactatgtgtgtcatatgaagctgtgaagagagagccttg 3945
|||||
Db 3780 acataagagcattgacatgactatgtgtgtcatatgaagctgtgaagagagagccttg 3839
QY 3946 tggaaactcttcatagattgatatgagcagctctcaagactgtggcatcttctagtatggca 4005
|||||
Db 3840 tggaaactcttcatagattgatatgagcagctctcaagactgtggcatcttctagtatggca 3899
QY 4006 tctcaagaagagccttgaaagaatattctcaaggtgtgcgaagaagagagagagagag 4065
|||||
Db 3900 tctcaagaagagccttgaaagaatattctcaaggtgtgcgaagaagagagagagagag 3959
QY 4066 ctgagacctcagatgtgacttgcacagcaagcaagcagggccttcggggagacaagc 4125
|||||
Db 3960 ctgagacctcagatgtgacttgcacagcaagcaagcagggccttcggggagacaagc 4019
QY 4126 agagctgtcttgcgcgttcaactgaagaatgactgtctgtatccaatgatcttgaacatg 4185
|||||
Db 4020 agagctgtcttgcgcgttcaactgaagaatgactgtctgtatccaatgatcttgaacatg 4079
QY 4186 acccaagaatcagaag 4245
|||||
Db 4080 acccaagaatcagaag 4139
QY 4246 tgaagaagctgaaacttacaacagcaagcttgtgagccttcttgaaagaagactgtaa 4305
|||||
Db 4140 tgaagaagctgaaacttacaacagcaagcttgtgagccttcttgaaagaagactgtaa 4199
QY 4306 ttgccaagagagatcgaaagagatcttctgaatgtctgtcagcagctgtgttct 4365
|||||
Db 4200 ttgccaagagagatcgaaagagatcttctgaatgtctgtcagcagctgtgttct 4259
QY 4366 gcaattgccttgttcaagctgtatgtgcacaccttggcaagtaaccaagcctgtgaac 4425
|||||
Db 4260 gcaattgccttgttcaagctgtatgtgcacaccttggcaagtaaccaagcctgtgaac 4319
QY 4426 ttcagccctgtatgtacaagaacagatcacatctgtcaagaatgatgtctccttgagaca 4485
|||||

Db 4320 ttacaccttgatgtacagacagatcacatcttgcacgaatgagctccctgagaca 4379
|||||
QY 4486 cgggaacccctggaaccttaacagccctcaccaaagacccctgtgttcggagcccggtga 4545
|||||
Db 4380 cgggaacccctggaacctttaaaccgcccctcacaaagacccctgtgttcggagcccggtga 4439
QY 4546 tgaagaagaaccccatctccagaacagcccttgcaagcagggagagagatgtgacaatg 4605
|||||
Db 4440 tgaagaagaaccccatctccagaacagcccttgcaagcagggagagagatgtgacaatg 4499
QY 4606 ccccaagttcccaagacacatgagaccccttccagaatlyggaactggaacatgcaaac 4665
|||||
Db 4500 ccccaagttcccaagacacatgagaccccttccagaatlyggaactggaacatgcaaac 4559
QY 4666 cttaacctgcattgcagatgtatgagcagcagaacatcaagaatgtgtgtgtgtgtccc 4725
|||||
Db 4560 cttaacctgcattgcagatgtatgagcagcagaacatcaagaatgtgtgtgtgtgtccc 4619
QY 4726 cagggcagggggt 4785
|||||
Db 4620 cagggcagggggt 4679
QY 4786 acctgacaggaagaaacatcttcagatctatctgtgtgaagcgtatgtgacatcatagcca 4845
|||||
Db 4680 acctgacaggaagaaacatcttcagatctatctgtgtgaagcgtatgtgacatcatagcca 4739
QY 4846 aaagcttaagaagaacagatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4905
|||||
Db 4740 aaagcttaagaagaacagatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4799
QY 4906 tcaagtaatactcaagacacttctccagatctcaagaagtaatgatalgcca tcaacaatga 4965
|||||
Db 4800 tcaagtaatactcaagacacttctccagatctcaagaagtaatgatalgcca tcaacaatga 4859
QY 4966 agaaacacctaagctgtgccaagagacagttctgtcagatcgatcttcaacagcttggaa 5025
|||||
Db 4860 agaaacacctaagctgtgccaagagacagttctgtcagatcgatcttcaacagcttggaa 4919
QY 5026 gatttataagagagctgtgacacacagaataatgtcaagttgtgtgtgtgtgtgtgtgtgt 5085
|||||
Db 4920 gatttataagagagctgtgacacacagaataatgtcaagttgtgtgtgtgtgtgtgtgtgt 4979
QY 5086 ggcattgcaatcagcttcttccagatcttcaatcaatcaatgcatcttccgggccaactgac 5145
|||||
Db 4980 ggcattgcaatcagcttcttccagatcttcaatcaatcaatgcatcttccgggccaactgac 5039
QY 5146 aaaagggagagaacccctagccattatggaatctactgtcttcaatcaatccctgaaatcca 5205
|||||
Db 5040 aaaagggagagaacccctagccattatggaatctactgtcttcaatcaatccctgaaatcca 5099
QY 5206 ccaagagagagctctcaag 5265
|||||
Db 5100 ccaagagagagctctcaag 5159
QY 5266 tctgtatcattcttgcaatgtcttccagcagcagcttgcgtatctctgacagag 5325
|||||
Db 5160 tctgtatcattcttgcaatgtcttccagcagcagcttgcgtatctctgacagag 5219
QY 5326 agcggtcagcaagaacaaacacctgacgttcaatcaagttgagttgaagcctgtcatctact 5385
|||||
Db 5220 agcggtcagcaagaacaaacacctgacgttcaatcaagttgagttgaagcctgtcatctact 5279
QY 5386 ggcctcctaatttctgtcttgagatgtatgaaatagctgttccctgcacacatgcatctta 5445
|||||
Db 5280 ggcctcctaatttctgtcttgagatgtatgaaatagctgttccctgcacacatgcatctta 5339
QY 5446 tcaatctcatctgtcttccagcagaaatccatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5505
|||||
Db 5340 tcaatctcatctgtcttccagcagaaatccatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5399
QY 5506 cccttactattgtctgtatgt 5565
|||||

QY	7726	tgctctggtgbcagtaaacgtgacacaaaaatgtaggtctctctctggaacgggaactgtg	7785
Db	7620	tgtttctgtgtgcagtaacatgcaacaaaaatgtgggtctctctgagcagcggaactgtgg	7679
QY	7786	ttccatgttatatcttccatgctctgagccatggtgctacaggtcatccatctataga	7845
Db	7680	ttccattgttatattgtctctatgtcttcgagccatgggtctcagaggtcatcttatgaga	7739
QY	7846	ctcttaataactatgatctccgtgtaagaagcgcaagaatcaacgccaactctgtggc	7905
Db	7740	ctctttaaataattactttgtgagatctgtgtaaggcgcaaaagatcaacgccaaatctgtgggc	7799
QY	7906	tgcaagctgtctgaagccagggcatggaattaaagatctgtgcgttccaaactgaaggaa	7965
Db	7800	tgcacagctgctgaagccagggcatggagattaaagattttgtgcgttccaaactgaaggaa	7859
QY	7966	ccgtgcccacattgtccctgactgtctgtctaacatgtaactgtcatctcaagtgttat	8025
Db	7860	ccctgtgcccttggctgtcctgactgtctgtcttaacatggtacactgcacatccaaagatttat	7919
QY	8026	ctgacacaaagtattattcttcggccttttgaattaaactgaagaaatgaagaatgaat	8085
Db	7920	ctgacacaaagtattattcttcggccttttgaattaaactgaagaaatgaagaatggaact	7979
QY	8086	tgtaatttgcaaaaaatgcttgtaactttttaaigttaattggaattaaagttctatcag	8145
Db	7980	tgtatttttgcaaaaaatgcttgtaactttttaaigttaattggaattaaagttctatcag	8039
QY	8146	tgactcttgatctcttagaatggccctcttgaagaacctgtgtaagagagatgagc	8205
Db	8040	tgaacttctgatatcccttgagatggccctcttgaagaacctgtgtaagagagatgagc	8099
QY	8206	cactgcccacatatttctatctctaigttaagtttgatctgcatcaatgactgaactgtcct	8265
Db	8100	cactgcccacatatttctatctctaigttaagtttgatctgcatcaatgactgaactgtcct	8159
QY	8266	agaaagcaatgtgtaatggttcaggaatccctcagcaatatatttgagtcttcttcagatcatt	8325
Db	8160	agaaagcaatgtgtaatggttcaggaatccctcagcaatatatttgagtcttcttcagatcatt	8219
QY	8326	taggaatcctcttaatcccaatcattcaatcaaatatttttgaigtatgtcgttagactga	8385
Db	8220	taggaatcctcttaatcccaatcattcaatcaaatatttttgaigtatgtcgttagactga	8279
QY	8386	aagagatctgtaactgataagaactagagagatatlaagctctcaactcactcctgtgc	8445
Db	8280	aagagatctgtaactgataagaactagagagatatlaagctctcaactcactcctgtgc	8339
QY	8446	catcttaactgaactcattgtttaaacaataagtgctgtctgtgtttagaagaccact	8505
Db	8340	catcttaactgaactcattgtttaaacaataagtgctgtgtgtgtttagaagaccact	8399
QY	8506	gtacaatatatgggcagcctttctttttttaaattgcaacaatgcaaaagccaaga	8565
Db	8400	gtacaatatatgggcagcctttctttttttaaattgcaacaatgcaaaagccaaga	8458
QY	8566	aagatataaggttcaacaagtttaacaatgaattcttccaagaaggaaaacagttagtga	8625
Db	8459	aagatataaggttcaacaagtttaacaatgaattcttccaagaaggaaaacagttagtga	8518
QY	8626	aaactgtctgaaaaaacaactctgttttaagcatcttagtaaccttcaaatatgtgct	8685
Db	8519	aaactgtctgaaaaaacaactctgtgtgtttatggcatttgatgacttcaaatatttgctgt	8578
QY	8686	ttgcagatatgtgataccccaataatctgaacagttcccaatttttcaatctcttaataac	8745
Db	8579	ttgcagatatgtgataccccaataatctgaacagttcccaatttttttcaatctcttaataac	8638
QY	8746	tagtcaagaanaataataaaaaacaataactcccatgtgagcatcttttcagagtcttc	8805
Db	8639	tagtcaagaanaataataaaaaacaataatctcccatgtgagcatcttttcagagtcttc	8698
QY	8806	taaccagctcttatcttctctagtcagtaaacattgtgaaanaaactgttccaataact	8865

Db	8699	TAACCCAGCTTATTTTCTAGCAGTAACATTTGTAAATAATCTGTTCACTAATACT	8758
Qy	8866	tactgttaactgtctctgagagaaagaaaataiyagagaactatgtcttgygggaagtc	8925
Db	8759	TACTGTAACTGCTCTTGAGGAGAAAAMAAAATATGAGGAACTATGTTTGGGGAAGTTC	8818
Qy	8926	aagtgatcttccaatatacttaactactctctccaactcttcccaaatcttgaacttaac	8985
Db	8819	AAGGATCTTTCATATCATTACTACTACTCTTCCACTTTTCCAAAATTTGAAATTTAAC	8878
Qy	8986	gctaaagiytaagactcagatltccaatlaactctctalatlcttlaaattltaacaga	9045
Db	8879	GCTAAAGGTGTAAAGACTTCAGATTTCCAAATATCTCTTCTATATTTTAAATTTACAGA	8938
Qy	9046	atatataataccacgtcgtgaaagaaasaaatgatgtgtttagaagttaaagtcgat	9105
Db	8939	ATATTATATATACCCACTGCTGAAAAAGAAAAATGATTTGTTTGAAGTTAAAGTCAT	8998
Qy	9106	atgattcttaataataagtaataiyagacalattccaatactagtgatgacoglt	9165
Db	8999	ATTGATTTTAAATATATAGTAATGATGAGCATATTTCCAAATACATGATGATGCAATCGTT	9058
Qy	9166	gcaatttaacgtagtacttccaasaaatacgaattatagaalaattctctccatlttaaat	9225
Db	9059	GCAATTTTACAGTACTCTCCAAAATAACAGATTTATAGAAATTAATTCCTCCTCAATTAATAT	9118
Qy	9226	tttccaatacaagatgatgtgttctccatlttactaaatcgataltccaattctcaat	9285
Db	9119	TTTTCCAAATATCAAGTTATATGTTTCCATTTTACTATAAATGATATGATATTCCTCAT	9178
Qy	9286	atagttaactctataggaactccttaactcttcogtctcgatlttcaaggccatatlttaa	9345
Db	9179	ATAGTAATCTATGAGCACTCTCTACTTCCTGCTGCTGATTTCAAGGCCATATTTTAA	9238
Qy	9346	aaatccaagaagcagcttgagacatlttgaagaaacagacatlttaatacagatltga	9405
Db	9239	AAAATCAAAAGGCATGTGACACTATTTTGAAGAAAACACACATTTTATACAGATTGAA	9298
Qy	9406	agagacctctctgtagagctagaaacaactatagtatatacctccaataatactgtgtta	9465
Db	9299	AGGACCTCTTCTGAAAGCTAGAAAACATCTATAGTATACATCTTCATTAATCTCTGTGA	9358
Qy	9466	ccctttaaatagaataatttttaacttctcgtgtfaaacctaatitgtagaataatt	9525
Db	9359	CTTTTAAATAGTAAATTTTTTACATTTTCTGTGTAACCTATATTTGCGTGAATTTT	9418
Qy	9526	taccaactctatactcaatacgaacaaattctcgatattccctgtggaatgtactaagt	9585
Db	9419	TACCAACTCTATACTCAATCAGCAAAATTTTGTATATTCCTGTGAATGTACTCTATG	9478
Qy	9586	tgaagttcagaataatctccaaaatcgtgttccaasaaattctgtcttttgatctcttggagc	9645
Db	9479	TGAGTTTTCAGAAATTTCTCAAAATATCGTGTCAAAAATTTCTGCTTTTGCATTTTGGGAC	9538
Qy	9646	acctcaagaanaactttaacaactgtgtaalatagaaatcagaagaanaataataagacc	9705
Db	9539	ACCTCAGAAAACCTTATTAACACACTGTAAATATAGAAATATACGAAATATAATTAAGCC	9598
Qy	9706	tctatacaataatgcccagacaatltcatltgttaasaaacaaccaaacctcaactactg	9765
Db	9599	TCTATACATTAATATCCAGCAACAATTCATTGTTAAAAAACACCAAACTCACACTACTCG	9658
Qy	9766	tattccatatacttactgaagaagaaatgtctgtgactataataatgttgacatcttc	9822
Db	9659	TATTTCACTATCTGACTGAAGCAATGCTTGTGTACTATTAAATGTTGCACATCATTC	9718
Qy	9826	atcca attca 9830	
Db	9719	ATTCA 9723	

RESULT 12

QY 4066 ctgaagctcagatgtagtactcttgcagcagaagaagcagggccttcggggagacaagc 4125
|||||
Db 3960 ctgaagctcagatgtagtactcttgcagcagaagaagcagggccttcggggagacaagc 4019
QY 4126 agagctgtcttcgcccgttcaactgaagaatgtagtctgtatccaaatgattctacatag 4185
|||||
Db 4020 agagctgtcttcgcccgttcaactgaagaatgtagtctgtatccaaatgattctacatag 4079
QY 4186 accaagaatccagaagagacacactgtctcagtggaatgtagtgcgaagagtcctacag 4245
|||||
Db 4080 accaagaatccagaagagacacactgtctcagtggaatgtagtgcgaagagtcctacag 4139
QY 4246 tgaagagctggaacttacaacagcaacagttgtgcgccccttctgtgaagagactgttaa 4305
Db 4140 tgaagagctggaacttacaacagcaacagttgtgtgccccttctgtgaagagactgttaa 4199
QY 4306 ttgcgcagacggaatccggaagaatcttctgtcagattgtcttcgagcctgtgttct 4365
Db 4200 ttgcgcagacggaatccggaagaatcttctgtcagattgtcttcgagcctgtgttct 4259
QY 4366 gcatctgcccctgtgtcagcctgtatcggtgcacccccttgcgaagttacccagcctgtgac 4425
Db 4260 gcatctgcccctgtgtcagcctgtatcggtgcacccccttgcgaagttacccagcctgtgac 4319
QY 4426 ttcaagcctgtgtagtacaacagacaglaacaattgtcagaatgtatgtctctgaagaca 4485
Db 4320 ttcaagcctgtgtagtacaacagacaglaacaattgtcagaatgtatgtctctgaagaca 4379
QY 4486 cgggaacccctgtgaactttaaagcccttcaacaaagacccctgtgttgggaacccgctgtta 4545
Db 4380 cgggaacccctgtgaactttaaagcccttcaacaaagacccctgtgttgggaacccgctgtta 4439
QY 4546 tgaagagaaacccaaatcccaagacagccctgcagcaggaaggaagatgtgacaactg 4605
Db 4440 tgaagagaaacccaaatcccaagacagccctgcagcaggaaggaagatgtgacaactg 4499
QY 4606 ccccaagtcccccagacacatcatgtgacctcttccaagaatgtggaactgtgacaatgtgacaac 4665
Db 4500 ccccaagtcccccagacacatcatgtgacctcttccaagaatgtggaactgtgacaatgtgacaac 4559
QY 4666 ctcaactgtatgtcagatgtgtagcagcagcaaaaatcaagaagatgtgcgctgtgtgtcccc 4725
Db 4560 ctcaactgtatgtcagatgtgtagcagcagcaaaaatcaagaagatgtgcgctgtgtgtcccc 4619
QY 4726 caggggagcagggggcgtgcctcctccacaagaagaacaaacactgtcagatatcctcag 4785
Db 4620 caggggagcagggggcgtgcctcctccacaagaagaagaacaaacactgtcagatatcctcag 4679
QY 4786 accctgacaggaagaagaatcttgatattatgtgtgaagcgtatgtgcagatcatagcca 4845
Db 4680 accctgacaggaagaagaatcttgatattatgtgtgaagcgtatgtgcagatcatagcca 4739
QY 4846 aaagcttaagaagaagaatcttgatattatgtgtgaagcgtatgtgcagatcatagcca 4905
Db 4740 aaagcttaagaagaagaatcttgatattatgtgtgaagcgtatgtgcagatcatagcca 4799
QY 4906 tcaatgaatcactcaagaactctcctgcgaagtcagaagttaatgaatgtccatcaaaaatga 4965
Db 4800 tcaatgaatcactcaagaactctcctgcgaagtcagaagttaatgaatgtccatcaaaaatga 4859
QY 4966 agaaacacccaagaagcgtgcgaagaagcagttctgcagatcagattctcaacagcttgagga 5025
Db 4860 agaaacacccaagaagcgtgcgaagaagcagttctgcagatcagattctcaacagcttgagga 4919
QY 5026 gattatgaagaagcgtgcgaagaagaataatgttcaaggtgtgtgttcaataaagaagcgt 5085
Db 4920 gattatgaagaagcgtgcgaagaagaataatgttcaaggtgtgtgttcaataaagaagcgt 4979
QY 5086 ggaatgaatgaagcgtcttcttcgaatgtcatcaaaatgtcgaatctcgggccaacgtgtgc 5145
Db 4980 ggaatgaatgaagcgtcttcttcgaatgtcatcaaaatgtcgaatctcgggccaacgtgtgc 5039
QY 5146 aaagaagagagaacccatagcattatgtgaattactgtcttcaatcatcccccgaatctca 5205
|||||
Db 5040 aaagaagagagaacccatagcattatgtgaattactgtcttcaatcatcccccgaatctca 5099
QY 5206 ccaagcagcagcctcagagatgtgtcgtatgataccatcagatgtatgtcctgtgtca 5265
Db 5100 ccaagcagcagcctcagagatgtgtcgtatgataccatcagatgtatgtcctgtgtca 5159
QY 5266 tctgtatcacttctgaaatgtcctcgtccagcagcagcttctgtatcctgtatcag 5325
Db 5160 tctgtatcacttctgaaatgtcctcgtccagcagcagcttctgtatcctgtatcag 5219
QY 5326 agcgggtcagaagaagaacacacgtgcagttatcaatgtgagatgtgaagcctgtcatctact 5385
Db 5220 agcgggtcagaagaagaacacacgtgcagttatcaatgtgagatgtgaagcctgtcatctact 5279
QY 5386 ggcctcctaatttctgtcgtgaatgtgataatgtatgttccctgtccacatgtcatca 5445
Db 5280 ggcctcctaatttctgtcgtgaatgtgataatgtatgttccctgtccacatgtcatca 5339
QY 5446 tcatcttcaatcgtcttccagcagaagtcctatgtgtctctccacaaatcgtcgtgtcag 5505
Db 5340 tcatcttcaatcgtcttccagcagaagtcctatgtgtctctccacaaatcgtcgtgtcag 5399
QY 5506 ccccttacttctgtcgtgaatgtgtgataatcaacacccctcaatgtacccagcctcctgt 5565
Db 5400 ccccttacttctgtcgtgaatgtgtgataatcaacacccctcaatgtacccagcctcctgt 5459
QY 5566 tgttcaagaatcccccagcagacactatgtgtgtcctacacagcgtgaacctctcatgtgca 5625
Db 5460 tgttcaagaatcccccagcagacactatgtgtgtcctacacagcgtgaacctctcatgtgca 5519
QY 5626 ttaatggcagcgtgtgcacacccctgtgtcgtgaagcgtgttaccagaataagcttgaata 5685
Db 5520 ttaatggcagcgtgtgcacacccctgtgtcgtgaagcgtgttaccagaataagcttgaata 5579
QY 5686 tcaatgataatcctgaagtcgtgtgttctgtatcttccacatcttctgtcctgtgagcagc 5745
Db 5580 tcaatgataatcctgaagtcgtgtgttctgtatcttccacatcttctgtcctgtgagcagc 5639
QY 5746 tcatcgaatcgtgtgaataaaccaggaatgtgtgtatgtgcctgtgaagaatcttgggaagaatc 5805
Db 5640 tcatcgaatcgtgtgaataaaccaggaatgtgtgtatgtgcctgtgaagaatcttgggaagaatc 5699
QY 5806 gcttctgtcacaatcattcttgggaactgtgtgtggaagcagcacttgcgcagctgtg 5865
Db 5700 gcttctgtcacaatcattcttgggaactgtgtgtggaagcagcacttgcgcagctgtg 5759
QY 5866 aaggggtgtgttcttccatctatctgtcgtatcagatcagatcttctcaacagccca 5925
Db 5760 aaggggtgtgttcttccatctatctgtcgtatcagatcagatcttctcaacagccca 5819
QY 5926 gacctgtatgaagaagaatcctcctcgtgaatgtgaagaatgtgaagatgtgaggggaaa 5985
Db 5820 gacctgtatgaagaagaatcctcctcgtgaatgtgaagaatgtgaagatgtgaggggaaa 5879
QY 5986 gacagaagaatcttctgtatgtgtgaagccagaatgtacatcttgaagaatacaagaatgtgaca 6045
Db 5880 gacagaagaatcttctgtatgtgtgaagccagaatgtacatcttgaagaatacaagaatgtgaca 5939
QY 6046 agatatataagaagaagcgtgaagcctgtgttgcagaagattgtcgtgtgacatcctcgt 6105
Db 5940 agatatataagaagaagcgtgaagcctgtgttgcagaagattgtcgtgtgacatcctcgt 5999
QY 6106 gtgagtgcttgggctccctgggaagttaatgtgagcgttgaagaatacaaaccttcaaatgt 6165
Db 6000 gtgagtgcttgggctccctgggaagttaatgtgagcgttgaagaatacaaaccttcaaatgt 6059
QY 6166 taacagaagatataccatgttataccagaagagatgtcttcttcaacaaaatagatctat 6225
Db 6060 taacagaagatataccatgttataccagaagagatgtcttcttcaacaaaatagatctat 6119
QY 6226 caaacatcattgaatgtatcatcagaagaatgtgtcctcagttgtatgtcatcag 6285
|||||


```

QY 8446 catgtltaacagctactggtttacaataatagtgctgtgtgttagagccact 8505
DB 8340 CATGTATTAAGCTCAGCTGGTTTACAATAATAGTTTCTCTTGTTGGTTAGAGCCACT 8399
QY 8506 gtaacaatattgagcagccttttttttttttttaattgcaacaalgcgaagccaga 8565
DB 8400 GTAACAATACTGGGCAACC-TTTTTTTTTTTTTTTTAAATTGCAACAATGCAAAAGCCACA 8458
QY 8566 aagataagaggtcaacagttttaaacaatgtaattcttcaacagaggaagaagcgtactga 8625
DB 8459 AAGATATAGGCTCACAAGTCTTAACAATGAAATCTTCAACAGGGAACACGTAAGCTTGA 8518
QY 8626 aaactgctgaaaaacaacacttgltttagtcatttagtacctcaaatattgagct 8685
DB 8519 AAATGCTGTGAAAAACACACTGTGTGTATGCACTTACTACTTCAATAATATGCGCTT 8578
QY 8686 tgcagatattgatacccaattaaatctgcagctcccaatttcaatctcctcaatc 8745
DB 8579 TGCAGATATTGATACCCCACTTAATCTGACAGTCTCAAAATTTTCACTCTCAATCAG 8638
QY 8746 taqtaagaataatataaacaacaataactccatataagagacatttccagagcttcc 8805
DB 8639 TAGTCAGAGAAATATATAAACAACAATATCTTCATATGAGACATTTTTCAGAGTTTTC 8698
QY 8806 taaccaagcttatttcttctagtcaglaaacatttgtaaaatactgcttccactaact 8865
DB 8699 TAACCCAGTCTATTTTCTTCTAGTCAGTAAACATTTTGAAAAATCTGTTTCACTAATAC 8758
QY 8866 tactgttaactgtctgagagaaagaataatataagagacattgtttggggaagctc 8925
DB 8759 TACTGTTAACTGTCTGAGAGAAAGAAATAATGAGAGAACTATGTTGGGAGGTTTC 8818
QY 8926 aagtgatcttcaataatcaataacttctcacttcttccaaatgtaatactaac 8985
DB 8819 AAGGATCTTCAATATCATATCTACTACTTCTTCCAAATTTGCAATATTAAC 8878
QY 8986 gctaaagtgtaagacttcaagattcaaatlaacttctctataattttaaattacaga 9045
DB 8879 GCTAAAGGTGTAGACTTCAGATTTCAAAATTAATCTTATATTTTAAATTTACAGA 8938
QY 9046 atattataaaccactgctgtaaaaaagaataatgattgttttaagaattaaagcact 9105
DB 8939 ATATTTATATACCCACTGCTGGAAGAAAGAAATATGTTTGAAGATTAAAGTCAAT 8998
QY 9106 attgattttaaataatagaatgaagacatatttccaaatactagatagatgcatcgt 9165
DB 8999 ATTGATTTTAAATATAGTAATGAAAGCATATTTCCAAATAGTATGATGACATCGTT 9058
QY 9166 gcaatttaacagtaacttcaaaaaatacagaattatagaataatttctcctcaattaat 9225
DB 9059 GCATTTTACAGTATCTTCAAAAATACAGAAATTAAGAAATATCTCTCAATTAATAT 9118
QY 9226 ttccaataatcaaatagatggttccctcaatttactaaatcgatcttcaatctcact 9285
DB 9119 TTTTCAAAATCAAAAGTTATGTTTCTCTCATTTTACTTAAATGTAATTCATTTTCANT 9178
QY 9286 atagaataactatggaacacttcttactcgttctcctgatttcaaggcaattttaa 9345
DB 9179 ATAGTAAATCTATGACCACTCTTAATCTGCTTCAATTTCAAGCCCAATATTTTAA 9238
QY 9346 aaatacaaaagacactgtaactatttgaagaacaacagacatttataagaatttaa 9405
DB 9239 AAAATCAAAAGGACACGTGTAATCTATTTGAGAAAACACMACATTTTATACAGATTTGA 9298
QY 9406 aggaactctctgaagctagaacaacataagatatacatcttcaataactgactgta 9465
DB 9299 AGGACCTCTTCTGAGAGCTAGAAACAATCATATGATATCATCTTCAATTAATCTGTGTTA 9358
QY 9466 cctttaaataagtaatttttaccatttccctggtttaaaccctaattggtgtagaatttt 9525
DB 9359 CTTTTTAAATATGTAATTTTACATTTTCTGCTTAAACCTAATTTGAGTAAGAAATTTT 9418
QY 9526 taaccaactlatactcaatcaagaacaatttctgtatatactccctgtgaagtactactg 9585

```

```

DB 9419 TACCAACTATATCTCAATCAACAAATTTCTGTATATTTCCCTGTGGAATGACTATG 9478
QY 9586 tgaatttcagaatacttcaaaatacgtgttcaaaaatttgcgttttgatctcttgagac 9645
DB 9479 TGAGTTTCAGAAATCTCAAAATATGCTGTCAAAAATTTTGCTTTTGCATCTTTGGGAC 9538
QY 9646 acctagaanaacttatacaacttgtaataatggaataacagaagaataataaagccc 9705
DB 9539 ACCTCAGAAAACCTTATTAACAACCTGTGAATATGAGAAATTAAGAAAATTAAGGCC 9598
QY 9706 tctatataatagccagcaaatctatctgtttaaacaacaacaactcaactactg 9765
DB 9599 TCTATACATTAATATGCGCAGCAACATTCATTTGTTAAAAACAACCAACTACACTACTG 9658
QY 9766 tatttcattatctgactggaagaacatgcttgcactatlaaagtgttcacatctc 9825
DB 9659 TATTTCAATTATCTGTACTGAAAGCAAAATGCTTGTGACTATTAATGTTGCACATCATTC 9718
QY 9826 attca 9830
DB 9719 ATTCA 9723

```

RESULT 13
 AX059973
 LOCUS
 DEFINITION Sequence 91 from Patent W0078970.
 ACCESSION AX059973
 VERSION AX059973.1 GI:12405631
 KEYWORDS
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 9497)
 Denefle, P., Rosler-Montus, M.F., Arnould-Reguigne, I., Prades, C.,
 Naudin, L., Lemoine, C., Duverger, N., Assmann, G., Rust, S., Funke, H.,
 and Brewer, H.B.
 Nucleic and proteinic acids corresponding to human gene abcl
 JOURNAL Patent: WO 0078970-A 91 28-DEC-2000.
 Aventis Pharma S.A. (FR)
 Location/Qualifiers
 FEATURES
 source
 1. 9497
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 2600 a 2115 c 2217 g 2564 t 1 others
 ORIGIN

Query Match 90.4%; Score 9444.6; DB 6; Length 9497;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 9464; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

```

QY 351 caacaatgtaagctgtaactggaagtgagcgtgacttattctctgactgacatc 410
DB 1 CAACATGTCAGCTGTACTGGAAGTGGCCGTCTTATTTATCTCCGATCTGATC 60
QY 411 tctttgagcgtgagctacccacccatgtaacaacataatgaatcttccaataaagcc 470
DB 61 TCTTTGGCTGAGCTACCCACCTATGAAACACATGAATGCCATTTTCCAAATTAAGCC 120
QY 471 atgcctctgagaacacttcttgggttcaaggagattactgtaatgcacaacaccc 530
DB 121 ATGCCCTCTCAGGAGACATTTCTTGGGTTCAGGGGATTATCTGTATATGCAACAACCC 180
QY 531 tgttcggttaaccgactcctctggggaggtcccgaggtgtgttgaaacttacaatcc 590
DB 181 TGTTCGTTACCCGACTCTCTGGGAGGCTCCGAGAGTTGTGGAACCTTTAACAATCC 240
QY 591 atgtgctgcgctgttctcagatgctcgaaggtccttatacagcagaagaagacc 650
DB 241 ATTTGCTGCTGGCTGTTCTCAGATGCTCGAGGCTCTTTTATACAGCCAGAAAGACACC 300

```

OY	651	agatgaggaacatgtgcgaagttcttggaaacattacagagatcaagaatccagctca	710
Db	301	AGCATGGAAGGACATGGGCAAAAGTCTCGAGAACATTACAGCAGATCAAGAAATCCAGTCA	360
OY	711	aacttgaagcttcaaaatttccgtgtgtgacaaatgaaacccctctctgtggttccatatacac	770
Db	361	AACTTGAAGCTTCAGAAATTTCCTGGTGGGCAATGAACCTTCTGGGTCTGTATAC	420
OY	771	aacctctctcccaagtctactgttgacaaagatgctgagagcttgatgtcatttccac	830
Db	421	AACTCTCTCTCCCAAAAGTCTACTGTGGCAAGATGTGAGGGGTGATGTATTCTCCAC	480
OY	831	aaggtatttttgcgaagctaccagatttcaatttgaaacagtcgtgtcaatlygatcaaatca	890
Db	481	AAGGTATTTTGGAAAGGTACACAGTTACTATTTGACAACATCTGTGCATATGATCAAAATCA	540
OY	891	gaagagatgatcaacttggltgacaaagaatttctgagcttgtgtgcttaccaaagag	950
Db	541	GAAAGATGATTTAACTTGGTGACCAAGAAAGTTTGTGAGCTTGTGGCTTACCAAGGAG	600
OY	951	aaactgtctcagcaagcagagacttgttccacaatggaacacccaaagccaatctgt	1010
Db	601	AAACTGCTCTCAGCAGACGACGAGTACTCTGTCCAAATGACATCTGTAAACCAATCTGT	660
OY	1011	agaacacataactatcatctcccttcccgacgaagagctgtgctgaagcccaaaaaa	1070
Db	661	AGAACACTTAAACTCTACATCTCCCTCCGACCAAGAGAGCTGCCGGAAGCCCAAAAACA	720
OY	1071	tgtgtcatatgtctcttggaactctgtgcacagagctgttccaaatgaagaagtgtgagtgac	1130
Db	721	TGTGCTGATAGTCTTGGGACTCTGGCCCAAGAGCTGTTCAGATGAGAACTGGAGTGAC	780
OY	1131	atgcgacaggaagtgatglttcttgaccaaagtgaacacagctccagctccctccaccaatc	1190
Db	781	ATGCGACAGGAGGAGATGTTCTTGACCAATGTGAACAGCTCAGCTCCTCCACCCAAATC	840
OY	1191	taccagagctgtgtcgttatgtctgtcggagctcccgagggagggaggtctaaagataag	1250
Db	841	TACCAAGGTGTGTCTGATATTGTCTGGGCAATCCGAGGGGGGGCTTAATAATTAAG	900
OY	1251	tctctcaacttgltatgtaggaacaaacacttcaaaagccctctttaggggaatlygacttgag	1310
Db	901	TCTCTCAACTGATGTAGGAGCAACACTMAAAGCCCTCTTGGAGCAATGGCACTGAG	960
OY	1311	gaagatgtctgaacacctctctatgacaactctacaactccttactgtcaatlygatgaag	1370
Db	961	GAAAGTGTGTGAACCTTCTATGACAACCTGTACAACTCTTACTGTGAATGATTTATGAG	1020
OY	1371	aatttgagcttagtctctcttccgaatctatctgaaagctctaaagcgtcgtcgtt	1430
Db	1021	AAITTTGGAGTAACTCTCTTCTTCCCGATTATCTGAAAGCTCTGAACCCCTGCTGTT	1080
OY	1431	gggaagatctgtlatacacttgaactccaagcccaagaagtcatagtgtgaagtgaac	1490
Db	1081	GGGAAGATCTGTTATACACTGTGACACTCCAGCCACAAAGCAAGTATGGCTGAGAGTGAC	1140
OY	1491	aagaccttccagagactggtgtgttccatgtcttggaaagatitgggaagaaactcagc	1550
Db	1141	AAGACTTTCGAGAACTGGCTGTGTTCATGATCTTGAAGSGATGTGGAGGAATCTGAC	1200
OY	1551	ccaagaacttgaccttccatlgagaacagccaagaatlygacctgtgtccgaagtgtgtg	1610
Db	1201	CCCAAGATCTGGACCTTCTATGGAAGAACGCAAGAAATGGACCTTGTCCGATGTGTTG	1260
OY	1611	gacagcaggaacaaatgacacatttgggaacagcaglttgatgtgcttgaatttgacagcc	1670
Db	1261	GACACAGGAGCAATGACACTTTTGGGAACACACACTTGGATGGCTGTAGATTGGACACCC	1320
OY	1671	caagacatcgtggagcttlttggccaagaccacagagagatgtccagctcaagtaatgttct	1730
Db	1321	CAGACATCTGTGGCCTTTTGGCCAGACACCACAGAGATGTCTAGTCCAGTATATGTCTT	1380

QY	1731	gttacaacctgagagagaagctttcaacgcgactaaacggagaatccggagacatatactcgc	1790
Db	1381	gtgtacacctctggagagaaagctttttcaacgcgagactaacacggcaatccggaccatattctgcg	1440
QY	1791	ttcaatgagatgtgtcaaacctccgaaacaactcagaaaccaatagaacaagaatcttgctcatc	1850
Db	1441	tttcattgagtgctgtcmaaccttgaaacaaagctatagaacccttatagcaacgaagtctgctcatc	1500
QY	1851	aacaagtcacatgagactcgtctcgtgaatgaagagaagcttcctggctglatgtgttcaactga	1910
Db	1501	aacaagttccatgagactgctgctgagatgagagaagaaattctggcgtgattgtttcactcga	1560
QY	1911	attactccaggcagcalttgagctgtgcccaatcatgttcaagtacaagaatccgaatgagacat	1970
Db	1561	attactccaggcaccatttgagctgtgcccaatcatgttcaaatcaamaatccgaatggaatt	1620
QY	1971	gacaaatgctggagaggaacaaataaatacaagatggttacttggaacctgtccctcgaagct	2030
Db	1621	gacaaatgtggagagagacaattaaaatccmaagatgggtacttgsgaacctcggtctcgagct	1680
QY	2031	gaacctcttgagagacatgctcgtgaatctcgtgggggcttcgcctacttgcaagatgtgtg	2090
Db	1681	gaacctcttgagagacatgctcgtgaatctcgtgggggcttcgcctacttgcaagatggtgtg	1740
QY	2091	gagcagcgaaatcacatccaggtgtgtcgaaggggacccggaaaanaaaactggtgtctatatgcaa	2150
Db	1741	gagcagcgaaatcatatcaggggtgtctacggggacccgaaamaaaatcgggtgtctatatgcaa	1800
QY	2151	cagatgacctatccctgttcaagttatgacatcttcctcgggtgtatgtagcgcgttcaatg	2210
Db	1801	cagatgacctatccctgttcaagttatgacatcttcctcggggtgatgagccggctaatg	1860
QY	2211	ccccctctcatgacgctgtgcctctgatttactcaagtggtcgtgtatcatcaagggcaatgtg	2270
Db	1861	ccccctctcatgacgctgtgcctctgatttactcagtcgctgtatcatcaagggcatgctg	1920
QY	2271	tatggaagagaggaagcgtctgaagaagaaacaatcggaatcaatggacctggaacaagacata	2330
Db	1921	tatggaagagaggaagcgtctgaagaagaaacaatcggaatcaatggacctggaacaagacatc	1980
QY	2331	cctctgatttaagctgttcaatlagtagcctaatccctctcttctgttgaagcgtgtgacctgta	2390
Db	1981	cctctgatttaagctgttcaatlagtagcctaatccctctcttctgttgaagcgtgtgacctgta	2040
QY	2391	gtgtgctatccttgaagatgaagaaacctgtgcctctacagatgataccagcgtgtgtgttgc	2450
Db	2041	gtgtgctatccttgaagatgaagaaacctgtgcctctacagatgataccagcgtgtgtgttgc	2100
QY	2451	ttccctgtctcgtgttgcctgtgtgtgaacaatccctgtagtctgttcctgattagaacaaccttc	2510
Db	2101	ttccctgtctcgtgttgcctgtgtgtgaacaatccctgtagtctgttcctgattagaacaaccttc	2160
QY	2511	tccaagaccaaactgtgacagcagcctgtgtgggggacatacctaacttaacgcgttaacctgcc	2570
Db	2161	tccaagaccaaactgtgacagcagcctgtgtgggggacatacctaacttaacgcgttaacctgcc	2220
QY	2571	taacgtctgtgtgtgtgcaatgacagagactacgtgtgggttcaaacactcaagaatctctgtacg	2630
Db	2221	taacgtctgtgtgtgtgcaatgacagagactacgtgtgggttcaaacactcaagaatctctgtacg	2280
QY	2631	ctgtgctctcctgtgtgcttlttggtgtgtgtgctgtgtgaglaattgtgcctltttgaagagcag	2690
Db	2281	ctgtgctctcctgtgtgcttlttggtgtgtgtgctgtgtgaglaattgtgcctltttgaagagcag	2340
QY	2691	ggcatttgaggtgcacatgagaaacacctlttgaaagtcctcgttggaagaagaatgtgttcaat	2750
Db	2341	ggcatttgaggtgcacatgagaaacacctlttgaaagtcctcgttggaagatgtgttcaat	2400
QY	2751	cttcaaacctctgatctccatgatgtctgttttgaacaaccttccctatgtgggtgtatgtaacctg	2810
Db	2401	cttcaaacctcttggtgtccatgatctctgttttgaacaaccttccctatgtgggtgtatgtaacctg	2460
QY	2811	tacatttgaggtctgtcttccagccgaabacgnaattcccaagccctgtatlttccctgtc	2870

|||||
Db 2461 TACATTAGAGCTGCTTTCCAGGCCAGTAGGAATTCGCCAGGCCCTGTATTTTCCCTGC 2520
Qy 2871 accaagtcctactggtttggcaggaagatgataagaagccacctggttccaacag 2930
Db 2521 ACCAAGTCTCTACTGGTTGGCGAGAAAGATGAGAAAGCCACCTGGTTCCAAACGAG 2580
Qy 2931 aagagaatgcagaatctcagcaggaaggaacccaccttgaagctggcgtctgc 2990
Db 2581 AAGGAATATCAGAAATCTCATGAGGAGGAACCCACCACCTTGAAGCTGGGCGTCTCC 2640
Qy 2991 attcagaacctggtaaaagctacccagatggaatgaagtggtctgatatgctgcga 3050
Db 2641 ATTTCAGAACTGGTAAAGCTTACCGAGATGGATGAAGTGGCTTCATGGCTGGCA 2700
Qy 3051 ctgaattttatagagccagatcacacctctctctggccacaaatggaacgggaagacg 3110
Db 2701 CTGAATTTTATGAGGGCCAGATCACCTCTCTGGCCACAAATGGACGGGGAAGAGG 2760
Qy 3111 accacatgtcaatctctgacccgggtgttcccccgaacctggggaacgcctacatctg 3170
Db 2761 ACCACATGTCAATCTCTGACCGGGTGTTCGCCGACCTCGGGCACCTACATCTCG 2820
Qy 3171 ggaagaacatctgcctgagatgagcacatccgcagaaacctgggggtctgtcccgag 3230
Db 2821 GGAAGAACATTTGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGGTCTGTCCCGAG 2880
Qy 3231 catacgtgctgttgcacatgctgactgtcgaagaacacatcgtgtctatgcccgtg 3290
Db 2881 CATACAGTGTCTTTGACATGTGCTGATGCAAGAACACATCTGGTTCATGCCCTCTTG 2940
Qy 3291 aaagggtctctcgaagaacagctggaagcggaatggaacagatgagccttgatgtgtg 3350
Db 2941 AAAGGGCTCTCTAGAGACGCGTGAAGCGGAGATGAGACAGATGGCCCTGATGTTGGT 3000
Qy 3351 ttgccatcaagcaagctggaagaacaaacaaagccagctgtcaggtggaatgcaagaag 3410
Db 3001 TTGCCATCAAGCAAGCTGAAACAAACAAAGCCACCTGTACAGTGAATGACAGAAAG 3060
Qy 3411 ctatcgtgagccttggccttctgcgggagatcgaaggtgtatcttgaatgaaccaca 3470
Db 3061 CTATCTGTGGCTTGGCCCTTTGTGGGGGATCTAAGGTGTCTATTTGTGATGAACCCACA 3120
Qy 3471 gctgtgtggaaccttactctccgcagaggaatatggaagctgctgtaataacagaca 3530
Db 3121 GCTGTGTGGACCTTACTCTCCGCAAGGGAATATGGAGCTGCTGTAATACGACAA 3180
Qy 3531 ggcgcagacattatctctctacacacacatgagatggaagcggaagctctggggagacg 3590
Db 3181 GGCAGCACATTTATCTCTCTACACACACATGAGATGAAGCGACGCTCTGGGGACAGG 3240
Qy 3591 attgcatcatctccatlggaagctgtgtgtgtggtctctccctgttctgaagaac 3650
Db 3241 ATTGCAATATCTCCATGGGAAGCTGTGCTGTGTGGCTCTCCCTGTTTCTGAAGAAC 3300
Qy 3651 cagctgggaacagagctactacacctgacctgtgtcaagaagaatggtgaaatccctccag 3710
Db 3301 CAGCTGGGAACAGGCTACTACCTGACCTTGTGTAAAGAAAGATGTGAATCCCTCCAT 3360
Qy 3711 tccctgagaacagtagtagcactgtgtcatacctgaanaaagagagacagtttctcag 3770
Db 3361 TCCCTGAGAAACAGTAGTAGCACTGTGTATACCTTAAGAAAGAGAGACAGCTGTCTCAG 3420
Qy 3771 agcagttctgtagtctggcctgggagagacatggaatgacacgtgcacatcagatgc 3830
Db 3421 AGCAGTTCTGATGCTGGCTGGGACGACCATGAGAGTGAACACCTGACCTCATGTGC 3480
Qy 3831 tctgcatctccaacctcaggaagacatgctgtcgaagcccgctgggtggaacata 3890
Db 3481 TCTGCTATCTCAACCTCATCAAGGAACATGTGTCTGAAGCCGGGTGTGGAACACATA 3540
Qy 3891 ggagcatgagctgacctgtgtgtgcacatacgaagctgtaaggaaggaaccttctgaa 3950
|||||

Db 3541 GGCATGAGCTGACCTATGTGCTGCATATGACGTGCTAAGAGAGAGCCTTGTGAA 3600
Qy 3951 ccttctcagatgtatgacccgctctcgaacctgggcatltttagtlatgcatctca 4010
Db 3601 CTCTTCTATGAGATGTATGACCGGCTCTCAGACCTGGGCATTTTCTATGTGATCTCA 3660
Qy 4011 ggaagacccttggaagataatctcctcaaggctggccgaagaagctgggtgtgactgag 4070
Db 3661 GAGAGACCTCTGGAAGAAATATCTCTCAAGGTGGCCCAAGAGATGGGGTGGATGCTGAG 3720
Qy 4071 acctgaatgttacctgtccagcaagacgaacagcgggccttcggggagacaagcagc 4130
Db 3721 ACCTGAGATGTATCTCTCCAGCAAGAACAGGGCGGCTTCGGGACCAACAGAGC 3780
Qy 4131 tgtctgcgcccttaactgaagatgtagtctgtatccaatgatatctgcatagacca 4190
Db 3781 TGTCTGCCCGCTTACATGAAGATGATCTCTCATCAATGATTTCTGACATGACCCA 3840
Qy 4191 gaatccagaagacagactgtctcagtggaatggaatggaaggtctctaccagtgaaa 4250
Db 3841 GAATCCAGAGAGACAGACTTCTCATGTGGATGGATGGCAAGGGGTCTACAGGTGAAA 3900
Qy 4251 ggttggaacttacaacagcaacaglttggtgccccttctgtggaagagactgctaattgc 4310
Db 3901 GGTGGAATCTTACACAGCAACAGTTGTGGCCCTTTGTGGAAGACATGCTAATTGGC 3960
Qy 4311 agaaggagtcggaaggaatlttctgtcagaatgttctgcagctgtgtgtctgcat 4370
Db 3961 AGACGAGTCCGAAAGGATTTTGTGCTACAGTGTCTTGGCAGCTGHTGTGCTGATTT 4020
Qy 4371 ggccttgtgtcaacgtgatgtgtgcaaccttggcaagaatccccagcctggaaactcag 4430
Db 4021 GCCCTGTGTACGCTGATGTGTCCACCTTGTGGCAAGTACCCACCTGGAACCTTCAG 4080
Qy 4431 ccttgatgttacaacagacagtlacacatltgttcagcaatgagctctcctggaacagcga 4490
Db 4081 CCTGAGATGTCAACGAAGATACATGATGCTGACATGATGCTCTGAGGACAGGGA 4140
Qy 4491 acccttgagactctaaagcgccttacaacaaagacctgtgtctggagaccgctatagaa 4550
Db 4141 ACCCTGGAATCTTAAAGCCCTCACCAAGACCTCTGGCTTGGGACCCCTGTATGAA 4200
Qy 4551 ggaacccaatcccaagacagcccttgcagagcagggaggaagagtggaacactgtccca 4610
Db 4201 GGAACCCAACTCCAGACAGACGCTGCAAGGAGGAGGAAGGTGAGCACTGCCCCA 4260
Qy 4611 gtccccaagacatcagagaccttctccagatggaagcagcaatgcagaaccttca 4670
Db 4261 GTTCCCCAGACCATATGAGACTTCTCCAGATGGGAATGGACAAATGCAAGAACCTTCA 4320
Qy 4671 cctgcatgcccagtgtaacaggaacaaatcaagaagaatgtctgctgtgttccccaagg 4730
Db 4321 CCTGATGCCAGTGTAGAGAGCAAAATCAAGAAAGATGTGCTGCTGTGCCCCAGGG 4380
Qy 4731 gcaagggggtgctgtctctccaagaagaacaaacacctgcagatatccttcagacctg 4790
Db 4381 GCAGGGGGGCTGCTCTCCACAAAGAAACAAACACTCAATATCTTCAGGACCTG 4440
Qy 4791 acagaagaacacatctcgatattcgttgaagacgtatgtgaatcatcagccaaagc 4850
Db 4441 ACAGAGAAAMAATTTGGGATATCTGTGAAGACGATGTGACATCAAGCAAAAGG 4500
Qy 4851 ttaagaacaagatcgtgtgaatggaatgaatgagcgttccctgggtgtcag 4910
Db 4501 TTAAGAACAAGATCTGGGTAATGATTAAGTATGGCGCTTTTCCCTGGGTGTACAGT 4560
Qy 4911 aatcactaagacactctctccagatcagaagaagttatgatatccataaacaatggaagaa 4970
Db 4561 AATACTCAAGCATTTCTCCAGTCAAGAAAGTTAATGATCCACCAACAAATGAAGAAA 4620
Qy 4971 caactaaagcttgccaagagacgttctgcagatcagatlttccaacagcttggaaagatt 5030
Db 4621 CACCTAAAGCTGGCAGAGGACAGTTCGAGATCGATTTCTCAACAGCTTGGGAATTT 4680
|||||

QY	5031	augcagagcttgtaacccagaataa	gtcaagtg	tgtgttc	taataac	agtgctgc	at	5090
Db	4681	ATGACAGAGCTGGACACCGA	AAATATG	CAAGAGTG	TGTTCAAT	AACAGGGCTGGCAT		4740
QY	5091	gcaacagccttcccttgaa	tatcatca	aaatgg	catctcc	cgsggcca	actg	5150
Db	4741	GCAATCAGCTCTTCTCTG	AATGTCAT	CAACAACTG	CAATTCCTCCGGGCA	CACTGCAAAAG		4800
QY	5151	ggagaagacccttagccat	tatagaa	tiaactgt	ttccaa	tcaatcc	cca	5210
Db	4801	GGAAGAAACCCCTAGCC	ATTATGGA	AAATACGTGTTCA	ATCCCTGAAATC	CACCAAG		4860
QY	5211	caagcagctc	caagag	tggctc	tga	tgacaca	tcagatg	5270
Db	4861	CAGCAGCTCTCAAGAGT	GGCTCGATG	AGACACATCATG	AGATGTCCTGTGTCCATCTGT			4920
QY	5271	gtacacttgcaatgtccct	tgttcc	agcagcct	tgtcc	atctcc	atg	5330
Db	4921	GTCATCTTTCGAATGTC	CTTCTGCCCCAGCA	ACTTGTGTCATTC	CGATCCGAAGACGG			4980
QY	5331	gtcagcaagaaca	aaacactg	tcag	tca	ag	tgaagcc	5390
Db	4981	GTCAGCAAGACCAAC	ACCCTGCGATTCA	TCATGTGA	AGTAAGACCTGTATCT	ACTGGCTC		5040
QY	5391	tctaattgtctc	tgga	tatgtga	caata	cgtttgc	ctcc	5450
Db	5041	TCTAATTTTGTCTGG	ATATGTGTCAAATTA	CGTTACGTTGCC	GCACACTGTCATATATCATC			5100
QY	5451	ttaactcgtctc	agagaag	tccat	tatgtgtcc	tccaca	atctgc	5510
Db	5101	TTTCACTGCTTCCAG	AGAAAGTCTATGTGTCCTCCACCA	ATCTGCTGTGTCAGCCCTT				5160
QY	5511	ctaactttgtc	tatgtg	gtgtca	tcaacactc	tca	tgtac	5570
Db	5161	CTACTTTTGTCTGAT	GGTGATGGTGTCAT	CAACACCTCTCATG	TACCAAGCTCCTTGTGTGTC			5220
QY	5571	aaga	tccca	gcagca	agc	at	tatgtgtc	5630
Db	5221	AAGATCCCGCCAG	CAAGCTATGTGGTGCTCACCA	CGTAGAACCTTCTCATTTGGCATTAAT				5280
QY	5631	ggcagcgt	tgga	ccacttt	gtc	gtga	gc	5690
Db	5281	GGCGCGCTGGCCAC	CTTGTGTGGAGGCTTTCACCGCA	ATAACCTGAAATAATATCAAT				5340
QY	5691	ga	tact	tgaa	gc	ctgtgt	cttgc	5750
Db	5341	GATATCTCTGAAG	TCTCGTGTTCATCTTCCACAT	TTTTTGTGCTGTGGACGAGGCTATCT				5400
QY	5751	gaca	tgt	tga	aaaa	caag	ga	5810
Db	5401	GACATGGTGA	AAAAACGAGCA	ATGGCTGATGGCTGGA	AAAGTTTGGGAGAAATCGCTTT			5460
QY	5811	gtgtc	ac	cat	tatc	ctt	gtg	5870
Db	5461	GTGTCAACCATTA	CTTGTGGGACTTGTGGAGCA	AAACCTTTCGCATGTGGCTGGAAGGG				5520
QY	5871	gtgg	tgt	ctt	cc	tca	tia	5930
Db	5521	GTTGGTCTTCTCTCAT	TACTGTCTTGATCCAGTAC	ATTTCTTCTATGAGCCCAAGACT				5580
QY	5931	g	t	aa	a	a	a	5990
Db	5581	GTAATATCA	AAAGCTATCTCTCTG	AATGATGA	AAAGATGTGAGCGGGA	AAAGACAG		5640
QY	5991	agaa	t	ct	t	g	a	6050
Db	5641	AGAAATTTTAT	GATGGTGAGGCCCA	GAATGTGCACTT	TGA	AAATCAAGAGATTGACCA	AGATA	5700
QY	6051	tata	ga	ag	ga	ag	a	6110
Db	5701	TATGAAAGGA	AGCGAAGCTCTGCTGTTG	ACAGAGATTTGTGGTGAGCATTC	CTCTGTGGTAG			5760

Oy	6111	tglttgagctcctggagagttaaatgggcttggaataatcaactcttaagaatlttaca	6170
Db	5761	TGCTTTGGGCTCCGGGAGTTAATGGGGCTGGAAATCATCACTTTTAAGATGTTAA	5820
Oy	6171	ggaataccactgttaccagaagagatgcttcccttaacaaatagtatcttacaac	6230
Db	5821	GGAAATACCACTGTTACCAAGAGGAGATGCTTTCCTTAACAGAAATAGTATCTTAACAAC	5880
Oy	6231	atccagtaagtaacatcagaacatlyggctacatgcctcaagtttgatgcatcaagagct	6290
Db	5881	ATCCATAGACATCATCAGAACATGGGCTACTGCCCCATGTTGAAGCCATCACAGAGCTG	5940
Oy	6291	ttgagctggagagaacacgfygagatcttgccttttgaagagaggtccagagaagaa	6350
Db	5941	TTGACTGGGAGAGAACCGTGGAGTTCTTGCCCTTTTGAAGGAGTCCCGAGAGAA	6000
Oy	6351	gttgacaaggtttgtagtggcgatctcgaaactbgccctglatgaatlatgagagaa	6410
Db	6001	GTTGGCAAGGTGGTGATGGGGGATTCGGAAACTGGGCTCGTAAGTATGAGAA	6060
Oy	6411	taigctglaactaagtagtaggacaacaaacgaagctcctacagcaatggcttgatc	6470
Db	6061	TATCTGGTAACTATAGTGGAGGCAACAAACGAACCTCTACAGCCATGGCTTTGATC	6120
Oy	6471	ggcgagcctcctgtggtgttcttgcgataccacacagcatgatatcccaaacggcg	6530
Db	6121	GGCGGGCTCCTGGTGGTTCGGATGGAACCCACCCAGGATGGATCCAAACCCGG	6180
Oy	6531	cgatccttgagaaatltgcccctaagtgtgttcaagaaaggagatacagtagtttaca	6590
Db	6181	CGGTTCTTGGAATTTGGCCCTAAGTGTGTCAAGAGAGGAGATCACTAGTGGTTACA	6240
Oy	6591	lctcataglatgagaagaatgtgaagctcttgcactagaatgagcaatcatgltcaatga	6650
Db	6241	TCTCATAGTATGAGAAAGATGTGAAGCTCTTTGCATAGAGATGGCAATGTCATGGA	6300
Oy	6651	aggttcaggtgacctgagcaatgtgcagcatctcaaaaataggtttggagatggttataca	6710
Db	6301	AGGTTCAAGTCCCTTGGCACTGTGCAGCATCTMAAAATAGGTTTGGAGATGGTTATCA	6360
Oy	6711	atagttgacgaatagcagggttccaaacccgagacctgaagccgtccagaattcttga	6770
Db	6361	ATAGTTGACCAATAGCAGGGSTCCAAACCCGAGCTTAAGCTGTCCAGGATTTCTTTGA	6420
Oy	6771	cttgcattccctggaagtgttctlaaagagaacacccggaatgctacaatacacgct	6830
Db	6421	CTTGATTTCTCGAATGTGTCCAAAAGAAACACCGAGACATGTCATATACCACTT	6480
Oy	6831	ccattctcatatctctctgtgccagagatatcagcatccctccagagacaagaacgca	6890
Db	6481	CCATCTTCATATTTCTCTGGCCAGAGATTTTCAGCATCTCTCCAGGCAAAAACGA	6540
Oy	6891	cttcaaatagaagcctactctgtttcttcagaacaaacttgacaagiatlttgaactt	6950
Db	6541	CTCCACATAGAGACTACTCTGTTTCTCAACACAACCTTGACCAAGTATTTGACTTT	6600
Oy	6951	gccaagagccaanaatgataatgacacttlaaagaaccttcatlacacaaacccaagca	7010
Db	6601	GCCAAAGACCAAAATGATGATGACCACTTAAAGACTCTCATTTACAAAAACACGACA	6660
Oy	7011	glagtgaacgttgcagttctcaacatcttctacagagatgagaagtgaagaagctat	7070
Db	6661	GTAGAGCACTTGGACGTTTTCACATCTTTTCTCACAGATGAGAAAGTGAAMAAGCTAT	6720
Oy	7071	gtaagaagaatccgttcatcagggggttgggttgaaglaaaggagaactagacttccctt	7130
Db	6721	GTAATGAACAATCTGTTTCATACGGGGGTGTGAATGAATGAAGGNNCTAGACTTTCCTT	6780
Oy	7131	gacacatgtgaagtgttgttgagaanaaacccaagatgtatgttggagaaglaaatcgt	7190
Db	6781	GCACCAATGTGAAGTGTGTGGAGAAAAGAACCCGAAGTTGATGTGGAGAAAGTAACTG	6840
Oy	7191	gatactgtaactgatactatcaatgcaatgcaatcaatgcaatgcaatgcaatcaatccat	7250

[illegible]

RESULT 14
AF165281

```

/!note="AB0 transporter; ABC1 protein"
/codon.start=1
/product="ATP cassette binding transporter 1"
/protein_id="AAPD9849.1"
/db_xref="GI:3734101"
/translation="MPSAGLIPWVQGIICNANPCERYPTPEAGVGVNKSIVAR
FSARAILLYSQDSTSKMKRMRYVLPRIQQIKSSSSNLDFQVLDNFEFSGLYHNH

```

[illegible]

QY	771	aaccctctctcccaaaatctactgttgacaagaatctgaaggtctatctctccac	830
Db	421	AACCTCTCTCCCAAACTCTACTGTGACAAGTCTGAGGCTGTATCTCTCCAC	480
QY	831	aaggtatctttgtcaagagctacacagttacatttgcacagltctgtgcaatlgatccaataca	890
Db	481	AAGGTATTTTGTGCAAGGCTTACCAATTCATTTGACAAAGTCTGTGCAAATGATCAAAATCA	540
QY	891	gaagatgatctcaactgtgtgaccaaagaattctgagacttgttgcttaccaaagag	950
Db	541	GAAAGATGATTCAACTTGTGTGACCAAGAAATTCTGAGCTTGTGTGCTTACCAAGGAG	600
QY	951	aaactgtgtcagaagagcgagtaactcgttccaacatlgacatccctgaagccaatcctg	1010
Db	601	AAACTGCTGCAGCAGACGACGAGTACTCTGTTCCAAACATGACATCCTGAAGCCATTCG	660
QY	1011	agaacactaaacttaactctccctctccgagaagaagctgtgtcgaagccaataaca	1070
Db	661	AGAACCTAAACTCTACTACTCTCCCTTCCGAGAAAGAGCTGTGCCCCAACCACCAAAATCA	720
QY	1071	ttgcgtcatctctgtgactctgtcccaagagctltcaagctgaagctcgtgtgtac	1130
Db	721	TTGCTGCAATCTTTGGGACTCTGTGGCCAGAGACTGTTCAGCATGAGAACTGTGAGTGC	780
QY	1131	atgcgaaggaaggtgtagtltctgaccaatgtgaacagctccaagctctctccaaactc	1190
Db	781	ATGCACACGAGGAGGTGATGTTCTCACAAATGTAACAGCTCCACAGCTCTCCACCAAAATC	840
QY	1191	taccagatctgtctctgtatgtctgtggtgcatcccaaggaaggggtgtgaagtaag	1250
Db	841	TACCAAGCTGTGTCTCGATTGTCTGTGGGGCATCCGAGAGAGGGGGCTGAAGTCAAG	900
QY	1251	tctctcaactgtgtatlgagacaacatacaaacgctcttlttgaggaatgtgactgtag	1310
Db	901	TCTCTCAACTGTGTATGTAGAGCAACAACTCAAAAGCCCTTTGTGAGGCAATGTGCCTAG	960
QY	1311	gaagatgtgtgaacctctctatgaacactacagccctactctgaatgatltgtag	1370
Db	961	GAAATGCTGAAACCTTCTATGACAACTCTACAACTCTTACTGCAATGATTTGTGTAAG	1020
QY	1371	aattggaagctagtcctctcttcccgatlatcttgaaagctctgaagcgtctgctgt	1430
Db	1021	AATTGGAGTGTATGCTCTTTCOCGATATCTGAAAGACTGTGAAGCCGCTGCTGCT	1080
QY	1431	gggaagatccctgtataaccttgaaactccagccagcaaggaagctatgtctgtaggtaac	1490
Db	1081	GGGAATCTCTGTATPACCTGTGAACTCCAGCCACCAAGCGAGGTATGGCTGAGGTGAAC	1140
QY	1491	aagaccttccaggaagctgtgttctccatgactctgaaagagcatgtggaaggaactcagc	1550
Db	1141	AAGACTCTCCAGSAATCTGTGCTGTTCATGATCTGGAAGGCTATGTGGAGGAACCTCAGC	1200
QY	1551	cccaagatctggaaccttcatatgtagaacaagccaagaatggaaccttgtccgagtctgtg	1610
Db	1201	CCCAAGATCTGTGACTTTCATGTGGAAGAACAGCAAGAAATGACCTTGTCCGATGCTGTGG	1260
QY	1611	gaacagagggagcaatgacacttlttggaacagcaatltgagtgtgttatgttagacagc	1670
Db	1261	GACAGCAGGACAAATGACACTTTTGGGAAACAGCACTGTGATGGCTTGAATTTGACAGACC	1320
QY	1671	caagacatcgtgtgcttlttggccaagcaccagagagatgtccagtccaagtatgtgtct	1730
Db	1321	CAAGACTCTGTGGGCTTTTGGCCAAAGCAACCAGAGATGTCCACTCCAGTAAATGTGCT	1380
QY	1731	gtggaacctggagagaagtttccaacgagacttaacacaggaatcccgaaatccatattcgc	1790
Db	1381	GTGTACACTGTGGAGAGAAAGTTTCAACGAGACTTAACACAGCAATCCGAGCACTATCTGC	1440
QY	1791	tctatggaagtgttcaaacctgaaacaagcttagaacatctagcaagaagctctgtctatc	1850
Db	1441	TTCATGAGATGTGTCAACCTGAACCAAGCTAGAAACCATATGCAACAGAAAGTCTGGCTCATC	1500
QY	1851	aacaaagtccatgagactgtctgtagtgaaggaagttcttgagctgtgatattgttcaactgga	1910

Db	1501	AAACAAGTCCATGAGACTCTGTAAGAGAGGAAGTTCGGCTGATNTGTTGCTACTGGA	1560
Qy	1911	attactccaagcagaattgaagctgtgcccacatcaltgcaagfacaaaga tccgaatgacatt	1970
Db	1561	ATTACTCCAGGAGCAATTGAGACTCCCCCATCATGTCAAGTACAAAGATCCGAATGGCAATT	1620
Qy	1971	gacaaatgtagagagagacaataaaataaagatgtaggtaactgggaacctgtgctcgaagt	2030
Db	1621	GACAATGTGGAGAGACAAATPAAATCAAGATGGGATCTGGGACCTGGTCTCGAGCT	1680
Qy	2031	gaacctcttgaggaatgcgttaacgtctgggggggctgcgcactgtgcaagatgtagt	2090
Db	1681	GACCCCTTGGAGACATCGGTACTGCTGGGGGGGCTTCCCTACTTGCAGATGTGGTG	1740
Qy	2091	ggcgagggcaatcattcaaggtgtctgaacgggcaacgagaagaanaacgtgtctatatgcaa	2150
Db	1741	GAGCAGGGCAATCATCAGGGTCTCACGGGACCGCAGAAAGMAAACTGGTGTCTAATGCA	1800
Qy	2151	gaagatgccctaccctgttcaagttgatacatcttctgagggtgtaga tggacggtcaatg	2210
Db	1801	CAGATGCCCTATCCCTGTATAGTTGATGACATCTTTCTGGGGGTGATGACCGCGTAAAG	1860
Qy	2211	ccctctctcaatgaagctgtgacctgtagatttactcagttgagctgtgaltcaagggacatg	2270
Db	1861	CCCCCTTCATGACGCTGGCCCTGGATTACTCATGATGGCTGTGATCATCAAGGCAATCGT	1920
Qy	2271	tatgtaagagagagcaagcgtctaaagaagaccatgcgaata tggacgttgcaacaagcata	2330
Db	1921	TATGGAAGAGAGCACGAGCTTAAGAAACACATGGCGATCATGGGACCTGGACAAACACATC	1980
Qy	2331	ctctgtgtttagctgtgttcaatagtaagcctatctctcttcttctgtgacgtgtgacctgta	2390
Db	1981	CTCTGTATTACTGATTGATCATGTAGAGCCCTATTCCTCTTGTGAGCCGTGGCCCTGCA	2040
Qy	2391	gtgtgtcctccgaagattaganaaacctgtcccttaagatgatacccaagcgttgtgtttgttc	2450
Db	2041	GGGTGTCATCTGAAGTTTAGGAACCTCTCCCTCAACAGTATCCAGCGTGGTGTTTGTTC	2100
Qy	2451	tctcgttccggttctgtgtgtgtgtacaaatcctgcagttgcttctctgtatgtgacaactcttc	2510
Db	2101	TTCCGTGCTCGTGTTCGTGTGGGTGACAAATCTGCAGAGTCTTCATGTAGCAACACTCTTC	2160
Qy	2511	tccagagccaacctggaagcaagcctgtgggggacatactacttcaagctgttaactgtccc	2570
Db	2161	TCCAAAGCCAACCTGGGACGACGCTGTGGGGCATCATCTACTTCACGCTGTACCTGTGCC	2220
Qy	2571	taagcctcgtgtgtgtacatgacaagaaatacgtgtgttcaactcaaga tctctgtcagc	2630
Db	2221	TACGTGCTGTTGTGGCATGAGCAAGATACGTGGGCTTCACACTCAAGATCTTCCGTAC	2280
Qy	2631	ctgctgtctcctgtgaccttgggttgtgctgtgagtaacttgcacctttagaagagag	2690
Db	2281	CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGATACTTTGGCCCTTTTGTAGAGACAG	2340
Qy	2691	ggcaatggaatgagagtagggacaacctgtttagaagctccgttggaggaagaatgcttcaat	2750
Db	2341	GGCATTTGGAGTGCAGTGGGACAACTGTTTGAAGACTCTGTGGAGAAATATGGCTTCAAT	2400
Qy	2751	ctcaacaacttgaactcctcaatgatactgtttagaaccttccatataaggggtgtagacccgg	2810
Db	2401	CTCACCACTTGGTCTCCATGATGCTGTGTGACACCTTCTCATATGGGGTGATGACCTGG	2460
Qy	2811	tacattgaagctgtcttccaagccagtaacgaattcccaagcctgtatatttccctgtc	2870
Db	2461	TACATTTGAGGCTGTCTTTCCAGGCGAGTACGGAATTTCCAGGCGCTGTATATTTCTCTTC	2520
Qy	2871	accaagttcactactgttttggcaggaagaatgataagaaagacacccctgtgttccaaacag	2930
Db	2521	ACCAAGTCTACTAGTTGTTGGCGAGAAAGTGAAGAAACGCCACCTGTGTTCCAAACAG	2580
Qy	2931	aaggaatgtcagaataatctgacatgtagaagaaaccaaccaacttgaagctgtggcgtgtcc	2990

Db 2581 AAGAGATATCAGAAATCTGCATGAGAGAGAAACCCACCTTGAAGCTGGCGGTGCC 2640
QY 2991 attcaaaacctgtaaaatctacccgagatggatgaaagtgtgctgtcgaatgcttgca 3050
Db 2641 ATTCAACACCTGGTAAATCTACCGAGATGGATGAAAGTGGCTGTCCATGGCTGGCA 2700
QY 3051 ctgaattcttaagaggccagatacaacctctctctctgagcacaatggacggggaagac 3110
Db 2701 CTGAATTTTATGAGGGCCAGATCACTCTCTCTCTGGCCACAATGAGAGGGGAAAGAC 2760
QY 3111 accaccaatgcaatccctgaaccgggtgtctcccccgcacctcgagcaccgtacatctg 3170
Db 2761 ACCACCATGTCAATCCTGACCGGGTGTCTCCCGACCTCGGGCACCCCTACATCTCTG 2820
QY 3171 ggaagaagaattcgtctctgagatgagaccaccacccgcaaaacctgggggtctgtccca 3230
Db 2821 GGAAGAAAGATTCGCTCTGATGATGAGCACCATCCGGCAACCTGGGGGTCTGTCCCG 2880
QY 3231 cataacgtgtctgttacaatgctgactgtctgaagaacacatctgtgtctatgcccgtg 3290
Db 2881 CATAAAGTGTCTGTTCATGCTGACTGCTGCAAGAAACATCTGTTCTATGCCCCCTTG 2940
QY 3291 aaagggtctctgagaagaacgltgaaggcgaatgagacagatggccctgagatgtgt 3350
Db 2941 AAAGGCTCTGTGAGAGACGAGGAGGCGGAGATGAGACAGATGGCCCTGGATGTGT 3000
QY 3351 ttggcatcaagcaagctgaaagaacaaacagccagctgtcaagtgagatgacagaaag 3410
Db 3001 TTGCCATCAAGCAAGCTGAAAGCAAAACACCCACTGTCTAGTGAATGAGAAAG 3060
QY 3411 ctactgtgacctgtgacctgtgcggggatctaagtggtcatcttgatgaaaccaca 3470
Db 3061 CTATCTGTGGCTTGTGGCTTGTTCGGGGGATCTAAAGTTGTCTATGATGATGACCCACA 3120
QY 3471 gctgtgtggaaccttaacctcccgaggggaataatggagctgtcgtgaaataacogaca 3530
Db 3121 GCTGTGTGGACCTTACTCTCCGCAAGGGAATATGGAGCTGCTGTAATATCCACAA 3180
QY 3531 gggcgacacattatctctctacacacacatgagatgaagcggaagctctctggggaacag 3590
Db 3181 GGGCGACCATTTATCTCTCTACACACACATGATGAAGCGGACCTCTGGGGGACAG 3240
QY 3591 attgcatcatctcccatatgggaagctgtgtgtgagctctccctgttctctgaagaac 3650
Db 3241 ATTGCCATCATCTCCATGGGAAGCTGTGCTGTGTGGCTCTCCCTGTCTGAAAGAC 3300
QY 3651 cagctgtggaacagctactactactgtcctgtgtcaagaagaatgtggaatctccctcag 3710
Db 3301 CAGCTGGGAACAGGCTACTACCTGACCTTGTCTCAAGAAAGATGTGAAATCTCCCTCAG 3360
QY 3711 tctctgagaacagtagtagcaactgtgtcatatactctgaagaagagacagtttctcag 3770
Db 3361 TCTCGAAGAAACGTAGTACACTGTGTCTATACCTTAAAAAGAGAGACAGTGTCTCAG 3420
QY 3771 agcagttctgagtctgagcgtggcagcagacatgagatgagacagctgtgacatctgact 3830
Db 3421 AGCAGTTCTGATCTGCGCTGGGACGACGACCATGAGAGACAGCTGACATCATGATGTC 3480
QY 3831 tctgcatatctcaactcatcaggaagaatgtgtctgaaagcccgctgtgtgaaacata 3890
Db 3481 TCTGCTATCTCCAACTCATACGAGAAAGCATGTCTGAAGCCCGGTGTGGAAGCATA 3540
QY 3891 gggcatgagctgacatctgtctgcatatgaagctgtcgaagaggagaccttgtggaa 3950
Db 3541 GGGCATGAGCTGACCTATGTGTGCTGCTATGAAGCTGTCTTAAGAGGAGGACCTTTGTGGA 3600
QY 3951 ctcttcatatgagtatgataccggtctcgaagctgtggacatcttcatgatatgcatctca 4010
Db 3601 CTCTTCATATGAGATGATGACGCGCTCTCAGACCTGGGCAATTTCTAGTTATGCAATCTCA 3660
QY 4011 gaaagacacctggaagaataatctctcaaggtgtgcgaagagagatgggtgtgactgtgag 4070
Db 3661 GAAAGCACTCTGGAAAGAAATTTCTCAAGGTGTGCGGAAGAGAGTGGGTGTGCTGTGAG 3720
QY 4071 aacctgaatggttacctgtccagcaagaacgaagcgcggtctctcgagggaacagagc 4130
Db 3721 ACCTGAGATGTGTACCTTGTCCAGCAAGAGAAAGGCGGCTTCTGGGGACACAGACG 3780
QY 4131 tgtctgcccccttcaactgaagatgagatgctgtatccaaatgatatctgacataagacca 4190
Db 3781 TGTCTGCCCGCTTCACTGAAGATGATGCTCTGATCCAAATGATCTGCATATGACCCA 3840
QY 4191 gaatccagaagaacagactgtctcaatgtgagatgagatgagcaaggtctctaccagtgaaa 4250
Db 3841 GAATCCAGAGAGACAGACTTCTCAGTGGATGAGCAAAAGGCTCTACACAGGTAAA 3900
QY 4251 ggtctgaaacttacaacgaacagtttggcccttctgtggaagagacgtcaatgtgc 4310
Db 3901 GGCTGGAATCTTACACACCAACAGTTTGTGGCTTTGTGGAAGAACACTGTAATTTGCC 3960
QY 4311 agaagagctggaaagagatttctgtcagaatgttctgtccagctgtgtgtctgcat 4370
Db 3961 AGACGAGCTCGAAAGATTTTGTCTCAGATGTGCTGCAGCTGTGTGTCTGAT 4020
QY 4371 gacctgtgttcaagctgtatctgtccaccttggcaagtaeccagcctggaaatctcag 4430
Db 4021 GCCCTTGTGTTCAGCTGATGCTGCTGACCTTTGGCAAGTACCCACCTGGAACTTCAG 4080
QY 4431 ccttgatgtacaacgaacagttacacattgttcaagcaatgttctctgaagacagga 4490
Db 4081 CCTGTGATGTACAAAGACAGTACATTTGTACCAATGATGCTCTGAGGACACGGGA 4140
QY 4491 aacctggaactcttaaaagccctcaccaaaagacctgtctcgagacccgtgtatgaa 4550
Db 4141 ACCCTGGAATCTTAAACGGCCCTCACCAAGACCCCTGGGACCCGCTGTATGAA 4200
QY 4551 ggaaaacccaatcccaagacagccttgcagcagggagggagaggtgagacatctgccc 4610
Db 4201 GGAACCCCAATCCAGACACCCCTGCGAGGAGGAGAGTGGACACACCTGCCCA 4260
QY 4611 gtccccagaccatcatgtgacctctccagaatggaaatggaactgacaatgcaaaccttca 4670
Db 4261 GTTCCCAAGACATCATGTGACCTCTTCCAGATATGGAACTGGACAAATGCAACACTTCA 4320
QY 4671 cctgcatgcccagtgtagcagcgaacaaatcaagaagatgtcgtgtgtgttccccaggg 4730
Db 4321 CCTGCATCCCATGTAGACGAGACGACAAATCAAGAAAGATGCTGTGTGTGTCCCGAGG 4380
QY 4731 gcaagggggtgtcctctcccaaaagaacaaacctgtgaatcttccctcaagactg 4790
Db 4381 GCAGGGGGGCTGCTCTCCCAAAAGAAACAAACACTGCAGATATCTTCAGGACCTG 4440
QY 4791 acaaggaagaacattctgagatctgttgaagacgtatgtgacatcatatagccaaagc 4850
Db 4441 ACAGGAAGAAACATTTGGGATTTATGTGTGAAGAGTATGTGAGATCATATGACCAAAAGC 4500
QY 4851 ttaagaagaacatctgggtgaatgagtttagtataggcgcttccctgtgtgtcagt 4910
Db 4501 TTAAGGAACAAGATGTGGGTGAATGAGTTAGTATGCGGCTTTTCCCTGGGTGTAGT 4560
QY 4911 aatctcaagacattcctccgagttcaagaagttlaatgagcatcaaaatgaagaa 4970
Db 4561 AATFACTCAAGCACTTCTCCGAGTCAAGAAAGTTAATGATGCGCCAAACAAATGAGAA 4620
QY 4971 caacctaaagctggcgaagaagcttctgacagatcgatttcccaacagcttggagaatt 5030
Db 4621 CACCTAAAGCTGGCAAGAGAGTCTCAGATGATGATTTCAACAGCTGGGAAGATTT 4680
QY 5031 atgacagagctggacacagaaataatgtcaaggtgtgttcaataaagagctgtgcat 5090
Db 4681 ATGACAGAGACTGAGACCAAGAAATATGTCAAGGTGTGTGTTCAATACAAAGGCTGCAT 4740
QY 5091 gcaatcagcttcttcttaatgataatcaaatgcatctccgggccaacctgtcaag 5150
Db 4741 GCAATCAGCTCTTCTTAATGTATCAACAATGACATTTCTCGGGCCAACTCTCAAAAG 4800

D	b	6961	TTAGTTTTTACCTAATACCATTGTGAACCTCATTATATGAAACCCCAATGGACATATGGCTT	7020
O	y	7371	tgaactacaccttttctttttttttgttcctcgtglatctcatcattggggttgacaacata	7430
D	b	7021	TGAACTCACACTTTTTTTTTTTTTTTTGTTCCGTGTAATCTCATTTGGGGTTGCAACAATA	7080
O	y	7431	atcataagaataatcatggccagcgatctatgatcaaaaatcaaaagttaatgcacacct	7490
D	b	7081	ATTATCATCAAGTAATACATGAGCGCACGCAGATTATGATCAAAAATCAAAGTAATGCACATCTC	7140
O	y	7491	cattcacctaagccaatgcacagcccagaagaccgtgttcccggtgacatccatctgctcgt	7550
D	b	7141	CATTCTACTAAGCCATGCCATGCCCGCCAGBAACHTGTTTCCCGGTGACATCTATTGGCTGG	7200
O	y	7551	caatgagltgccaagagtlattagtgccaagtttttcagnaaggittgaagcaccatggtg	7610
D	b	7201	CAATGAGTGTGCCAGAGTWTATAGTSCCAAGTTTTTCAAGAAAGTTTGAAGCACCATGGTG	7260
O	y	7611	tgtaatgctaacatttttgtgaagctgctctgctcaagagctctatcaaatltgaataagct	7670
D	b	7261	TGTCATGCTCACTTTTGTGAAACCTGCTCGCTGCACAGCTATCAACATTTGAATATACGT	7320
O	y	7671	tgcagaatgtgtgcacatgcgtgtgctctaacactccgtccttattccctcgtataagctgtc	7730
D	b	7321	TGCAGAAATGCTGCCATGCGCTGGCTACTACATCCTGCTTTATTTCCCTCTGATTAAGCTGTC	7380
O	y	7731	tggtgycagataacatgtgcaaaaaatgtgtgtgltccttagcagcagygaaacttggtlcca	7790
D	b	7381	TGTTGGCAGTAACATGCAACMAAAATGTGGGTGTCCTTAGCAGCGGAACCTTGTTCCA	7440
O	y	7791	ttgttatatgttctctaatgcttgcagccaigggtctacaggtctacaccttaagaaactctt	7850
D	b	7441	TTGTTAATATGTGCTTATGCTTTCAGGCATGTGGGCTTACAGGGTCATCTTATAGACCTCTT	7500
O	y	7851	aaatactactagatccctggytaagagcaaaagaatcaacaagccaactcgtgaggtcga	7910
D	b	7501	AAATATATCTTAGATCCCTGCTGTAAGAAGCAAGAAATCAACAGCCMAACTGCTGGGGCTGCA	7560
O	y	7911	gcgcgcgaagccagygacatgggaattaaagatatgtgcgttcaaacctagaaggaagcctgt	7970
D	b	7561	GCTGCTGAAGCCAGAGCGCATGGGATTTAAAGAGATTGTGCGTTCAAACTTAGGAACCCCTGT	7620
O	y	7971	gcccaatttgctcagcagctgtcgtlaacacatggtacactgcatctcaagatglttacatgc	8030
D	b	7621	GCCCATTTGCTCAGCTGCTGTGCTAACATGTAACACTGATCTCAAGATGTTTATCTTAC	7680
O	y	8031	aacaagtatattacttcgcgctttttaataatcctagaanaatggaagaatggaagtgtat	8090
D	b	7681	ACAAAGTATATTATTTCTGCGCTTTTGTGAATTATCTGAANAATGAANAAGATGAGTGTGAT	7740
O	y	8091	tttgacaaaaatgcttbtactttttaagttaattbgaaattttaagttotlacatgact	8150
D	b	7741	TTTGACAAAAATGTTTGTACTTTTTTATATGTAATTTGGAATTTTAAAGTCTATACATGACT	7800
O	y	8151	tcgtaatcccttagaagayggcctcttgtlagaaaccctgtgtlatagagagatlgcgcactg	8210
D	b	7801	TCTGAATCTTAGAGATGGCCTCTTTGTAGAACCCCTGTGTAATAGAGAGATATGAGCCACTG	7860
O	y	8211	ccccacatttttaatttcttaagtaagttitgatabtaagtcagtcagtagtgcctcaga	8270
D	b	7861	CCCCACTATTTTTTATTTTCTTATGTAAAGTTTGCATATGAGTACATGATGCTCCCTTA	7920
O	y	8271	gcaatgatagtatcagaagatcctcatgacatataattggatcttccttcagatcaattaga	8330
D	b	7921	GCAATGTATAGTGTGAGATCTCTCATGACATTATTTTGAAGTTTCTTTCAATCATATTAGGA	7980
O	y	8331	tactcttaatctcaactcatalcaaatcaaatatttttgagtglatgctgtagcttgaagaag	8390
D	b	7981	TACTCTTATATCTCACTTCATCATCAATCAAAATTTTTTGAAGTATGCTGATGAGCTGAAGAG	8040
O	y	8391	tatgtatgtaagtataagaactatagagagataattaagctcctaagtaacactccctgtgcacatg	8450
D	b	8041	TATGTACGTACGTATTAAGACTTAGAGAGATTTTAAAGTCTAGTAACATTTCTCTGTGCACGT	8100

[illegible]

QY 9531 acctatactcaatcaagcaaaattctgtatatctccctgtggaatgtacctatgtgagt 9590
|||||
Db 9180 ACTGTATACCTCAATCAAGCAAAATTTCTGTATATTCCTGTGAATGTAATCTGTAGAT 9239
QY 9591 ttcaagaattctcaaaataagtggttcaaaaattcttgcttttcacattctggagacccctc 9650
|||||
Db 9240 TTCGAAATTTCTCAAAATACGTTGTTCAAAATTTCTGCTTTTGCACTTTGGGACACCTC 9299
QY 9651 agaaacttatacaactgtgaaatagagaataacagaaataataagccctcat 9710
|||||
Db 9300 AGAAACTATTAACAACTGTGAATATGACAATATACGAAAGAAATATATAGCCCTCTAT 9359
QY 9711 acataaatgcccgcagcaaatctatgtttaaanaaaacaaacctcaactactgtatlt 9770
|||||
Db 9360 ACATTAATGCCCAGCAATTCATGTATTAATAAAACCAACCACTCACTACTGTATTT 9419
QY 9771 catatctgtactgaagcaaatgtctgtgaactatlaattgttgcacatctcatctca 9830
|||||
Db 9420 CATATCTGTATGTAAGCAATGCTTTGTGACTATTAATGTGTGCAATCATCTCATTC 9479

RESULT 15
AX059978 9495 bp DNA linear PAT 22-JAN-2001
LOCUS AX059978
DEFINITION Sequence 96 from Patent WO0078970.
ACCESSION AX059978
VERSION AX059978.1 GI:12405636
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 9495)
AUTHORS Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,
Naudin, U., Lemoine, C., Duverger, N., Assmann, G., Rust, S., Funke, H.
and Brewer, H.B.
TITLE Nucleic acid and proteinic acids corresponding to human gene abcl
JOURNAL Patent: WO 0078970-A 96 28-DEC-2000;
Aventis Pharma S.A. (FR)
FEATURES
source location/Qualifiers
1.9495
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2599 a 2115 c 2216 g 2564 t 1 others
ORIGIN

Query Match 90.3%; Score 9430.6; DB 6; Length 9495;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 9462; Conservative 0; Mismatches 15; Indels 3; Gaps 2;

QY 351 caaacatgctagctgttactggaagtgagcctgacctatattcttcctgactccgatac 410
|||||
Db 1 CAAACATGTAGCTGTTACTGGAAGTGCGCTGCGCTCTATTATTTCTTCCTGATCCTGATC 60
QY 411 tctgtctgctgagctacccacccatgaaacaatgaaatgacatlttccaaataagcc 470
|||||
Db 61 TCTGTTCTGCTGAGTACCCACCCCTATGAAACAATGAATGACCATTTTCCAAATAAAGCC 120
QY 471 atcccccttcaggaacactctctgtgttcagggatattctgtaatgcacaacacccc 530
|||||
Db 121 ATGCCCCCTTCAGGAACACTTCTCTGGGTTCAAGGGATATATCTGTATGCAACCAACCCC 180
QY 531 tgttcctgtacccgactcctcgtggagagctcccgagctgtgtggaactttaaacaatcc 590
|||||
Db 181 TGTTCCTGTAACCCGACTCTCTGGGAGGCTCCCGGAGTTGTGGAATCTTAAACAATCC 240
QY 591 atgtgtgctgctgttctcagaatgctcggagagctctttaaagccagaagaagacc 650
|||||
Db 241 ATTGTGGCTGCTGTTCTCAGATGCTCGAGGCTCTTTTATACGCGCAAGAAAGACACC 300
QY 651 agcatgaagacatgacgaagctctggaacattacacagatcgaagaatccacatca 710
|||||

Db 301 AGCATGAAGGACATGCGCAAAAGTTCTGAGAACATTACAGAGATCAAGAAATCCAGCTCA 360
QY 711 aacttgaagcttcaagattctcgtgtgacaatgaaacctctctggtttctatatac 770
|||||
Db 361 AACTTGAACTTCAAGATTCTCTGCTGACAAATGAACAACTCTCTGSGTTCTGATACAC 420
QY 771 aacctctctcccaagctactgtgtgacaagaatgctcgaaggtgtatgtcatctccac 830
|||||
Db 421 AACCTCTCTCTCCAAAGCTTACTGTGGAAGATGCTGAGAGGGCTGATGTATTTCTCCAC 480
QY 831 aaggtatlttgcagaggtcaccagtacattgacaatctcgtgcaatggaataatca 890
|||||
Db 481 AAGGTATTTTTCAGAGGCTACCAATTATTTGACAACTCTGTGCAATGATTCAAATCA 540
QY 891 gaagagatgattcaacttgtgtgaccaaagaatttctgaacttltgtgcttaccaaagag 950
|||||
Db 541 GAAAGATGATTCACACTTGTGTGACCAAGATTTCTGAGCTTTGTGGCTTACCAAGGAG 600
QY 951 aaactggtctgcagagacgagtaacttctgtccacaatgacatccctgaaagcaactctg 1010
|||||
Db 601 AAACGTGGCTGACGACGACCGAGTACTTGTTCACCAATGACATCTGAAACCAATCTCG 660
QY 1011 agaacactaaactctacatctcccttcccgagcaagagctggtctgaaagccacaanaa 1070
|||||
Db 661 AGAACACTTAATCTATACATCTCTCTTCCGAGCAAGAGCTGCGCGAAGCCCAAAAAACA 720
QY 1071 ttgtgtcatagctctgtggaactctgcccagagagctgttcaagcatgagaagctgtgag 1130
|||||
Db 721 TTGCTGCAATGACTTGTGGGACTCTGGCCGAGGAGCTGTTCACATGAGAGAGTGAAGTGC 780
QY 1131 atgagcagagagtgatgttcttcgacaatgtgacaactcagctccctccacccaatc 1190
|||||
Db 781 ATGCCACAGAGAGTATATTTCTGACCAATGGAACAGCTCCAGCTCTCCACCCCAATC 840
QY 1191 taccagagctgtctcgtatctgtctgcggacatcccgagggaggggctgtgaatacag 1250
|||||
Db 841 TACCAGGCTGTCTCGTATTTGTCTGCGGATCCCGAGGAGGGGCTGAATGATCAAG 900
QY 1251 tctctcaactggtatgagaacaacactacaagaagccctcttgaaggaatgagactgag 1310
|||||
Db 901 TCTCTCAACTGATATGAGACACACATACAAAGCCCTTGTGAGGCAATGAGCACTGAG 960
QY 1311 gaagatgttgaacactctatagacaactctacaactccttacttgaatgtatgtgaag 1370
|||||
Db 961 GAAGATGCTGAACCTCTGTATGACAACTTCAACTCTTACTGCAATGATTGATGAGAG 1020
QY 1371 aatttgaagctagctccctcttcccgcatctcgtgaagactcgtgaagccgctcgtct 1430
|||||
Db 1021 AATTTTGAAGTCTAGTCCCTCTTCCGCAATATCTGGAAGGCTGTGAAGCCGCTCTCGTT 1080
QY 1431 ggaagatccctgtatataccctgcacatccagccacaagagcagtcacatgagctgag 1490
|||||
Db 1081 GCGAAGATCTGTATACACCTGACACTCCAGCCACCAAGAGCATGTGCTGAGAGTGAAC 1140
QY 1491 aagacttccaggaactgtgtgttccatgatactgtgaagagcatgtgtggaagactcaagc 1550
|||||
Db 1141 AAGACTTCCAGGAAGTCTGTGTCTTCATGATGTGGAAGGCAATGTGGAGAACTGAGC 1200
QY 1551 cccaagatctgagactatagagaacagcaagaagaatgagacttgcggatgtctgtt 1610
|||||
Db 1201 CCCAAGATCTGAGCTTATGAGAACAGCCCAAGAAATGACCTTGTCCGATCTCTGTG 1260
QY 1611 gacagcagaggaacaatgacaacttlttggaagaagagatgtgtgacttagattgagaccc 1670
|||||
Db 1261 GACACAGAGGAGCAATGACCACTTTTGGGAACAGCAGTTGATGTGCTTAGATTGACAGCC 1320
QY 1671 caagacatcgtgtgttlttgccaagacccagaagatgttccagtcagtaatgttct 1730
|||||
Db 1321 CAAGCATCTGTGGCTTTTGTGGCAAGCACCAGAGATGTCAGTCAAGTAATGTGTTCT 1380
QY 1731 gtgtacacttggagagagcttcaacagagactaacagaggaatccggacatatctcgc 1790
|||||
Db 1381 GTGTACCTGTGAGAGAGCTTTCAACGAGACTAACCAAGGCAATCCGACCATATCTCGC 1440

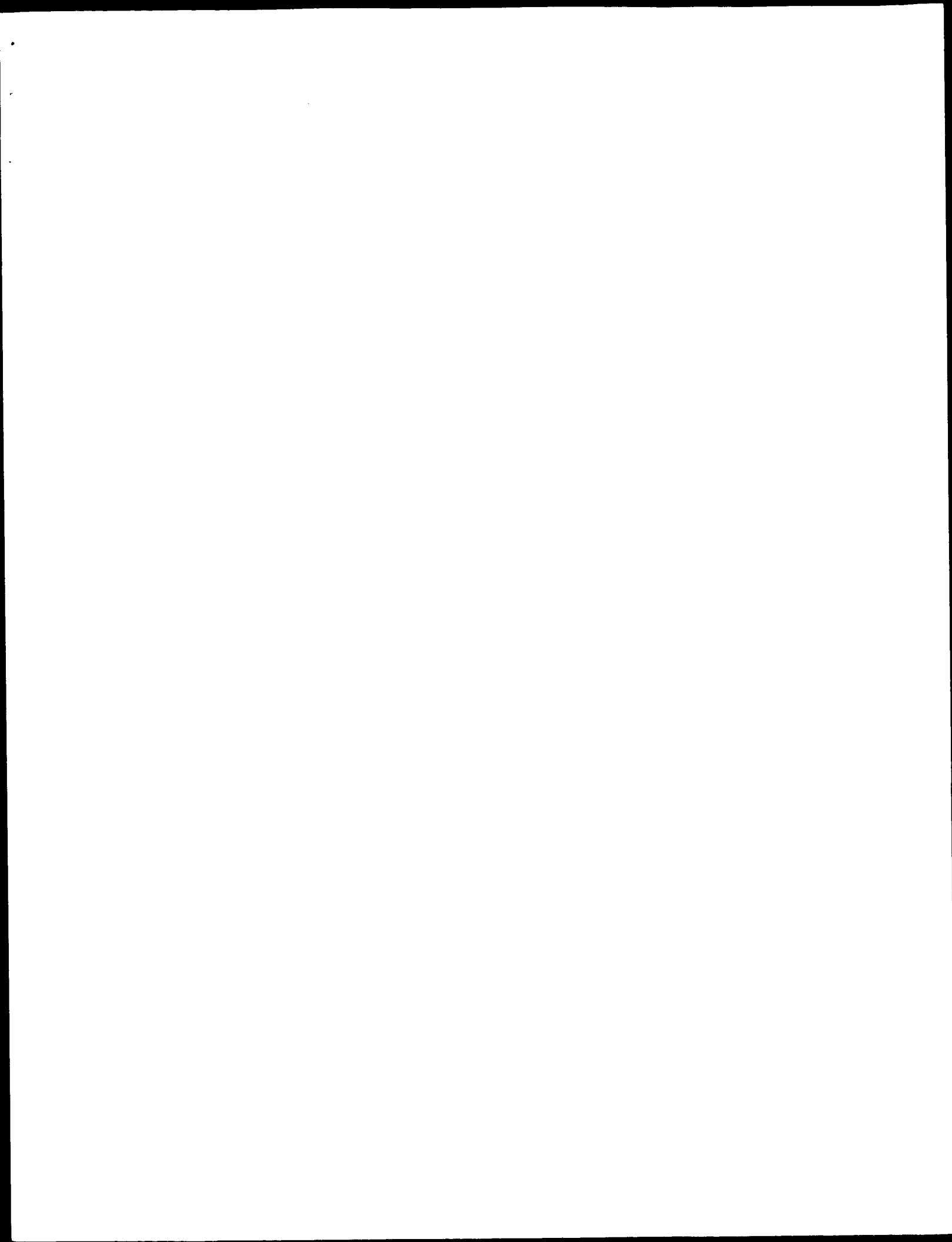
QY	1791	ttcatggaagtgtgtcaaaccccggaacaaagctagaacccaataagaaacagaagtctggtctacac	1850
Db	1441	TTTCATGAGATGTGTCAACCTGGAACAAAGCTAGAACCCATAGACAACAAGACTGTGGCTATC	1500
QY	1851	aaagaagcctatgagacgtgcgtgagatgagagaagtctctgagctgtgtattgtgtcatctga	1910
Db	1501	AACAAAGTCCATGAGAGTGTGCTGAGATGAGAGGAAGTCTTGAGGCTGATGTGTGTCACTGGAA	1560
QY	1911	attactccaggcagcagcatctgagctgccccacalcaltcaagtagacaagaatccgaatctgacatt	1970
Db	1561	ATTACTCCAGGACACATTGAGCTGGCCCATCATGTGTCAAGTAGACAAGATCCGAATGAGACATT	1620
QY	1971	gacaaatgtgagagagaaataataataaagaatggtgtactcgggaacccctggtctctgaagct	2030
Db	1621	GACAAATGTGAGAGGACAAATTAATAATCAAGATGGGTACTGGGAGACCTGGTCTCCAGACT	1680
QY	2031	gaaccccttgagagacatgagctgacgtctgtgggggggcttcgacactctgacagatgtgagt	2090
Db	1681	GACCCCTTTTGAAGGACATGGCGGTAGCTGTGGGGGGGCTTCCGCTCACTTGGCAGATGTGTG	1740
QY	2091	gagcaggcaatcalcaagagtgctgacgggacacgagagaagaanaacatggtgtctataltgcaa	2150
Db	1741	GAGCAGGCAAAATCAATCAGAGGTGCT--CGGGACCCAGAGAAAGAAACGTGGTCTATATGCAA	1798
QY	2151	cagatggccataccctcttctgattgtagacatcttctgtaggttgatgagccggtcaatg	2210
Db	1799	CAGATGCCCTATCCCTCTTACGTGTGATGATCATCTTCTTGCGGGTGATGAGACCGGCTCAATG	1858
QY	2211	ccccctctcaltgacgctgcgctgattactcagtggtctgtgacatcaltgacataggcagctgtg	2270
Db	1859	CCCCCTTCATGAGCGTGGCGCTGGATTACTCATGATGCTGTGATCATCAAGGGGCATCGTGG	1918
QY	2271	tatagaagaagagacagcgtcgaagaagaaacacatcgagatcatgtggctgtgacaacagcata	2330
Db	1919	TATAGAAGAGGAGGACGCGCTGAAGAACACATGCGGATCATGTGGCCCTGGACAACAGATAC	1978
QY	2331	ctcgtgattagctgtgtcatagtagcctcatctctctctctgtgagcgtctggcctgtcta	2390
Db	1979	CTCCTGTGTACCTGGTTCATTAGTAGGCTCATCTCTCTTCTGTGGAGCGCTGGGCTGTCTA	2038
QY	2391	gtggtcalccctgaagttagaanaacctgtcgcctacagtagatcccaagcgtgtgtttgttc	2450
Db	2039	GTGGTCATCTCGAAGTTAGGAACACTGTGCTCCCTACAGTATCCCAACGCGTGGTGTGTC	2098
QY	2451	ttctcgttcgcggtttgcgtgctgtgataaatccttgagatgcttccctgattaaacaactcttc	2510
Db	2099	TTCCGTCCGTTGTGTGCTGTGTGACAAATCCTGCAAGTGTTCCTCGATTACACACTCTTTC	2158
QY	2511	lccagaagcaaacctgcgcagcagcagcctgtgtgggggcaatcaactcaacgcgtgataccctgc	2570
Db	2159	TCCAAGGCCAATCTGGGAGCGAGCGCTGTGGGGGCATCATCTACAGCTGTACTCCCTCCC	2218
QY	2571	taagtcctgtgtgtgtgaatgagcagaagtaogtgggtcttacaactcaagaatctctcgtatgc	2630
Db	2219	TACGCTCCTGTGTGTGGCATGTGGACAGACTACCTGTGGCTTCAACATCAAGATCTTTCGTAGC	2278
QY	2631	ctgctgctcctgtgtgacctgttggtgttgagcgtgtgaftaactttgaccttttgaagaagcag	2690
Db	2279	CTGCTGTCTCCTGTGGGCTTTTGGGTTTGGCTGTGAGTACTTGTGCCCTTTTGAAGAGACAG	2338
QY	2691	ggcattgagatgtcagttgagacaacctgtttgaagctccctgtgagaagaatgtgcttcaat	2750
Db	2339	GGCATTGTGAGTGCAGATGGGACAACTGTTGTGAGAGTCTCTGTGGAGGAAGATGGCTTCAT	2398
QY	2751	ctcaccactctgactctcaatgactgtgtttgaacaacttccctctatctgggagtgaatacctgtg	2810
Db	2399	CTCACCACTTGTGGTCTCATATGCTGTGTTTACACCTTTCCTATGTGGGGTGAATCACTGG	2458
QY	2811	taacattgagcgtgtcttctccagccagtaacgaaatccccaagccctgtgatatcttccctgc	2870
Db	2459	TACATTGTGAGGCTGTCTTTCACAGGCCAGTACGAATTCACAGGCGCTGTGTATTTTCTCTTGC	2518
QY	2871	accaaagtccctactggtttgtggcgagaaagatgtgataagaagaagccaacctgtgttccaacag	2930
Db	2519	ACCAAGTCTCTACTGGTTTGGGAGAGAAATGATGAAGAGCCACTCGTGTCCATCCACAG	2578
QY	2931	aagaaatctcagaatctgcatgtagagagaacccaaccaacttgaagctgtggcgtgtcc	2990
Db	2579	AAGAAATATCAGAAATGTGATGAGAGGAAACCAACCCACTTGAAGCTGTGGGCTGTCC	2638
QY	2991	altcagaacctgtgtaaagaatctaccagatgagatgtgaagtgtgctgtcgatgacctgtgca	3050
Db	2639	ATTCAAGAACTGTGAAAAAGTGTACCGAATGGATGGAAGGTGCTGTGTATGGCTGTGGCA	2698
QY	3051	ctgaaatttttatgagggccagatcaacctccctctctgtggccaatgtgaagcgggagaagcg	3110
Db	2699	CTGAATTTTATGAGGGCCAGATACCTCTCTCTGCGGCACATGTGAACGGGGAAACAGC	2758
QY	3111	accacacatgcaatccctgacggggtgtgttcccccagacctcgggacgcgcctacatccctg	3170
Db	2759	ACCACCATGTCAATCTGACCGGGGTTGTTCCCCCGACCTGTGGGCACCGGCTCATATCCTG	2818
QY	3171	ggaaaagacatctgctcttgaaatgagacacatcccggaagaacctgagggtgtctgtccccag	3230
Db	2819	GGAAAAGACATTGCTGTGGAATGAGCAACCATCCGCGCAAGACCTGGGGGTGTGCCACAG	2878
QY	3231	caataagctgtcgttttgacatctgtgactctgaaagaacacatctgttctatgtcccccttg	3290
Db	2879	CATTAAGTGTCTGTTTGACATGCTGACTGTGCAAGAACATCTGTTCTATATGCCGCTTG	2938
QY	3291	aaaaggctctcttgagaagacgltgaaggcgagatlgagaacagatgtgccctgagatgtgtgt	3350
Db	2939	AAAGGCTCTCTGAGAAACACAGTGAAGCGGAGATGTGAGCGAATGGCCCTGTGATGTTGGT	2998
QY	3351	ttgcacataagaaagcttgaagaagcaaaacaaagccagcgtgtcaagttgaaatgcagaagaag	3410
Db	2999	TTGCCATCAAGCAACCTGAAAAAGCAAAACAGCAGCTGTAGGTGGAATGCAGAAAG	3058
QY	3411	ctatctgtgacctgtgaccttgcgtggggatctaaggttgttcatctgaltgaltgaaccaca	3470
Db	3059	CTATCTGTGGCTTGTGGCTTGTTCGGGGGATCTTAAGTGTTCATTCTGTGATGAACCCACA	3118
QY	3471	gctggtgtggaaccttactcccgcgaagggaatatgaggcgtgcgtctgaaatlacaggcaa	3530
Db	3119	GCTGTGTGTGACCTTTACTTCCCGAGGGGAATATGGAGCTGTCTGTGAATATCCGACAA	3178
QY	3531	ggcgcacacatlatctctcttcaacaacacatgta.tgaagagacgctctcctgagggaagcag	3590
Db	3179	GGCCGACCATTATTCTGTCTACACACCAACATGATGAAGCGGAGCGTCTGTGGGACAGG	3238
QY	3591	attgcacatcctccacatggaagaactgtgtcgtgtgtgtggctccctccctgttctgaagaac	3650
Db	3239	ATTGGCATATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCTCCCTCCTGTTCTAAGAAC	3298
QY	3651	cagcttgaggaaagcgtctactaacctctgtgtgcaagaagaatgtg	

Db 3599 CTCTTTTCATGAGATTGATGACGGCTCTCAGACCTGGGCACTTTCAGTTATGAGCATCCCA 3658
OY gagagacccttggaaataataatctcaagg tggccgaagagtggtgtgagctgag 4070
Db 3659 GAGAGACCTCTGAGAGAAATATCTCTCAAGTGGCCGAGAGAGTGGGCTGATGCTGAG 3718
OY 4071 acctagatgttaccttgcagcaagagaacagcgagcctccgggagacaagcagc 4130
Db 3719 ACCTGATGATGATCTTCCAGCAAGAGCAAGAGGCGGCTTCGGGAGCAACAGCAGC 3778
OY 4131 tgtctgcgcccttcaactgaagatgctgtgatcccaatgattctgacatagacca 4190
Db 3779 TGTCTGCCCGCTTCACGAGATGATGCTGCTGATCCAAATGATTCGACATAGACCA 3838
OY 4191 gaatccagaagaagacagacttgcagtgagtgagtgagcaagggtccctaccagtgaaa 4250
Db 3839 GAATCCAGAGAGACAGACTTCTCAGTGGATGATGGCAAGGGTCTCTACAGCTGAAA 3898
OY 4251 ggtcgaacttacacaagcaacagttgtgaccttctgtgagaagagactgtaattgcc 4310
Db 3899 GGCTGGAAACTTACACACACAAAGTTGTGSCCTTTTGTGAGAGAGACTTAATTGCC 3958
OY 4311 agaagagtcggaagagatttttgcagatgtcttgcagactgtgtgtgtgtgact 4370
Db 3959 AGACGAGCTCGGAAAGCATTTTGTCTCAGATGCTGTGACAGCTGTGTGTGCTGACTT 4018
OY 4371 gcccttgttcaagccttgatgtgacaccttggcaagtaaccacacgtgaaacttcag 4430
Db 4019 GCCCTGTGTTCAAGCTGATGCTGACACCTTTTGCAAGATGCCACACCTGGAACCTTTCAG 4078
OY 4431 ccttgatgtacaacagaaacagttatctacagcaatgtgtctcttgagacaagcga 4490
Db 4079 CCTGTGATGTACAAAGAAACAGTATACATTTGTGACATGATGCTCTGAGAGACGGGA 4138
OY 4491 acctgtgaaccttaaaagcccttaacaaagacccctgtgtctggagccgtgtatgaa 4550
Db 4139 ACCCTGGAACTCTTAAAGGCCCTCACCAAAACACCTGCTGGGACCGCTGTATGAA 4198
OY 4551 ggaaccacacacccagacagcctgtcagcagggaggaagagtgagacactggccca 4610
Db 4199 GGAACACCAATCCAGACACGCCCTTGCCAGGAGGAGAGAGTGGACCACTGCCCA 4258
OY 4611 gtccccaagacatcatgagaccttccaaatgagaaactgagacatgcaaaccttca 4670
Db 4259 GTTCCCAAGACATCATGAGACTTCTCAGATGGAACTGGAACATGCAAAACCTTCA 4318
OY 4671 ccttcagtgccagttgtagcagcagcaaaataaagaagaagtgtgtgtgtgtgtgtgt 4730
Db 4319 CCTGCTATGCCAGTGTAGCAGGACAAATCAAGAGATGCTGCTGTGTGTGTGTGTGTGT 4378
OY 4731 gcaaggggggtgtcctctccaaagaacaaacacactgcagatctccttcagagactg 4790
Db 4379 GCAGGGGGGCTGCTCTCCCAAAAGAAACAAACACTGCAGATATCTTTCAGAGACTG 4438
OY 4791 acagaagaacacatttcggatlatctgtgagaagcgtatgtgcagatcatgccaaagc 4850
Db 4439 ACAGGAAAGAAACATTTGGATTATCTGTGTGAAGCGTATGTGAGATCATAGCCAAAGC 4498
OY 4851 ttaagaacaagaactcgtgtgaatgagttgagttatgagggctttccctgggtgtcagt 4910
Db 4499 TTTAAAGAACAGATCTGTGGTGAATGACTTTAAGGTATGGCGGCTTTTCCGTGGGTGTGACT 4558
OY 4911 aataactcaagacttctccagatcaagaagttaatatgcatcaacaacaaatgaaagaa 4970
Db 4559 AATACTCAAGCAGCTCTCTCCGAGTCAAGAGTTAATGATGCCAACAAATGAGAGAAA 4618
OY 4971 caactaaagcttgcgaagacagttctgcagatcgatlttccaacgcttgggaagatt 5030
Db 4619 CACCTAAAGCTGGCAAGGACAGTGTGCGAGATCGATTCTCAACAGCTTGGAGAAATTT 4678
OY 5031 atgacagactgtgacaccaaataatgtcaaggtgtgttcaataacagggctggcag 5090
|||||

Db 4679 ATGACAGGACTGGACACAGAAATAATGTCAGAGTGTGTTCAATTAACAAGGCTGGCAT 4738
OY 5091 gcaatcaagcttctctgaatgtcatcaacaatgtccattcccgagccaactgtcaaaag 5150
Db 4739 GCATCAGGCTCTTCTCGTAATGTCAATCAACATGCAATTCCTCCGGGCCAAGCTGCAAAAG 4798
OY 5151 ggaagaacaccttagccattatgaaatgactgtcttcaatccatccctgaaatccaaga 5210
Db 4799 GGAGAGAACCCCTAAGCCATTATGGAATTAAGTGTTCATTAATCAATCCCTGATCTCACAG 4858
OY 5211 cagcagctcacaaggttgcctcagatgacacataagtgagatgtctgtgtgtgtgtgtgt 5270
Db 4859 CACAGCTCTCAGAGGTGGCTCGATGACCAATCAATGAGATGTCTGTGTGTGTGTGTGTGT 4918
OY 5271 gtcaatcttgaaatgtccttccagcagcagcttgcgtatctcctgataccaagagcgg 5330
Db 4919 GTCATCTTGCATGTCTTCGTCGACAGCAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4978
OY 5331 gtccagaagaacaaacactgtcagttcatcagtgagtgagtgagtgagtgagtgagtgagtg 5390
Db 4979 GTACGAAAGCAAAACACTGCAATTCATCAGTGGAGTGAAGCTGTGTGTGTGTGTGTGTGTGT 5038
OY 5391 tctaatttgcctggagatagtgaatlaactgtgtccctgcagacactgtgcatlatac 5450
Db 5039 TCTAATTTGTCTGGGATATGTGCAATTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5098
OY 5451 ttcatctgtccagaagaagttcctatgtgtcctcaacacactgtcgtgtgtgtgtgtgtgt 5510
Db 5099 TTTATCTGTCTCCAGCAAGAGTCTATGTGTCTCCACCAATCTGCTGTGTGTGTGTGTGTGTGT 5158
OY 5511 ctacttctgtatagtggt 5570
Db 5159 CTACTTTTGTCTGTATGT 5218
OY 5571 aagatccccaagcaacagcctatgt 5630
Db 5219 AAGATCCCAAGCAAGCCTATGT 5278
OY 5631 ggcagcgttgccaacctgt 5690
Db 5279 GGCAGGCTGGCACTTTGT 5338
OY 5691 gatatactgaatccgt 5750
Db 5339 GATATCTGAATGCTGT 5398
OY 5751 gacatgt 5810
Db 5399 GACATGT 5458
OY 5811 ggtcacacatlatcttgagactgt 5870
Db 5459 GTGTACCATTTATCTTGT 5518
OY 5871 gt 5930
Db 5519 GT 5578
OY 5931 gtaaatgtcaaaactatccctcttgatgaatgaatgaatgaatgaatgaatgaatgaatgaat 5990
Db 5579 GTTAATGTCAAAAGCTATCTCTCTGTAATGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5658
OY 5991 agaattcttgatgt 6050
Db 5639 ACAATTTGTGATGT 5688
OY 6051 tatagaagaaacggaagcctgt 6110
Db 5699 TATAGAAGAAAGCGGAACCTGT 5758
OY 6111 tgccttggt 6170
Db 5759 TGTCTTGGGCTCTGGGAGTTAATGGGCTGTGAAATCATCAACTTCAAGATGTTAACA 5818
|||||

OY	6171	ggagaaaccacgttataccagagagatgcttcttccttaacaaataglatcttataac	6230
Db	5819	GGAGATACCACTGTATCCAGAGAGATGCTTCTTAAACAGAAATGATCTTATCAAC	5878
OY	6231	atccataaatacatcaagaacatgggtctacttgccttaagtttgatgcatcaagaacgtg	6290
Db	5879	ATCCATTAAGATCATCAGAACATGGGCTACTGCGCTCAGTTGATGGCATACAGAGCTG	5938
OY	6291	ttgacttggagagaaacacgttgaattcttctgccttttgaagagagtcctccagagaaag	6350
Db	5939	TTGACTGGGAGAGAACCGTGGAGTCTTGTGCGCTTTTGAAGAGAGTCCAGAGAAAGAA	5998
OY	6351	gttggcaaggttgtgtgagtggtgcgaltcggaaacttgggcctgtgaaglatgtsgaaana	6410
Db	5999	GTTGGCAAGGTTGGTGTGGCGGATTCGGAAACATGGGCGCTGTGAACATGAGCAAAAA	6058
OY	6411	tatctgttaactatagttgagggcaacaaagcaagctctcraagcgatgttctatc	6470
Db	6059	TATCTGTGTAACATATGATGAGGCAACAAACGAAAGCTCTTACAGCCATGGCTTTGATC	6118
OY	6471	ggcgagcctcctgtgtgttctctgaagaaccacacagcagatgatgcccaagccgg	6530
Db	6119	GGCGGGCGCTCCTGTGTGTCTTGATGAACCCACACAGCATGGAATCCCAAGCCCGG	6178
OY	6531	cggltcttgtggaattgtgtccaaagtgtgtccaagagggagatacagtagtgttaca	6590
Db	6179	CGGTTCTTGTGGAATGTGGCCCTTAAGCTGTGTGTCAGAGAGGGAGATCATGTGTGTACA	6238
OY	6591	tctatagtatgtgaagaatgttgaagctctcttcgaatgaatgtgcatatgttcaatga	6650
Db	6239	TCTCATATGTGAGAGAAATGTGAAGCTCTTTGCACTAGCATGGCAATATGTGCTAATGGA	6298
OY	6651	aggltcaggtgtccttggcagtggtccagcatctcaaaaaatagtttgaagatgtgtataca	6710
Db	6299	AGGTTCAAGTGCCCTTGCCAGTGTCCAGCATCTTAAAAAATAGTGTGGAGATGGTTATACA	6358
OY	6711	atagtttagaataagaaaggttccaaacccggacgtgaagcctgtccaagatttctttga	6770
Db	6359	ATAGTGTGACGAATGAGAGGGGTCCAACCCGAGACTGTAACCCGTGTCAGGATTTCTTTGGA	6418
OY	6771	cttgcattcctgtgaagtgcttcaaaaagagaacacccgaaacatgtcacaatacacgctt	6830
Db	6419	CTTGCAATTTCTGSAATGTGTCCAAAAGAGMAACCGGAAACATGCTCATATACAGCTT	6478
OY	6831	ccatctcatatctctctctgtccagagatatacgaatcctctccagagcaaaaaagcga	6890
Db	6479	CCATCTTCATATATTTCTTCTGCGCAGAGATATTCAGATCTCTCCCAAGCAAAAAAGCGA	6538
OY	6891	ctccacatagaagactactctgtttctagaacaacacttgaccagatittgtgaactt	6950
Db	6539	CTCCACATAGAAAGCTACTGTTGTTCTCAGACACACTTGACCAAGTATTTGTGAACCTT	6598
OY	6951	gccaaagaccaaagtgtatgaaccacttaaaagacctctctatcaacaaaaaacagaca	7010
Db	6599	GCCAAAGCAAAAGTGTATGATGACCACTTAAAAAGACCTCTCATACACAAAAACAGACA	6658
OY	7011	gtatgtgaacgttgcagttctccacatcttttctacagatgtgaagaatgtgaagaagctat	7070
Db	6659	GTAATGTGACGTTGTGACGTTTCCACATCTTTTCTACAGATGAGAAAGTGAAMAAAAAGCTAT	6718
OY	7071	gtatgaagaatccgtgttcatcaaggggtgtcgtgaagttaagaaggaactagacttccctt	7130
Db	6719	GTAATGAGAAATCCGTTTCATACGGGGGTGCTGAAGATTAAGAGGNAATGAGATTTCCTTT	6778
OY	7131	gcacaaatgtgaagtgtgtgtgagaaaaagaccgaagtltgatgtgtggaagaatlaaactg	7190
Db	6779	GCACCAATGTGAAGTGTGTGGAGAAAAAGACCAGAGTGTGATGTGGAAAGATGTAACTG	6838
OY	7191	gatatctgactgatactattccaatgaatgaatlaatgaatgaatgaatgaatgaatgaat	7250
Db	6839	GATATCTGACTGATACATTTCAATTCAGATTCGAATTCGAATTCGAATTCGAATTCGAATTC	6898

QY	7251	tacaggggcagtgcccttctgttagacctatgctctgttaagctcccaagtgaaagccttgaat	7310
Db	6899	TACAGGGGCAGTGCCTTTGTAGGCTATGTCCTGTATAGGCTCTCAAGTGAAGACTTGAT	6958
QY	7311	ttagcttttaccataaccatagtgaacaccttaatggaaaccaatgacataagttc	7370
Db	6959	TTAGTTTTTACCCTATACCTATGTGAACCTCTATTGTGAACCCAAATGGACATATAGGTT	7018
QY	7371	tgaactccaccttt	7430
Db	7019	TGAACTCACACTTTTTTTTTTTTTTTTTTTTGTCTGTATTCATTTGGGGTTCACAACATA	7078
QY	7431	atctcaagaatcatcatgcccagcatatctgaatcaaatcaaaagttaatgcacacct	7490
Db	7079	ATTCTCAAGTAATCAATGCGCAGCGATTTATGTATCAAAATCAAAAGTAATGCACATCT	7138
QY	7491	cattcaactaaagccatgcccaggaagacgtgttcccggttgacaatccatctgcg	7550
Db	7139	CATTCACTAACCCATGCGCATGCGCCAGGAGCTGTGTTCCGGTGACACTTCATTGCTGG	7198
QY	7551	caatgagtgccgaagttatctagtcgaagttttcagaagaatttgaagcccaatggt	7610
Db	7199	CATATAGTGTCGACGAGTATTATGTGCAGTTTTCAGAAAGTTTGAAGCACCATGGTG	7258
QY	7611	tgctatgctcaacttttctgtgaagctgctctgctccagagttcatcaacatgaaatcag	7670
Db	7259	TGCTATGCTCACTTTTGTGAAGCTGCTGTCAAGACTCTATCAAGCTATTCAACTTAATATCAGT	7318
QY	7671	tgacgaatggtgcacagcgtgtggttaacatccctgctttgattccctctgataagctgtc	7730
Db	7319	TGACGAATGAGTGCATGCGCATGCGCTAACATCTCGTTTATTCCTCTGATTAAGCTGTTC	7378
QY	7731	tgtgtgcagtaacatgcaacaaaatttgggtgtctctctagggcaagggaaacttggttcca	7790
Db	7379	TGCTGCGAGTAACATGCAACAAAATGTGGGTGTCTTAGCGACGGGAACCTTGGTGTCCA	7438
QY	7791	ttgttatattgtccolatgcttcgaagcaatgggtctccagggttcatcccttaagaacctt	7850
Db	7439	TGTGTATTTGTCTCTATGCTTCCAGCCATGGGCTCTACAGGGTCACTCCTTATATAGACTTT	7498
QY	7851	aaatactacttgatccctggtlaaagggaagaatcaacagccaacttgttgggttcgaa	7910
Db	7499	AAATTACTTATGATCTGTGTGAAGGCAAAAGTAACAAGCCAAACTGCTGGGCGTGCAA	7558
QY	7911	gctgtctgaagccaggaatgagatctaaagatcttgctctcaaaccttaggaagacgct	7970
Db	7559	GCTGCTGAAGCCAGGCGCATGGGATTAAGAAGATTGTCCGTTCAAACTAGGCAACCTGT	7618
QY	7971	ggcccatctgtccctgacagtctgctaaacatgtaacatgcaatcctcaagatgtttalcgac	8030
Db	7619	GGCCATTTTGTCTGACTGTCTGTAAACATGTGACATGCATCTCAAGAGTTTATCTGAC	7678
QY	8031	acaaatgtatatatttctggtcttttgaatatactagaanaatgaaagaatggaagtgtat	8090
Db	7679	ACAAATGTATTAATTCGTGGCTTTTGTGAATTAATCTGAAAAATCAAAAAGATGGAATGTAT	7738
QY	8091	tttggcaaaaatgtttgaccttttaagtatcttgaatttaagtcttccatcagtgact	8150
Db	7739	TTTGCACAAAATGTTTGTACTTTTATGTATTGTTGGAATTTTAATGTTTATCACTAGACT	7798
QY	8151	tctgaatcccttagaagtgccctcttgtagaaccctgtglatagaggagtagtgccactg	8210
Db	7799	TCTGAATCCTTAAGATGCGCTCTTTGTAGAACCCTGTGGTATGAGAGAGTATGCGCCACTG	7858
QY	8211	cccacacttt	8270
Db	7859	CCCCACTATTTTATTTTCTTATGTATTAAGTTTGTGATATCACTCATGCTATGCTCAGAAA	7918
QY	8271	ggcaatgtatgtcaggaatcctgaacatataattgagtttcttccaatcaatttaga	8330
Db	7919	GCAATGTGATGTGCGAGATCTCAAGACATTAATTGAGAGTTTCTTTCAAGATCATTTAGGA	7978
QY	8331	tactcttaatccatccatccatcaatcaaatatttttgaagtglatgctgtagctgaagaag	8390



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: September 13, 2002, 11:38:08 : Search time 1589.81 Seconds (without alignments)
11276.832 Million cell updates/sec

Title:	US-09-595-526B-1
Perfect score:	10442
Sequence:	1 ggcgcgacccgcagagccg.....aaaaaaaaaaaaaaaaaa 10442

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

```
Searched:      1736436 seqs, 858457221 residues
Total number of hits satisfying chosen parameters: 3472872
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

```
1: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1960.DAT.*
2: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT.*
```

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	10438	100.0	10442	22	AAE244680	Nucleotide sequen
2	10438	100.0	10442	22	AAE244702	Nucleotide sequen
3	10429	99.9	10474	22	AAE24685	Nucleotide sequen
4	10429	99.9	10474	22	AAE24686	Nucleotide sequen
5	10429	99.9	10474	22	AAE24707	Nucleotide sequen
6	10429	99.9	10474	22	AAE24708	Nucleotide sequen
7	9777.8	93.6	9854	22	AA506121	Human ABC1 DNA se
8	9672.8	92.6	9741	22	AA506120	Human ABC1 DNA se
9	7825.8	74.9	7860	22	AAE92835	Human ABC1 CDNA.

10	7822.6	74.9	7860	22	AAFP8389.6	Human ABC1 nucleot
11	7791.8	74.6	7864	21	AAAC69120	Human ABC1 cholest
12	7790.2	74.6	7864	21	AAAC69385	Human ABC1 cholest
13	7790.2	74.6	7864	21	AAAC69386	Human ABC1 cholest
14	7790.2	74.6	7864	21	AAAC69389	Human ABC1 cholest
15	7775.8	74.5	7861	21	AAAC69387	Human ABC1 cholest
16	7767.8	74.4	7857	21	AAAC69388	Human ABC1 cholest
17	7198.8	68.9	7260	22	AAAD1333.6	Human ATP binding
18	7198.8	68.9	7260	22	AAAD1333.6	Human ATP binding
19	7194	68.9	7281	22	AAAK51683	Human polynucleoti
20	7038.6	67.4	7086	22	ABA09200	Human polynucleoti
21	7038.6	67.4	7086	22	AAKS52667	Human ATP binding
22	6862.4	65.7	6880	21	AAZ94734	Human ATP binding
23	6862.4	65.7	6880	22	AAIT7031.4	Human ATP binding
24	6852.2	65.7	6880	22	AAAD21325	Human stomach canc
25	4952	47.4	5037	22	AAI939313	Human cDNA sequenc
26	4952	47.4	5037	22	AAHI82233	Nucleotide sequenc
27	3362	32.2	3366	22	AAAF24684	Nucleotide sequenc
28	3362	32.2	3366	22	AAAF24706	Human ABC1 gene, p
29	3282.8	31.4	5352	22	AAAS04049	Human ABC1 genomid
30	3227.6	31.4	5352	22	AAAF92831	Human ABC1 gene ex
31	2107.8	20.2	5138	21	AAAC659147	Human ATP binding
32	1929.8	18.5	7323	21	AAAZ93746	ATP binding cassete
33	1929.8	18.5	7784	19	AAAV33392	Nucleotide sequenc
34	1906.6	18.3	2011	22	AAAF24683	Nucleotide sequenc
35	1906.6	18.3	2011	22	AAAF24705	Human PD-ATP-bindi
36	1735.8	16.6	6522	22	AAAS08706	Nucleotide sequenc
37	1696	16.2	6607	22	AAAF54812	Nucleotide sequenc
38	1531.6	14.7	5762	22	AAAF54792	Nucleotide sequenc
39	1528.8	14.6	5811	22	AAAD05626	Human secreted prote
40	1465	14.0	5669	22	AAAS08707	Human PD-ATP-bindi
41	992.6	9.5	1556	22	AAHI16606	Human cDNA sequenc
42	985	9.4	8040	22	AAAF57452	Human ABCA2 transp
43	985	9.4	8195	22	AAAH75187	Nucleotide sequenc
44	953.6	9.1	6792	22	AAAD07222	Human ATP binding
45	949.2	9.1	6437	23	AAAF73965	DNA encoding novel

PN	W0200078972-A2.
XX	
PD	28-DEC-2000.
XX	
PF	16-JUN-2000; 2000WO-US16765.
XX	
PR	18-JUN-1999; 99US-0140264.
PR	14-SEP-1999; 99US-0153872.
PR	19-NOV-1999; 99US-0166573.
XX	

Db 1621 acaatgaccatttggagacagcagttgagctgattgagatgagacccaagacatcg 1680
Qy 1681 tggcgctttggccagacccaagagatgctcagttcaagtaatgtgttcgtgacacct 1740
Db 1681 tggcgctttggccagacccaagagatgctcagttcaagtaatgtgttcgtgacacct 1740
Qy 1741 ggaagaagcttccaaacgagactaaacgaacatccgagacatactcgtctcaagagat 1800
Db 1741 ggaagaagcttccaaacgagactaaacgaacatccgagacatactcgtctcaagagat 1800
Qy 1801 gctcaacctgtaacaagctagaaacccaatagcaacagaagctcgtctcatcaacaagtc 1860
Db 1801 gctcaacctgtaacaagctagaaacccaatagcaacagaagctcgtctcatcaacaagtc 1860
Qy 1861 tggagctgtgtagatgagagaagttctcgtgctgattgtgttcaactggaattactccag 1920
Db 1861 tggagctgtgtagatgagagaagttctcgtgctgattgtgttcaactggaattactccag 1920
Qy 1921 gcaagcattgagctgccccatctcagaaagtacaagaatccgaatgagacattgacaattgag 1980
Db 1921 gcaagcattgagctgccccatctcagaaagtacaagaatccgaatgagacattgacaattgag 1980
Qy 1981 agagagacaataaatacaagatgagatgagacccctggtccctgagctgagccctctg 2040
Db 1981 agagagacaataaatacaagatgagatgagacccctggtccctgagctgagccctctg 2040
Qy 2041 agagacatgctgtagctgtgagagagcttcgtcctactctgcaagatgtgtgtgagagagca 2100
Db 2041 agagacatgctgtagctgtgagagagcttcgtcctactctgcaagatgtgtgtgagagagca 2100
Qy 2101 tcaatcaggtgtgtagcagggcaccgagaagaacacgtgtctatctgacaagatgacct 2160
Db 2101 tcaatcaggtgtgtagcagggcaccgagaagaacacgtgtctatctgacaagatgacct 2160
Qy 2161 atccctgtatcgttgaatgaacatctctcgtcgggtgagatgagacccgtcaatgcccccttca 2220
Db 2161 atccctgtatcgttgaatgaacatctctcgtcgggtgagatgagacccgtcaatgcccccttca 2220
Qy 2221 tgaagctgagctgagatcttcaatcagtgagctgtgatacaagagacatcgtgtatgagaag 2280
Db 2221 tgaagctgagctgagatcttcaatcagtgagctgtgatacaagagacatcgtgtatgagaag 2280
Qy 2281 agagcagctggaagaagacacatgagacatgagacatgagacatgagacatgagacatg 2340
Db 2281 agagcagctggaagaagacacatgagacatgagacatgagacatgagacatgagacatg 2340
Qy 2341 gctggttcatctagtagcctcatctctctctctctctctctctctctctctctctctctct 2400
Db 2341 gctggttcatctagtagcctcatctctctctctctctctctctctctctctctctctctct 2400
Qy 2401 tgaagctggaagaac 2460
Db 2401 tgaagctggaagaac 2460
Qy 2461 tgttctgttggtagaacaac 2520
Db 2461 tgttctgttggtagaacaac 2520
Qy 2521 acctgagcagcgtgtgagagacatcatctacttcaacgctgtagacacacacacacacacac 2580
Db 2521 acctgagcagcgtgtgagagacatcatctacttcaacgctgtagacacacacacacacacac 2580
Qy 2581 gctgtagcagcgtgtgagagacatcatctacttcaacgctgtagacacacacacacacacac 2640
Db 2581 gctgtagcagcgtgtgagagacatcatctacttcaacgctgtagacacacacacacacacac 2640
Qy 2641 ctgtgcttggtagctgtgagac 2700
Db 2641 ctgtgcttggtagctgtgagac 2700
Qy 2701 tgcagctgagac 2760
Db 2701 tgcagctgagac 2760

Qy 2761 cgatccatgatgctgttggac 2820
Db 2761 cgatccatgatgctgttggac 2820
Qy 2821 ctgcttccagcagctagcgaattccacagccctgtgatacttctcttgcacacagctcct 2880
Db 2821 ctgcttccagcagctagcgaattccacagccctgtgatacttctcttgcacacagctcct 2880
Qy 2881 actggttggcagagagagatgagatgagagagacacacacacacacacacacacacacacacac 2940
Db 2881 actggttggcagagagagatgagatgagagagacacacacacacacacacacacacacacacac 2940
Qy 2941 cagaatctgtagcag 3000
Db 2941 cagaatctgtagcag 3000
Qy 3001 tgttgaagaagcttaccagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 3060
Db 3001 tgttgaagaagcttaccagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 3060
Qy 3061 atgagagcagacatcactcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 3120
Db 3061 atgagagcagacatcactcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 3120
Qy 3121 caatcctgagcagagctgtgtcccccagacacacacacacacacacacacacacacacacacacac 3180
Db 3121 caatcctgagcagagctgtgtcccccagacacacacacacacacacacacacacacacacacacac 3180
Qy 3181 ttcgctcctgagatgagac 3240
Db 3181 ttcgctcctgagatgagac 3240
Qy 3241 tgttggagacatgctgagctgagac 3300
Db 3241 tgttggagacatgctgagctgagac 3300
Qy 3301 ctgagagcagctgagagcagagatgagagcagatgagagcagatgagagcagatgagagcagatgag 3360
Db 3301 ctgagagcagctgagagcagagatgagagcagatgagagcagatgagagcagatgagagcagatgag 3360
Qy 3361 gcaagctggaagaagac 3420
Db 3361 gcaagctggaagaagac 3420
Qy 3421 ccttggccttgcctgagagatcagagctgagagctgagagctgagagctgagagctgagagctgag 3480
Db 3421 ccttggccttgcctgagagatcagagctgagagctgagagctgagagctgagagctgagagctgag 3480
Qy 3481 acccttaccacagagagagatgagagcagctgagagcagctgagagcagctgagagcagctgagag 3540
Db 3481 acccttaccacagagagagatgagagcagctgagagcagctgagagcagctgagagcagctgagag 3540
Qy 3541 ttatctctctac 3600
Db 3541 ttatctctctac 3600
Qy 3601 tctccacatggaagcgt 3660
Db 3601 tctccacatggaagcgt 3660
Qy 3661 caggttacttaccac 3720
Db 3661 caggttacttaccac 3720
Qy 3721 acagtagtagcagctgt 3780
Db 3721 acagtagtagcagctgt 3780
Qy 3781 atgctgagcctgagagac 3840
Db 3781 atgctgagcctgagagac 3840

Db 10381 aa 10440
 QY 10441 aa 10442
 Db 10441 aa 10442

RESULT 2

AAF24702
 ID AAF24702 standard; DNA; 10442 BP.

XX AAF24702;

XX 20-APR-2001 (first entry)

XX Nucleotide sequence of a human ABC1 polypeptide.

XX Human: adenosine triphosphate binding cassette protein 1; ABC1;

KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;

KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;

XX atherosclerosis; cholesterol transport; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 291..7076

XX /tag= a

XX /product= "ABC1 polypeptide"

XX WO20078971-A2.

XX 28-DEC-2000.

XX 16-JUN-2000; 2000WO-US16591.

XX 18-JUN-1999; 99US-0140264.

XX 14-SEP-1999; 99US-0153872.

XX 19-NOV-1999; 99US-0166573.

XX (CVNH-) CV THERAPEUTICS INC.

XX (UNIV) UNIV WASHINGTON.

XX Lawn RM, Wade D, Oram JF, Garvin M;

XX MPI; 2001-137811/14.

XX P-PSDB; AAB31365.

XX Adenosine triphosphate (ATP) binding cassette protein (ABC) 1

XX polynucleotides and polypeptides, useful for treatment of heart disease

XX PT and other disorders associated with hypercholesterolemia and

XX atherosclerosis -

XX Claim 3; Page 117-123; 211pp; English.

XX The present sequence encodes a human adenosine triphosphate (ATP)

XX binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell

XX membranes and utilizes ATP hydrolysis to transport a wide variety of

XX substrates across the plasma membrane. ABC1 is a pivotal protein in

XX the apolipoprotein-mediated mobilisation of intracellular cholesterol

XX stores. ABC1 is defective in Tangier disease, a genetic disorder

XX characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is

XX localised to chromosome 9q22-9q31. The ABC1 genes and proteins are

XX useful for developing pharmaceutical agents for the treatment of heart

XX disease and other disorders associated with hypercholesterolemia and

XX atherosclerosis. The genes are useful for developing screening assays to

XX screen for compounds that regulate the expression of genes associated

XX with cholesterol transport. The genes and proteins are also useful for

XX are also useful as diagnostic indicators of cardiovascular disease and

XX other disorders associated with hypercholesterolemia.

XX Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match 100.0%; Score 10438; DB 22; Length 10442;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 10442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggcggagaccgagagccgagccgacccctctctccgggctgcygcaaggcggcg 60
 Db 1 ggcggagaccgagagccgagccgacccctctctccgggctgcygcaaggcggcg 60
 QY 61 ggaagtcgcgcgacacacagagagccggttctcaggcgcttgctccctgttttcccg 120
 Db 61 ggaagtcgcgcgacacacagagagccggttctcaggcgcttgctccctgttttcccg 120
 QY 121 gtctgtttctccctctccggaagcgtgttcaagggttagagaaagagacgcaac 180
 Db 121 gtctgtttctccctctccggaagcgtgttcaagggttagagaaagagacgcaac 180
 QY 181 acaaaagtgaacacagttatgacccagccagcgctccctgtgagctctggcgcg 240
 Db 181 acaaaagtgaacacagttatgacccagccagcgctccctgtgagctctggcgcg 240
 QY 241 tgcctccagggctccgagccacacgctggcgctgtgctgtagggagacatgctgt 300
 Db 241 tgcctccagggctccgagccacacgctggcgctgtgctgtagggagacatgctgt 300
 QY 301 ggcctcagctgaggttgcctgtgtaggaagacccctacttcagaagagacacatgtc 360
 Db 301 ggcctcagctgaggttgcctgtgtaggaagacccctacttcagaagagacacatgtc 360
 QY 361 agctgtactgtaggtgctgctgtctattatcttctcgtatcctgtctgtcgcg 420
 Db 361 agctgtactgtaggtgctgctgtctattatcttctcgtatcctgtctgtcgcg 420
 QY 421 tgaagctaccacccatgaacacacatgacatgacatttccaaataaagcctgtc 480
 Db 421 tgaagctaccacccatgaacacacatgacatgacatttccaaataaagcctgtc 480
 QY 481 caggaacacttccctgtggttcagggatctatctgaagcaaacacccctgttcgt 540
 Db 481 caggaacacttccctgtggttcagggatctatctgaagcaaacacccctgttcgt 540
 QY 541 accgcagctcctgggagcctccggagctgttggaacttaacaatcattgtgctc 600
 Db 541 accgcagctcctgggagcctccggagctgttggaacttaacaatcattgtgctc 600
 QY 601 gctgttctcagatgctcggagcgtcttatacaagccagaagacccagcatgaag 660
 Db 601 gctgttctcagatgctcggagcgtcttatacaagccagaagacccagcatgaag 660
 QY 661 acatgcgcaaaattctggaacattacagcagatcaaaatccagctcaacttgaagc 720
 Db 661 acatgcgcaaaattctggaacattacagcagatcaaaatccagctcaacttgaagc 720
 QY 721 ttaagattcctgtgtagacaatgaaccttctgtggttccctatatcaaacctctc 780
 Db 721 ttaagattcctgtgtagacaatgaaccttctgtggttccctatatcaaacctctc 780
 QY 781 tcccaagttactcttgtagacaagatgctgagggcgtgagatcttccacaagttatt 840
 Db 781 tcccaagttactcttgtagacaagatgctgagggcgtgagatcttccacaagttatt 840
 QY 841 tgaagagctaccagttacatttgacaagctgtggaatgagatcaaatcagaagatga 900
 Db 841 tgaagagctaccagttacatttgacaagctgtggaatgagatcaaatcagaagatga 900
 QY 901 ttaactgtgtagcaagaagtcttgagcttggccttaccagaaggaactgtgtc 960
 Db 901 ttaactgtgtagcaagaagtcttgagcttggccttaccagaaggaactgtgtc 960
 QY 961 cagcagagagagtagctgttccacatgagacatcccttgaagcactaa 1020
 Db 961 cagcagagagagtagctgttccacatgagacatcccttgaagcactaa 1020
 QY 1021 acttaccatctccttcccgagcaaggagctgtgtagcagcaaaacattgtcgtata 1080

Db 1021 actcaatccctccctcccgagcaagagctgctgaaagcccaaaaacatgtctgata 1080
Qy 1081 gtcttggaactctgcccagaagctgttcaagcatgaaagctgagtgacatgccaag 1140
Db 1081 gtcttggaactctgcccagaagctgttcaagcatgaaagctgagtgacatgccaag 1140
Qy 1141 agtgaatcttctgaacaaatgtaacagctccagctccctcccaacaaatccaaagctg 1200
Db 1141 agtgaatcttctgaacaaatgtaacagctccagctccctcccaacaaatccaaagctg 1200
Qy 1201 tgtctgatttctgctgggcatcccgagagaggggctgaaagataaagcttccaaact 1260
Db 1201 tgtctgatttctgctgggcatcccgagagaggggctgaaagataaagcttccaaact 1260
Qy 1261 ggtatgaggaacaaacaaacaaagcctcttggagagcaatgagctgaggaagaatgctg 1320
Db 1261 ggtatgaggaacaaacaaacaaagcctcttggagagcaatgagctgaggaagaatgctg 1320
Qy 1321 aaactctatgacaactcaactcaactctactctactctgaatgttgaatgaatltgagt 1380
Db 1321 aaactctatgacaactcaactcaactctactctgaatgttgaatgaatltgagt 1380
Qy 1381 ctgaatctcttcccgcaatctggaagagctcgaagcgcgtctgctggtggagaatcc 1440
Db 1381 ctgaatctcttcccgcaatctggaagagctcgaagcgcgtctgctggtggagaatcc 1440
Qy 1441 tgtataacccctgacaactcccaagcgaagcagtcagtcagtgagtgaaacagacttcc 1500
Db 1441 tgtataacccctgacaactcccaagcgaagcagtcagtcagtgagtgaaacagacttcc 1500
Qy 1501 aggaactgctgctgttccatgatctggaagagcagtggaagagcaatccagcccaagatc 1560
Db 1501 aggaactgctgctgttccatgatctggaagagcagtggaagagcaatccagcccaagatc 1560
Qy 1561 ggaactcctcagtgaggaacagcccaagaaatggaactgtccggatgctgtggaacagag 1620
Db 1561 ggaactcctcagtgaggaacagcccaagaaatggaactgtccggatgctgtggaacagag 1620
Qy 1621 acaatgacacacttctgggaacagcagctggaatgtggaatgtggaacagcaagacatc 1680
Db 1621 acaatgacacacttctgggaacagcagctggaatgtggaatgtggaacagcaagacatc 1680
Qy 1681 tggcgttcttggccaagcaacccagaagatgctccagctcaatgctgtctgttacaact 1740
Db 1681 tggcgttcttggccaagcaacccagaagatgctccagctcaatgctgtctgttacaact 1740
Qy 1741 ggaagaagaacttcaagaagacttaacaggaactcaacagcaatccggaacatatactcgttcaatgagt 1800
Db 1741 ggaagaagaacttcaagaagacttaacaggaactcaacagcaatccggaacatatactcgttcaatgagt 1800
Qy 1801 gctcaacactgaaacaaagctagaacccaatagaacagaagctgctcatcaacaagaatcca 1860
Db 1801 gctcaacactgaaacaaagctagaacccaatagaacagaagctgctcatcaacaagaatcca 1860
Qy 1861 tggagctgctgagtgaggaagaaatcttctgggctgtgtatgtgttcaactggaattactccag 1920
Db 1861 tggagctgctgagtgaggaagaaatcttctgggctgtgtatgtgttcaactggaattactccag 1920
Qy 1921 gcaacatctgagctggcccatcagtgtaagtgacaagatccgaatgagacattggaacaatgtg 1980
Db 1921 gcaacatctgagctggcccatcagtgtaagtgacaagatccgaatgagacattggaacaatgtg 1980
Qy 1981 agaggaacaaataaatacaagatgagtgactggaagcctgtgctcctgagctgaccccttgg 2040
Db 1981 agaggaacaaataaatacaagatgagtgactggaagcctgtgctcctgagctgaccccttgg 2040
Qy 2041 aggaacatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2100
Db 2041 aggaacatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2100
Qy 2101 tcatcagagtgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2160
Db 2101 tcatcagagtgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2160
Qy 2161 atccctgttaacgttgaatgaacatcttctgagggtgagtgagccggtcaatgcccccttca 2220
Db 2161 atccctgttaacgttgaatgaacatcttctgagggtgagtgagccggtcaatgcccccttca 2220
Qy 2221 tgaactgctgagcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2280
Db 2221 tgaactgctgagcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2280
Qy 2281 aggaacagcgtgaagaagaaacatgagcagatgagtgagcctggaacaaagcagatctgttta 2340
Db 2281 aggaacagcgtgaagaagaaacatgagcagatgagtgagcctggaacaaagcagatctgttta 2340
Qy 2341 gctggttcaatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2400
Db 2341 gctggttcaatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2400
Qy 2401 tgaagttaagaaacccgtgctgagcagtgagtgagtgagtgagtgagtgagtgagtgag 2460
Db 2401 tgaagttaagaaacccgtgagcagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2460
Qy 2461 tgttctgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2520
Db 2461 tgttctgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2520
Qy 2521 acctggcagcagcctgctgggagcagcagcagcagcagcagcagcagcagcagcagcagc 2580
Db 2521 acctggcagcagcctgctgggagcagcagcagcagcagcagcagcagcagcagcagcagc 2580
Qy 2581 gtagtgacatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2640
Db 2581 gtagtgacatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2640
Qy 2641 ctgagccttctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2700
Db 2641 ctgagccttctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2700
Qy 2701 tgcagtgaggaacaaacccgttgaagtgagtgagtgagtgagtgagtgagtgagtgag 2760
Db 2701 tgcagtgaggaacaaacccgttgaagtgagtgagtgagtgagtgagtgagtgagtgag 2760
Qy 2761 cgaatcccaatgaatgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2820
Db 2761 cgaatcccaatgaatgctgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2820
Qy 2821 ctgctcttccagcagcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2880
Db 2821 ctgctcttccagcagcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2880
Qy 2881 actggttctgagcagcagcagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2940
Db 2881 actggttctgagcagcagcagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2940
Qy 2941 cagaatctcagcagcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3000
Db 2941 cagaatctcagcagcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3000
Qy 3001 tggtaaaatctcaacagcagcagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3060
Db 3001 tggtaaaatctcaacagcagcagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3060
Qy 3061 atgagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3120
Db 3061 atgagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3120
Qy 3121 caatccctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3180
Db 3121 caatccctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3180
Qy 3181 ttcgctctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3240
Db 3181 ttcgctctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3240

Db 5401 tcttggaatgtgcaattagctgtccctgcacacatgctgcatattatcatcttcacgtc 5460
Qy 5461 tccagcagaagctctatgtgtccctccacacatctgcctgtgctagcccttctacttgc 5520
Db 5461 tccagcagaagctctatgtgtccctccacacatctgcctgtgctagcccttctacttgc 5520
Qy 5521 tgtatggtgtgcatcaacacatctcatgtacccagccctctgtgttcaagaatccca 5580
Db 5521 tgtatggtgtgcatcaacacatctcatgtacccagccctctgtgttcaagaatccca 5580
Qy 5581 gcaacagcctatgtgtgtctcaacagcgttgaacotcttcatttgcatatgtgcagctg 5640
Db 5581 gcaacagcctatgtgtgtctcaacagcgttgaacotcttcatttgcatatgtgcagctg 5640
Qy 5641 ccacactgtgtgagcgtgtctcaacacataagctgataatataatgatactctga 5700
Db 5641 ccacactgtgtgagcgtgtctcaacacataagctgataatataatgatactctga 5700
Qy 5701 agtcggtgtgtctcatctccacatcttgcctgtgagcagaggtctcatcgacatgta 5760
Db 5701 agtcggtgtgtctcatctccacatcttgcctgtgagcagaggtctcatcgacatgta 5760
Qy 5761 aaaaacggcgaatgctgcatgctctggaagaagtttgaggagatcgcttgttccat 5820
Db 5761 aaaaacggcgaatgctgcatgctctggaagaagtttgaggagatcgcttgttccat 5820
Qy 5821 tatcttggaactgtgtgagcagaacactctgcacatgacgttgaaggggtgtct 5880
Db 5821 tatcttggaactgtgtgagcagaacactctgcacatgacgttgaaggggtgtct 5880
Qy 5881 tcccatctactgttctgatacagatgatttctcatcaagccacagccctgtataagca 5940
Db 5881 tcccatctactgttctgatacagatgatttctcatcaagccacagccctgtataagca 5940
Qy 5941 agcatctcctctgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 6000
Db 5941 agcatctcctctgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 6000
Qy 6001 atgtgtgagcgcaggaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 6060
Db 6001 atgtgtgagcgcaggaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 6060
Qy 6061 agcggaaagcctgcctgtctgaacagatgttgcgttgagcattctcctgtgagcttgggc 6120
Db 6061 agcggaaagcctgcctgtctgaacagatgttgcgttgagcattctcctgtgagcttgggc 6120
Qy 6121 tccctggaggttaatgtgggctcggaataatcatcaacttcaagaatgttaacagagatacca 6180
Db 6121 tccctggaggttaatgtgggctcggaataatcatcaacttcaagaatgttaacagagatacca 6180
Qy 6181 ctgttaccagaagagatgctgttcccttaacaaatagtaacttatcatcaacataccagaag 6240
Db 6181 ctgttaccagaagagatgctgttcccttaacaaatagtaacttatcatcaacataccagaag 6240
Qy 6241 tacatcaagaacatgagctgactgcccctgattgtatgccaacacagagctgttgaactgga 6300
Db 6241 tacatcaagaacatgagctgactgcccctgattgtatgccaacacagagctgttgaactgga 6300
Qy 6301 gagaaacagctgagatcttctgccttttgagagagatcccaagagaaagatgtggcaag 6360
Db 6301 gagaaacagctgagatcttctgccttttgagagagatcccaagagaaagatgtggcaag 6360
Qy 6361 ttggtgagctgagcagatctcggaactggtcgttgaagtaaggagaataatgactgtgta 6420
Db 6361 ttggtgagctgagcagatctcggaactggtcgttgaagtaaggagaataatgactgtgta 6420
Qy 6421 acctatgtgagcagcaaaaacagcaagctctctacagccatgcttgcagcgggctc 6480
Db 6421 acctatgtgagcagcaaaaacagcaagctctctacagccatgcttgcagcgggctc 6480
Qy 6481 ctgtggtgttctcgatgaacccaacagcatgatacccaagcccggttctgt 6540
Db 6481 ctgtggtgttctcgatgaacccaacagcatgatacccaagcccggttctgt 6540

Db 6481 ctgtggtgttctcgatgaacccaacagcatgatacccaagcccggttctgt 6540
Qy 6541 ggaattgtgccctaagtgttctcaaggaggagatcagtagtcttcatcatcatgta 6600
Db 6541 ggaattgtgccctaagtgttctcaaggaggagatcagtagtcttcatcatcatgta 6600
Qy 6601 tgaagaatgtgaagctcttgcactagatgcatgaatgaatgaatgaatgaatgaatgaat 6660
Db 6601 tgaagaatgtgaagctcttgcactagatgcatgaatgaatgaatgaatgaatgaatgaat 6660
Qy 6661 gccctggcagtgctcagcatctaaataaagtttgagatgttatacaatagtgtac 6720
Db 6661 gccctggcagtgctcagcatctaaataaagtttgagatgttatacaatagtgtac 6720
Qy 6721 gaataagcaggtgcccaacccggagcctggaagcctgtccagatcttcttgacttgatc 6780
Db 6721 gaataagcaggtgcccaacccggagcctggaagcctgtccagatcttcttgacttgatc 6780
Qy 6781 ctggaagtgtctaaagaagaacacaggaacatgctacaataccagcttccatctcat 6840
Db 6781 ctggaagtgtctaaagaagaacacaggaacatgctacaataccagcttccatctcat 6840
Qy 6841 tatcttctgcagcagatattcaacatctctccagagaaagaagcactccacatag 6900
Db 6841 tatcttctgcagcagatattcaacatctctccagagaaagaagcactccacatag 6900
Qy 6901 aagactactctgttctcagacaacacttgacaaagtattgtgaacttgcagaagcc 6960
Db 6901 aagactactctgttctcagacaacacttgacaaagtattgtgaacttgcagaagcc 6960
Qy 6961 aagatgatagtacacacttaaaagcctctcatcaacaaaacagacagatgtgagc 7020
Db 6961 aagatgatagtacacacttaaaagcctctcatcaacaaaacagacagatgtgagc 7020
Qy 7021 ttgcagttctcagcatcttctcagcagatggaagaagttaagaagcagatgtatgaagaa 7080
Db 7021 ttgcagttctcagcatcttctcagcagatggaagaagttaagaagcagatgtatgaagaa 7080
Qy 7081 tccgtgtcaaggggtgtgtgtgaagaatgaagaagcacttcccttgcacatgtg 7140
Db 7081 tccgtgtcaaggggtgtgtgtgaagaatgaagaagcacttcccttgcacatgtg 7140
Qy 7141 aagctgtgtgagaaagacagcagatgtgattgtgaagaagttaaacctgatactgac 7200
Db 7141 aagctgtgtgagaaagacagcagatgtgattgtgaagaagttaaacctgatactgac 7200
Qy 7201 tgatactatcaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 7260
Db 7201 tgatactatcaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 7260
Qy 7261 gtccttctgaacatgtctgtatgtgctcagagtgaaagacttgatattttt 7320
Db 7261 gtccttctgaacatgtctgtatgtgctcagagtgaaagacttgatattttt 7320
Qy 7321 acctataactatgtgaactctatataggaaaccaaaggacatagttggaactaca 7380
Db 7321 acctataactatgtgaactctatataggaaaccaaaggacatagttggaactaca 7380
Qy 7381 ctt 7440
Db 7381 ctt 7440
Qy 7441 taatcatgcccagcatatttgatcaaaaatcaaaaaggaatgacatcccatcactaa 7500
Db 7441 taatcatgcccagcatatttgatcaaaaatcaaaaaggaatgacatcccatcactaa 7500
Qy 7501 gccatgcatgcccagcagatgttcccggtgacacatccatctgtggaatgagtg 7560
Db 7501 gccatgcatgcccagcagatgttcccggtgacacatccatctgtggaatgagtg 7560
Qy 7561 gccagatattatgtgccaagtttctcagaagatttgaagcaccatgtgtgcatgtc 7620
Db 7561 gccagatattatgtgccaagtttctcagaagatttgaagcaccatgtgtgcatgtc 7620

QY	8701	ccatlaaatctgacagtcctcaaatcttctctctccatccatgacaggaataa	8760
Db	8701	cccatlaaatctgacagtcctcaaatcttctctctccatccatgacaggaataa	8760
QY	8761	taaaacaacaatctccatctgagcatcttctcaagcttctcaaccagctctatt	8820
Db	8761	taaaacaacaatctccatccatctgagcatcttctcaagcttctcaaccagctctatt	8820
QY	8821	ttctcagtcagtaaacatttgttaaaaatacgtttccataactactgtaactgct	8880
Db	8821	ttctcagtcagtaaacatttgttaaaaatacgtttccataactactgtaactgct	8880
QY	8881	tggagagaagaagaaaaataatgagagacatctgtgttgggaagttaagtgcttccat	8940
Db	8881	tggagagaagaagaaaaataatgagagacatctgtgttgggaagttaagtgcttccat	8940
QY	8941	atcatctactactctccactcttcccaaatcttcaatataacgcaagctgtgaag	9000
Db	8941	atcatctactactctccactcttcccaaatcttcaatataacgcaagctgtgaag	9000
QY	9001	cttcagatcttcaaatlaactcttccatattttttaaatttaccagatatataacca	9060
Db	9001	cttcagatcttcaaatlaactcttccatattttttaaatttaccagatatataacca	9060
QY	9061	ctgctgtaaaaaagaaaaatgattgtgtttgagaagttaaagcaatattgattttaaat	9120
Db	9061	ctgctgtaaaaaagaaaaatgattgtgtttgagaagttaaagcaatattgattttaaat	9120
QY	9121	aagtaataaggaatcttcccaatataatgataagcatcggttgcaattaccagatc	9180
Db	9121	aagtaataaggaatcttcccaatataatgataagcatcggttgcaattaccagatc	9180
QY	9181	ttcaaaaaatacagaattatagaataatcttccctcaatttaattttucaaaatcaag	9240
Db	9181	ttcaaaaaatacagaattatagaataatcttccctcaatttaattttucaaaatcaag	9240
QY	9241	ttatggttccctcaatttactaaatcgtatcttaattccatatagtataactatga	9300
Db	9241	ttatggttccctcaatttactaaatcgtatcttaattccatatagtataactatga	9300
QY	9301	gcaactcttactcgttctcctcgatttcaagggcaattttaaaaaatcaaaaggac	9360
Db	9301	gcaactcttactcgttctcctcgatttcaagggcaattttaaaaaatcaaaaggac	9360
QY	9361	tgtgacattcttgaagaaaaacagcaattttaatcagatgtgaaggaccccttcgaa	9420
Db	9361	tgtgacattcttgaagaaaaacagcaattttaatcagatgtgaaggaccccttcgaa	9420
QY	9421	gctagaacaacatctatagttatatacatctcattataactggttacctttaaaatga	9480
Db	9421	gctagaacaacatctatagttatatacatctcattataactggttacctttaaaatga	9480
QY	9481	atttttcatcttccctggtgttaaacctaatctgtgtgagaatcttttaccactctact	9540
Db	9481	atttttcatcttccctggtgttaaacctaatctgtgtgagaatcttttaccactctact	9540
QY	9541	caatcaagcaaaattctctgatactccctgttgaatgttaacctatgtgattcagaat	9600
Db	9541	caatcaagcaaaattctctgatactccctgttgaatgttaacctatgtgattcagaat	9600
QY	9601	ctcaaaaatagtggttcaaaaattctgtccttttgcatcttttggacaacctcagaanaacta	9660
Db	9601	ctcaaaaatagtggttcaaaaattctgtccttttgcatcttttggacaacctcagaanaacta	9660
QY	9661	ttaaacaactgtgataatgagaataacagaaataataaagccctctataactaatgac	9720
Db	9661	ttaaacaactgtgataatgagaataacagaaataataaagccctctataactaatgac	9720
QY	9721	ccagacaattcatgtgttaaaaaacaacaacctcaactcgtatattcattatcgt	9780
Db	9721	ccagacaattcatgtgttaaaaaacaacaacctcaactcgtatattcattatcgt	9780
QY	9781	actgagaagcaaatgcttctgtgactataaatgttgacatacatcaatcactgataag	9840

|||||
Db 454 gggctacccacccctatgaaacaatgaaatgccaatttccaaataagcaatgcccctcgc 513
Qy 482 aggaacactctcttggttcgaaggattatctgtaatgccaaacccctgttccgtta 541
Db 514 aggaacactctcttggttcgaaggattatctgtaatgccaaacccctgttccgtta 573
Qy 542 cccgactcttgaggaggtcccgaggttggttgaaactttaacaatcatgttgctgc 601
Db 574 ccgaaactccggaggagcccgaggttggttgaaactttaacaatcatgttgctgc 633
Qy 602 ccgtttcaagatgctcgaaggctcttcttaacagccgaagaagcacagcatgaaga 661
Db 634 cctgtttcaagatgctcgaaggctcttcttaacagccgaagaagcacagcatgaaga 693
Qy 662 catgycgaagtcttgagacatltacagcagatcaagaatcccaagctcaacttgaagct 721
Db 694 catgycgaagtcttgagacatltacagcagatcaagaatcccaagctcaacttgaagct 753
Qy 722 tcaagattccctggttgagaaatgaaaccttctcgtgttccatatacaactctctct 781
Db 754 tcaagattccctggttgagaaatgaaaccttctcgtgttccatatacaactctctct 813
Qy 782 cccaaagtctactggtgagacaatgctgagggctgagtgcatcttcccaaggtatttt 841
Db 814 cccaaagtctactggtgagacaatgctgagggctgagtgcatcttcccaaggtatttt 873
Qy 842 gcaaggctacccagttacatlttgacaagtctgtgcaatgtagatcaaaaatcagaagatgat 901
Db 874 gcaaggctacccagttacatlttgacaagtctgtgcaatgtagatcaaaaatcagaagatgat 933
Qy 902 tcaacttggtgacaaagaagttcttgagtttggtgcttccaaaggaaagaaactgtgctgc 961
Db 934 tcaacttggtgacaaagaagttcttgagtttggtgcttccaaaggaaagaaactgtgctgc 993
Qy 962 agcagagcagatcactcgttccacaatgagacatccgaaagccaatccctagaacaactaa 1021
Db 994 agcagagcagatcactcgttccacaatgagacatccgaaagccaatccctagaacaactaa 1053
Qy 1022 ctctacatctcccttcccgagcaaggagctgctgtagaagcccaaaaaaatctgtgcatag 1081
Db 1054 ctctacatctcccttcccgagcaaggagctgctgtagaagcccaaaaaaatctgtgcatag 1113
Qy 1082 tctctggaactgtgcccgaagagctgttccagatgaagaactggaagtcgaatccgaaga 1141
Db 1114 tctctggaactgtgcccgaagagctgttccagatgaagaactggaagtcgaatccgaaga 1173
Qy 1142 ggtgagttcttgacaatgtagaacagctccagctccctccacaacaaatctacagagctgt 1201
Db 1174 ggtgagttcttgacaatgtagaacagctccagctccctccacaacaaatctacagagctgt 1233
Qy 1202 gttctgtatgtctgcgggcatcccgaggagggtgcggaagatcaagtctctcaactg 1261
Db 1234 gttctgtatgtctgcgggcatcccgaggagggtgcggaagatcaagtctctcaactg 1293
Qy 1262 gttctgaggaacaacacacacacccctcttcttgaggcaatgtagcagtcgaagaatctcta 1321
Db 1294 gttctgaggaacaacacacacacccctcttcttgaggcaatgtagcagtcgaagaatctcta 1353
Qy 1322 aaactctatgacaactctacaactcccttacttgacaatgtttagaagaatlttgagctc 1381
Db 1354 aaactctatgacaactctacaactcccttacttgacaatgtttagaagaatlttgagctc 1413
Qy 1382 tagtcccttctccgcatatcttgaaagctcgaagccggtcgtctgttggggaagctct 1441
Db 1414 tagtcccttctccgcatatcttgaaagctcgaagccggtcgtctgttggggaagctct 1473
Qy 1442 gtataacccgagacatccacacaaagcgagtcagtgctgagagtgaaacaagccttcca 1501
Db 1474 gtataacccgagacatccacacaaagcgagtcagtgctgagagtgaaacaagccttcca 1533
Qy 1502 gtaactgctgtgttccatgactggaagcagtggtggaagaaactcaagcccaagatctg 1561
|||||

Db 1534 gtaactgctgtgttccatgactcgaagcagtggtggaagaaactcaagcccaagatctg 1593
Qy 1562 gactttatgagaacagccagaagaatggaactgttccggatgctgttggacagcaagga 1621
Db 1594 gactttatgagaacagccagaagaatggaactgttccggatgctgttggacagcaagga 1653
Qy 1622 caatgacacacttctgggaacagcagcttgatgctcttaagttgagcaagcccaagacatct 1681
Db 1654 caatgacacacttctgggaacagcagcttgatgctcttaagttgagcaagcccaagacatct 1713
Qy 1682 ggcgttlttggccaagcaccagaagatgtccagttccagttaaatggtctgttaccctg 1741
Db 1714 ggcgttlttggccaagcaccagaagatgtccagttccagttaaatggtctgttaccctg 1773
Qy 1742 gagagaagcttccaacgagatccaacgggaatcccgaaatcatctcgtctcatgaggtg 1801
Db 1774 gagagaagcttccaacgagatccaacgggaatcccgaaatcatctcgtctcatgaggtg 1833
Qy 1802 tgtcaacctgacaagctagaaacccatagacaagaagctggtctcatcaacaagtccat 1861
Db 1834 tgtcaacctgacaagctagaaacccatagacaagaagctggtctcatcaacaagtccat 1893
Qy 1862 ggaagctgtgagtagaagaaagctctggtcgtgatatgtgttcaactggaattactccag 1921
Db 1894 ggaagctgtgagtagaagaaagctctggtcgtgatatgtgttcaactggaattactccag 1953
Qy 1922 cagcatltgagctgccccatcatgttcaagttacaagaatccgaatlgacatltgacaatgtgga 1981
Db 1954 cagcatltgagctgccccatcatgttcaagttacaagaatccgaatlgacatltgacaatgtgga 2013
Qy 1982 gaggacaataaatacaagatgtggtgactggaagctgtgctctcgaagctgaaccccttga 2041
Db 2014 gaggacaataaatacaagatgtggtgactggaagctgtgctctcgaagctgaaccccttga 2073
Qy 2042 ggaacatgagtaagctctggtgggggtcttcgactacttgcaggaatgtgtgtggaagcaat 2101
Db 2074 ggaacatgagtaagctctggtgggggtcttcgactacttgcaggaatgtgtgtggaagcaat 2133
Qy 2102 catcaggtgtctggaagggcaccggaagaagaactggtctcatatgacaagatgccccta 2161
Db 2134 catcaggtgtctggaagggcaccggaagaagaactggtctcatatgacaagatgccccta 2193
Qy 2162 tccctgttaagttgatacatcttctcgggtgtatgtagagccggtcaatgtccccttcat 2221
Db 2194 tccctgttaagttgatacatcttctcgggtgtatgtagagccggtcaatgtccccttcat 2253
Qy 2222 gaagctgtgctggaattactcaatgagctgtatcatcaagggcatgtgtatggaagga 2281
Db 2254 gaagctgtgctggaattactcaatgagctgtgtatcatcaagggcatgtgtatggaagga 2313
Qy 2282 ggcagagctggaagaagacatgagcagatcatgagccttgacaacagacatctggttag 2341
Db 2314 ggcagagctggaagaagacatgagcagatcatgagccttgacaacagacatctggttag 2373
Qy 2342 ctggttcatatgtaagcccatctctctctgtgtagcgctggtcgtgtagtgtcatcct 2401
Db 2374 ctggttcatatgtaagcccatctctctctgtgtagcgctggtcgtgtagtgtcatcct 2433
Qy 2402 gaagttaggaacccgctgcgccttaagatgataccagcggtgtgtgtgtcttccgttcgt 2461
Db 2434 gaagttaggaacccgctgcgccttaagatgataccagcggtgtgtgtgtcttccgttcgt 2493
Qy 2462 gtttctgtgtgtgacaatccctgacgtctccgtatgtagacacactctctccagaagccaa 2521
Db 2494 gtttctgtgtgtgacaatccctgacgtctccgtatgtagacacactctctccagaagccaa 2553
Qy 2522 cctggaagcagctgttggtgggcatcatctacttcaagctgtactgtccctacgtcgtgtg 2581
Db 2554 cctggaagcagctgttggtgggcatcatctacttcaagctgtactgtccctacgtcgtgtg 2613
Qy 2582 tgttgcatgagcagagctatggtgttcaactcaagaatcttggctagcgtcgtgtccc 2641
Db 2614 tgttgcatgagcagagctatggtgttcaactcaagaatcttggctagcgtcgtgtccc 2673
|||||

QY 2642 tttgtgcttttggttttggtcgtgagtaacttgccttttttgagagcaaggcaattgagt 2701
Db 2674 ttgtgtcttttggttttggtcgtgagtaacttgccttttttgagagcaaggcaattgagt 2733
QY 2702 gcaagtggacaacgtgttttagagtcctgtgtgaggaagatggtcttaactcaccacttc 2761
Db 2734 gcaagtggacaacgtgttttagagtcctgtgtgaggaagatggtcttaactcaccacttc 2793
QY 2762 gatctccaatgactgttttgacaacttcctctatgtgggttgatgaaactgtgtacattgagac 2821
Db 2794 gatctccaatgactgttttgacaacttcctctatgtgggttgatgaaactgtgtacattgagac 2853
QY 2822 tttctttccagggccaggaatctcccaagccctgtgtatcttctcttgacaagaagcccta 2881
Db 2854 tttctttccagggccaggaatctcccaagccctgtgtatcttctcttgacaagaagcccta 2913
QY 2882 ctggtttgaggaagatgatagagaagcccaactgtgtttccaacagagaagatgtc 2941
Db 2914 ctggtttgaggaagatgatagagaagcccaactgtgtttccaacagagaagatgtc 2973
QY 2942 agaaatctgataaggaaggaagaaaccccaacttgaaagctgggagctgtccattcagaacct 3001
Db 2974 agaaatctgataaggaaggaagaaaccccaacttgaaagctgggagctgtccattcagaacct 3033
QY 3002 ggtcaaaagctacagagatgaga tgaaggtgtcgtcgtatgagcttgagcaatgaatttta 3061
Db 3034 ggtcaaaagctacagagatgaga tgaaggtgtcgtcgtatgagcttgagcaatgaatttta 3093
QY 3062 tgaaggccagatacactcctctcttgagcaaca tgaagcgagggaagacagaccatactc 3121
Db 3094 tgaaggccagatacactcctctcttgagcaaca tgaagcgagggaagacagaccatactc 3153
QY 3122 aatcccgaaacgggtttttcccccaagcctcgggcaaccgctatactcttgaggaaagacct 3181
Db 3154 aatcccgaaacgggtttttcccccaagcctcgggcaaccgctatactcttgaggaaagacct 3213
QY 3182 tgcctctgagatgagacacatccggcagagaactggtgggtgtgtccccaacataacgtgtc 3241
Db 3214 tgcctctgagatgagacacatccggcagagaactggtgggtgtgtccccaacataacgtgtc 3273
QY 3242 gtttgacatgctgactcgtcgtgaagaacacatctgtgtctctatgcgcgcttgaaagggtctc 3301
Db 3274 gtttgacatgctgactcgtcgtgaagaacacatctgtgtctctatgcgcgcttgaaagggtctc 3333
QY 3302 tgaagaagcagtgaaagcgagagatgagacagatggccctggatgtgtgttcacatcaag 3361
Db 3334 tgaagaagcagtgaaagcgagagatgagacagatggccctggatgtgtgttcacatcaag 3393
QY 3362 caagctgaaagaaagcaaacagacagctgtcaggtggaatgacagagaagactatctgtgac 3421
Db 3394 caagctgaaagaaagcaaacagacagctgtcaggtggaatgacagagaagactatctgtgac 3453
QY 3422 ctgtgacctgttcgggggagatcaaggtgtcattctgatacccaagctgtgtgga 3481
Db 3454 ctgtgacctgtgtcgggggagatcaaggtgtcattctgatacccaagctgtgtgga 3513
QY 3482 ccccttactccgagaggagatatggagctgtctgtcgaataacgacaagggccagacat 3541
Db 3514 ccccttactccgagaggagatatggagctgtctgtcgaataacgacaagggccagacat 3573
QY 3542 tattctcttaacacacacatgagatgaaagcgagctcctgtgggagacagatgtccatcat 3601
Db 3574 tattctcttaacacacacatgagatgaaagcgagctcctgtgggagacagatgtccatcat 3633
QY 3602 ctcccaatgagaagctgtgtgtgtgtgtgtgtcctcctcctgtttctgaagaacagctvggaac 3661
Db 3634 ctcccaatgagaagctgtgtgtgtgtgtgtgtcctcctcctgtttctgaagaacagctvggaac 3693
QY 3662 aggtactactccagactgtgtcaagaagaatgtgaaatcctccctcagttccttgagaa 3721
Db 3694 aggtactactccagactgtgtcaagaagaatgtgaaatcctccctcagttccttgagaa 3753
QY 3722 cagtagtagcaactgtgtatactccgaaaaaggaagacagtggtttctcaagacattctga 3781
Db 3754 cagtagtagcaactgtgtatactccgaaaaaggaagacagtggtttctcaagacattctga 3813
QY 3782 tgtgtgctgggcaagcagacatgaaagatgacacgtcagctacatgattctgtctatctc 3841
Db 3814 tgtgtgctgggcaagcagacatgaaagatgacacgtcagctacatgattctgtctatctc 3873
QY 3842 caactctcaaggaagcatgtgtctgaaagcccggtcgtgtgaaagacataagggcatgact 3901
Db 3874 caactctcaaggaagcatgtgtctgaaagcccggtcgtgtgaaagacataagggcatgact 3933
QY 3902 gaactatgtctgcacataagaaagctgtcgaaggaagggactttgtgaaactcttcatga 3961
Db 3934 gaactatgtctgcacataagaaagctgtcgaaggaagggactttgtgaaactcttcatga 3993
QY 3962 gatgatgacgggtcctcagacacttgagacttctagatgatgacatccagagacacct 4021
Db 3994 gatgatgacgggtcctcagacacttgagacttctagatgatgacatccagagacacct 4053
QY 4022 ggaagaataatctctcaaggtgtgcccgaagagatggtgggttgatgactcagatgag 4081
Db 4054 ggaagaataatctctcaaggtgtgcccgaagagatggtgggttgatgactcagatgag 4113
QY 4082 tactctgcagcaagacgaacaaagcgagctctggggagacaagaagctgtcttgccc 4141
Db 4114 tactctgcagcaagacgaacaaagcgagctctggggagacaagaagctgtcttgccc 4173
QY 4142 gtccaatgaaatgatagtgtctgtatccaatgatactcgtacataaaccacaatccaaga 4201
Db 4174 gtccaatgaaatgatagtgtctgtatccaatgatactcgtacataaaccacaatccaaga 4233
QY 4202 gacagactgtctcagtgagatgagatgagcaaaaggtcctaccaggtgaaagctgtgaact 4261
Db 4234 gacagactgtctcagtgagatgagatgagcaaaaggtcctaccaggtgaaagctgtgaact 4293
QY 4262 tacacaagaacagttgtgtgagccctttgtgaaagaagactctaattgccagaagatcag 4321
Db 4294 tacacaagaacagttgtgtgagccctttgtgaaagaagactctaattgccagaagatcag 4353
QY 4322 gaaaggaattttgtcctcaagatgtctgtcagcagctgtgtgtgtcgtacatgtccctgtgt 4381
Db 4354 gaaaggaattttgtcctcaagatgtctgtcagcagctgtgtgtgtcgtacatgtccctgtgt 4413
QY 4382 cagctgtgtgtcagacccctttggcaagatgaccccaagccttgaaacttaagccctgagatga 4441
Db 4414 cagctgtgtgtcagacccctttggcaagatgaccccaagccttgaaacttaagccctgagatga 4473
QY 4442 caacgaagaatgacacattgtgacgaacatgatactcctgagagacacggaaacccctgagat 4501
Db 4474 caacgaagaatgacacattgtgacgaacatgatactcctgagagacacggaaacccctgagat 4533
QY 4502 cttaaaagcctcaacaaagaacccctgtcggagacccgctgtatgtgaaagaaacccaat 4561
Db 4534 cttaaaagcctcaacaaagaacccctgtcggagacccgctgtatgtgaaagaaacccaat 4593
QY 4562 cccagacaacggcctcgtcgaagcgaggaggagatggaacacatggcccaattccccagac 4621
Db 4594 cccagacaacggcctcgtcgaagcgaggaggagatggaacacatggcccaattccccagac 4653
QY 4622 catcatggaactctctcaagaatggaactggaacatgtcagaacacccctcaactcatgacca 4681
Db 4654 catcatggaactctctcaagaatggaactggaacatgtcagaacacccctcaactcatgacca 4713
QY 4682 gtgtagcagcgacaataatcaagaagatgtcgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4741
Db 4714 gtgtagcagcgacaataatcaagaagatgtcgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4773
QY 4742 ggcctcccaaaaagaaacaaaacatgagatalccttcagagactcagcaagaaagaa 4801
Db 4774 ggcctcccaaaaagaaacaaaacatgagatalccttcagagactcagcaagaaagaa 4833
QY 4802 cattcgatgatctgtgtgaagacgtatgtcagatcatagccaagaagcttaagaacaa 4861

Db	4834	 catttcggatlaatccggtgaaagcgtatgacagatcaatagccaaagcttaagaacaa	4893
Qy	4862	gattctggagaaatgaatttaagtaatgagcgcgtcttccttggtgtcgaataactaacg	4921
Db	4894	gattctgggtgaattgatttagatgagcgcgtcttccttggtgtcgaataactaacg	4933
Qy	4922	actctctccgagtaagaagttaatgataatcaacaatagaagaacacttaagct	4981
Db	4954	actctctccgagtaagaagttaatgataatcaacaatagaagaacacttaagct	5013
Qy	4982	ggccaaggaacagttcttgacagatcgattctccaacagcttgggaagattatgacagact	5041
Db	5014	ggccaaggaacagttcttgacagatcgattctccaacagcttgggaagattatgacagact	5073
Qy	5042	ggacaacgaagaaatgtaacaggtgtgtgttcaataacaagggtgcgtatgaatcagctc	5101
Db	5074	ggacaacgaagaaatgtaacaggtgtgtgttcaataacaagggtgcgtatgaatcagctc	5133
Qy	5102	ttctctgaatgtaacaaatgacatctctccgggccaacctgtgcaaaagggaagaaacc	5161
Db	5134	ttctctgaatgtaacaaatgacatctctccgggccaacctgtgcaaaagggaagaaacc	5193
Qy	5162	tagccattatggaattactgtcttcaatcatcccttgaaatctccaacgaagcagctctc	5221
Db	5194	tagccattatggaattactgtcttcaatcatcccttgaaatctccaacgaagcagctctc	5253
Qy	5222	aagaggtgctcgcgaatgacacatcaatcaatgagatgtgtgtcgaatctgtgtacatcttg	5281
Db	5254	aagaggtgctcgcgaatgacacatcaatcaatgagatgtgtgtcgaatctgtgtacatcttg	5313
Qy	5282	aatgtccttcgtccacgacagacttgtcgtatctctgaatccagaagcgggtcgaacagc	5341
Db	5314	aatgtccttcgtccacgacagacttgtcgtatctctgaatccagaagcgggtcgaacagc	5373
Qy	5342	aaaaaacctgcgaatcgaatgagatgagagcctgtcaactactatggtctcttaattgt	5401
Db	5374	aaaaaacctgcgaatcgaatgagatgagagcctgtcaactactatggtctcttaattgt	5433
Qy	5402	ctgggatatgtgcaattacgtgtgtccctgcacacatggtcaattactctctcatctgtc	5461
Db	5434	ctgggatatgtgcaattacgtgtgtccctgcacacatggtcaattactctctcatctgtc	5493
Qy	5462	ccagcagaagatcctaagtgtccctccacaacatctgcctgtgtgaaccccttaacttgc	5521
Db	5494	ccagcagaagatcctaagtgtccctccacaacatctgcctgtgtgaaccccttaacttgc	5553
Qy	5522	gtatgggtggatcaatacaacctctcaatgtaacccagcctcttgtgttcaagatccccag	5581
Db	5554	gtatgggtggatcaatacaacctctcaatgtaacccagcctcttgtgttcaagatccccag	5613
Qy	5582	cacaacatgtgtgtgtccacacagcgtgaacacttctatgtgacatgaattatggcagcgtgc	5641
Db	5614	cacaacatgtgtgtgtccacacagcgtgaacacttctatgtgacatgaattatggcagcgtgc	5673
Qy	5642	caacttgtgtgtggaagctgttaccacgaacaataagctgaataataataatgataatcctgaa	5701
Db	5674	caacttgtgtgtggaagctgttaccacgaacaataagctgaataataataatgataatcctgaa	5733
Qy	5702	gtccgtgttcttgatcttccacaatttttgcctgggaacgaggtctcatcgacatgvgaa	5761
Db	5734	gtccgtgttcttgatcttccacaatttttgcctgggaacgaggtctcatcgacatgvgaa	5793
Qy	5762	aaacaaaggaatgtgtgaatgcccctggaaaggtttggggagaatctgttgttacaat	5821
Db	5794	aaacaaaggaatgtgtgaatgcccctggaaaggtttggggagaatctgttgttacaat	5853
Qy	5822	atcttgggaacttgtgtgagcaaaacctcttcgccaatgagcgttgaaggggtgtgtctt	5881
Db	5854	atcttgggaacttgtgtgagcaaaacctcttcgccaatgagcgttgaaggggtgtgtctt	5913
Qy	5882	cctcaattactgttctgatacagatcttcatcaaggcccaagactgttaaatgcaaa	5941
Db	5914	cctcaattactgttctgatacagatcttcatcaaggcccaagactgttaaatgcaaa	5973
Qy	5942	gctatctcccttgaaatgataagatgaaatgttgagcggggaagaacagaatcttga	6001
Db	5974	gctatctcccttgaaatgataagatgaaatgttgagcggggaagaacagaatcttga	6033
Qy	6002	tgttggagggccaagatgacatcttgaagaatcaagaagatgtgacaagaatataagaagaa	6061
Db	6034	tgttggagggccaagatgacatcttgaagaatcaagaagatgtgacaagaatataagaagaa	6093
Qy	6062	gcggaagcctgtctgttgaacagatcttgcgttggcatctccctcgttgatgcttgggtc	6121
Db	6094	gcggaagcctgtctgttgaacagatcttgcgttggcatctccctcgttgatgcttgggtc	6153
Qy	6122	cctgggaagttaagggtgcggaaatctcaacttccaagtgttaacagaagatataccac	6181
Db	6154	cctgggaagttaagggtgcggaaatctcaacttccaagtgttaacagaagatataccac	6213
Qy	6182	tgttaccagaaggagatgtcttcttcaacaanaatagtatctatcaacatcgaat	6241
Db	6214	tgttaccagaaggagatgtcttcttcaacaanaatagtatctatcaacatcgaat	6273
Qy	6242	acatcagaacatggtgactgctccctcaagtttgaatgcatacagaagcgtgtgactvgag	6301
Db	6274	acatcagaacatggtgactgctccctcaagtttgaatgcatacagaagcgtgtgactvgag	6333
Qy	6302	agaaacacgtggaggttcttgcctttagaaggaatcccaagaagaagtgtgcaagt	6361
Db	6334	agaaacacgtggaggttcttgcctttagaaggaatcccaagaagaagtgtgcaagt	6393
Qy	6362	tgttgaatgagcgaatcggaaactgggcctcgttgaagatataagaanaatatgtcgtgaa	6421
Db	6394	tgttgaatgagcgaatcggaaactgggcctcgttgaagatataagaanaatatgtcgtgaa	6453
Qy	6422	ctataatggaagccaacaaacgcaagcctctacaagcatalggtcttgcgtgggcctcc	6481
Db	6454	ctataatggaagccaacaaacgcaagcctctctacaagcatalggtcttgcgtgggcctcc	6513
Qy	6482	tgtgtgttcttggaatgaaacccaacagggcatgatatcccaagcccggttcttgt	6541
Db	6514	tgtgtgttcttggaatgaaacccaacagggcatgatatcccaagcccggttcttgt	6573
Qy	6542	gaatttgcacctaaatgtgttcaaaaggaggatgacaaatgattgtcttaactcataat	6601
Db	6574	gaatttgcacctaaatgtgttcaaaaggaggatgacaaatgattgtcttaactcataat	6633
Qy	6602	ggaagaatgtgaagccttcttgacatagaatggaacatctgttcaatggaaggtccaagt	6661
Db	6634	ggaagaatgtgaagccttcttgacatagaatggaacatctgttcaatggaaggtccaagt	6693
Qy	6662	ccttggcagtggtccagactcttaaaaataggtttggaaatgtgtataaataagttgacg	6721
Db	6694	ccttggcagtggtccagactcttaaaaataggtttggaaatgtgtataaataagttgacg	6753
Qy	6722	aataagaggttccaaaccccggaacctgaagcctgttccagaattcttggacttgcattcc	6781
Db	6754	aataagaggttccaaaccccggaacctgaagcctgttccagaattcttggacttgcattcc	6


```

|||||
Db 9214 tcaaaatcacgaatttatagaataattccctccatttaatttccaaatcgaatf 9273
Qy 9242 tatgtttccctatttactaaatcgtatctatcttcattatagtaactatgag 9301
Db 9274 tatgtttccctatttactaaatcgtatcttcattatagtaactatgag 9333
Qy 9302 caaccctactcgttcctcctgatttcaagcgcatatttaaaaaacaaaggcact 9361
Db 9334 caaccctactcgttcctcctgatttcaagcgcatatttataaaatcaaaaggcact 9393
Qy 9362 gtgaactatttgaagaacacagacatttatacagattgaaggcctcttcgaag 9421
Db 9394 gtgaactatttgaagaacacagacatttatacagattgaaggcctcttcgaag 9453
Qy 9422 ctgagaacatctatagttatatacatctcattatacgtgttaccctttaaataagtaa 9481
Db 9454 ctgagaacatctatagttatatacatctcattatacgtgttaccctttaaataagtaa 9513
Qy 9482 tttttacatttccgtgtgaacctaattgtgtagaataatttaccactatactc 9541
Db 9514 tttttacatttccgtgtgaacctaattgtgtagaataatttaccactatactc 9573
Qy 9542 aatcaagcaaaattctgtatatactccctgtggaatgtacattgtgaattcagaattc 9601
Db 9574 aatcaagcaaaattctgtatatactccctgtggaatgtacattgtgaattcagaattc 9633
Qy 9602 tcaaaatacgtgtcnaaaatctcgtcttgcattcttggacacactcagaanaactat 9661
Db 9634 tcaaaatacgtgtcnaaaatctcgtcttgcattcttggacacactcagaanaactat 9693
Qy 9662 taacaactgtgaatagagaataacagaagaataaataaagccctctataataatagcc 9721
Db 9694 taacaactgtgaatagagaataacagaagaataaataaagccctctataataatagcc 9753
Qy 9722 caacacattcatgtttaaaaaaacacacacacacactacactatgtattcattctgta 9781
Db 9754 caacacattcatgtttaaaaaaacacacacacacactacactatgtattcattctgta 9813
Qy 9782 ctgaagcaaatgtcctgtgactataaagtgtgcacatcatcattcaactgtatagtaa 9841
Db 9814 ctgaagcaaatgtcctgtgactataaagtgtgcacatcatcattcaactgtatagtaa 9873
Qy 9842 tcatctactaaagcattcgtcgtgttctctcctgtgtgtnatatacgaataaata 9901
Db 9874 tcatctactaaagcattcgtcgtgttctctcctgtgtgtnatatacgaataaata 9933
Qy 9902 ttttccaaagcagctgtcattgataatactgaacccttgaatgtgagacattattg 9961
Db 9934 ttttccaaagcagctgtcattgataatactgaacccttgaatgtgagacattattg 9993
Qy 9962 gaccctgtgatactactagataaatacgtgaatactcgaataatctgtcctaattctt 10021
Db 9994 gaccctgtgatactactagataaatacgtgaatactcgaataatctgtcctaattctt 10053
Qy 10022 caaaatgttcaccccttaaaangttcatttccataagattagttgcttatccc 10081
Db 10054 caaaatgttcaccccttaaaangttcatttccataagattagttgcttatccc 10113
Qy 10082 ttcttataccctaaagatgaagctgttttgtcctttgttcatcatgtggccctatcc 10141
Db 10114 ttcttataccctaaagatgaagctgttttgtcctttgttcatcatgtggccctatcc 10173
Qy 10142 aagcacttaagctgtctgttaatgagatcattttgacatgtaataatcgtgaattgta 10201
Db 10174 aagcacttaagctgtctgttaatgagatcattttgacatgtaataatcgtgaattgta 10233
Qy 10202 aaactagacaaagattcacaaagatttctaagttaaatcatttcattaaagaagaa 10261
Db 10234 aaactagacaaagattcacaaagatttctaagttaaatcatttcattaaagaagaa 10293
Qy 10262 aagaanaaaatttgtatgtcaataacttataatgaagattaaatgcatatttctat 10321
|||||

```

```

Db 10294 aagaanaaaatttgtatgtcaataacttataatgaagttataaagtcatattctat 10353
Qy 10322 gtgttaataatagtcacaaataaagctgtgacagttctgtttaaaaaaaaaaaaaa 10381
Db 10354 gtgttaataatagtcacaaataaagctgtgacagttctgtttaaaaaaaaaaaaaa 10413
Qy 10382 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 10441
Db 10414 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 10473
Qy 10442 a 10442
Db 10474 a 10474

RESULT 4
AAF24686
ID AAF24686 standard; DNA; 10474 BP.
XX
AC AAF24686;
XX
DT 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW Apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW Chromosome 9q22-q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 323..7108
FT FT /tag=a
FT FT /product="defective ABC1 polypeptide"
XX
PN MO200078972-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000: 2000MO-US16765.
XX
PR 18-JUN-1999; 990S-0140264.
PR 14-SEP-1999; 990S-0153872.
PR 19-NOV-1999; 990S-0166573.
XX
PA (CVTH-) CV THERAPEUTICS INC.
XX
PI Lawn RM, Wade D, Garvin M;
XX
DR WPI: 2001-137812/14.
XX
PT Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT useful for the development of agents for the treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX
PS Disclosure: Page 170-176; 215pp: English.
XX
CC The present sequence encodes a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC ATP hydrolysis to transport a wide variety of substrates across the
CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC Tangier disease, a genetic disorder characterised by abnormal
CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC 9q22-q31. The ABC1 genes and proteins are useful for developing
CC pharmaceutical agents for the treatment of heart disease and other
CC disorders associated with hypercholesterolemia and atherosclerosis. The
CC genes are useful for developing screening assays to screen for compounds
CC that regulate the expression of genes associated with cholesterol

```

CC transport. The genes and proteins are also useful for are also useful
 CC as diagnostic indicators of cardiovascular disease and other disorders
 CC associated with hypercholesterolemia.

XX Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;

Query Match 99.9%; Score 10429; DB 22; Length 10474;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 10436; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

QY      2 ggcggagcccgagagccgagccgacccctctctccgggctgcgcaaggcgagcg 61
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      34 ggcagagccgagagccgagccgacccctctctccgggctgcgcaaggcgagcg 93
QY      62 ggcgctccgagccagagccgagcttccagggcgcttctctcttcttcccg 121
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      94 ggcctccgagccagcaagagccgcttccagggcgcttctctcttcttcccg 153
QY     122 tctgtttctccctctccggaagcttgcaggggtagagaaagagagcaaa 181
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     154 tctgtttctccctctccggaagcttgcaggggtagagaaagagagcaaa 213
QY     182 caaaagtgaaaaacattatagaccgcaacggcgctccctgcgtgagctcggcgct 241
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     214 caaaagtgaaaaacattatagaccgcaacggcgctccctgcgtgagctcggcgct 273
QY     242 gcttccagggctcccgagccacacgctggcgctgctgctgagagagacatgctgtg 301
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     274 gcttccagggctcccgagccacacgctggcgctgctgctgagagagacatgctgtg 333
QY     302 gcttcgctgagagctgctgctgctgagagacacacacacacacacacacacac 361
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     334 gcttcgagctgagagctgctgctgagagacacacacacacacacacacacacac 393
QY     362 gctgttactgagagctgctgctgcttcttctctctctctctctctctctctctct 421
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     394 gctgttactgagagctgctgctgcttcttctctctctctctctctctctctctct 453
QY     422 ggcgtaccccaacacatgaacatgaatgcacatttccaaataaagccatgctctgc 481
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     454 ggcgtaccccaacacatgaacatgaatgcacatttccaaataaagccatgctctgc 513
QY     482 aggaacactctctggttccagagatattctgtaattccaaacacacacacacacacac 541
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     514 aggaacactctctggttccagagatattctgtaattccaaacacacacacacacac 573
QY     542 cccgactctgaggagctcccgagctgtgtggaactttaacaatccattgtgctcg 601
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     574 cccgactctgaggagctcccgagctgtgtggaactttaacaatccattgtgctcg 633
QY     602 cctgttctcagaatgctcgagagctcttcttctacagccagaaacacacacacacac 661
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     634 cctgttctcagaatgctcgagagctcttcttctacagccagaaacacacacacacac 693
QY     662 catgctgcaaaagtctcagaaacatcacagcagatcaagaatcccgctcaaaacttgagct 721
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     694 catgctgcaaaagtctcagaaacatcacagcagatcaagaatcccgctcaaaacttgagct 753
QY     722 tcaagaattctctggtgagcaatgaacacttctcgggttccctatatcaaacactctct 781
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     754 tcaagaattctctggtgagcaatgaacacttctcgggttccctatatcaaacactctct 813
QY     782 cccaagtctactgtgagcaagatgctgagagctgagctcatctctccacaagattttt 841
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     814 cccaagtctactgtgagcaagatgctgagagctgagctcatctctccacaagattttt 873
QY     842 gcaaggtcaccagttacatttgaaagtctgtgcaatgagtcacaatccagaagagatg 901
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     874 gcaaggtcaccagttacatttgaaagtctgtgcaatgagtcacaatccagaagagatg 933
QY     902 tcaactgtgtaccaaagaattctgagcttctgagcttccaaagagaaactgtgctg 961
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```

Db     934 tcaactgtgtaccaaagaattctgagcttctgagcttccaaagagaaactgtgctg 993
QY     962 agcagagcgagtaattctgttccaaatgagacatctcgaagccacacacacacacacac 1021
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     994 agcagagcgagtaattctgttccaaatgagacatctcgaagccacacacacacacac 1053
QY    1022 ctctaacatctctctcccgagagagctgtgctgagccacacacacacacacacacacac 1081
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1054 ctctaacatctctctcccgagagagctgtgctgagccacacacacacacacacacacac 1113
QY    1082 tcttgagactctgagccagagctgttcaagcttgagagagctgagctgagacagagga 1141
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1114 tcttgagactctgagccagagctgttcaagcttgagagagctgagctgagacagagga 1173
QY    1142 ggtgagttcttgcagcaatgagacagctccagctccctccacacacacacacacacac 1201
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1174 ggtgagttcttgcagcaatgagacagctccagctccctccacacacacacacacacac 1233
QY    1202 gttctgattgtctgagagcaccgagaggggaggggctgagagatcctcctcaactg 1261
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1234 gttctgattgtctgagagcaccgagaggggaggggctgagagatcctcctcaactg 1293
QY    1262 gttctgagagcaacacacacacacacacacacacacacacacacacacacacacac 1321
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1294 gttctgagagcaacacacacacacacacacacacacacacacacacacacacacac 1353
QY    1322 aacctctctatgcaacacacacacacacacacacacacacacacacacacacacacac 1381
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1354 aacctctctatgcaacacacacacacacacacacacacacacacacacacacacacac 1413
QY    1382 tagtctctctcccgacatctctgagagagctgagagcctgctgtgtgagagatcct 1441
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1414 tagtctctctcccgacatctctgagagagctgagagcctgctgtgtgagagatcct 1473
QY    1442 gttatacactgacacacacacacacacacacacacacacacacacacacacacac 1501
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1474 gttatacactgacacacacacacacacacacacacacacacacacacacacacac 1533
QY    1502 ggaactgctgtgtgtcagatctcgaagagcagtgaggaggaactcagccacacacac 1561
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1534 ggaactgctgtgtgtcagatctcgaagagcagtgaggaggaactcagccacacacac 1593
QY    1562 gaccttcatgagagacagccagaaatgagacctgtctcggatgctgtgagacagcgagga 1621
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1594 gaccttcatgagagacagccagaaatgagacctgtctcggatgctgtgagacagcgagga 1653
QY    1622 caatgacacacttgggagacagcaggttggttgatgagatgagacagccacacacac 1681
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1654 caatgacacacttgggagacagcaggttggttgatgagatgagacagccacacacac 1713
QY    1682 ggcgtttttggcagagcaccagagagatgtccaggtccagtaatggttctgtgacacctg 1741
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1714 ggcgtttttggcagagcaccagagagatgtccaggtccagtaatggttctgtgacacctg 1773
QY    1742 gagagaagcttccaagagacacagcagcagcagcagcagcagcagcagcagcagcagc 1801
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1774 gagagaagcttccaagagacacagcagcagcagcagcagcagcagcagcagcagcagc 1833
QY    1802 tgcacaactgagcaagctatagaacccatagcaacagagatgtgctcatatacaagaagctat 1861
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1834 tgcacaactgagcaagctatagaacccatagcaacagagatgtgctcatatacaagaagctat 1893
QY    1862 ggaactgctgtgagatgagagagatgtggtgctggtatgtgttccactggaattcctcag 1921
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1894 ggaactgctgtgagatgagagagatgtggtgctggtatgtgttccactggaattcctcag 1953
QY    1922 cagcattgagctgcccacatgtccaagtacaaagatccgaatgagacattgagaaatgtgga 1981
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1954 cagcattgagctgcccacatgtccaagtacaaagatccgaatgagacattgagaaatgtgga 2013
QY    1982 gaggacaataaatacaagatgagtgatgagacccctgtctcagctgagctgacaccccttga 2041
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    2014 gaggacaataaatacaagatgagtgatgagacccctgtctcagctgagctgacaccccttga 2073

```

QY	2042	ggaacatcgttaacgtctcgtggggggtccgcctactctgcaggaatgctgtgagcaggcat	2101
Db	2074	ggaacatctgtgaacgtctctcgtgggggtccgcctactctgcaggaatgctgtgagcaggcat	2133
QY	2102	catcaaggctgtctgcagggccacccaggaagaacatcgtgtctatctatctgaacagatgcctta	2161
Db	2134	catcaaggctgtctgcagggccacccaggaagaacatcgtgtctatctatctgaacagatgcctta	2193
QY	2162	tcocctgtacgtctgaatgacatctctctcgtgggtgaatgagccggttcaatgtgcctctcat	2221
Db	2194	tcocctgtacgtctgaatgacatctctctcgtgggtgaatgagccggttcaatgtgcctctcat	2253
QY	2222	gacgcctgcctcggatcttaactacgtcgtgtgatcatcaagggtactgtatgatgaagga	2281
Db	2254	gacgcctgcctcggatcttaactacgtcgtgtgatcatcaagggtactgtatgatgaagga	2313
QY	2282	ggcaaggtctgaagaagacacatcgcgcgatalcatgtgcctgcgaacacagcatcctgtttag	2341
Db	2314	ggcaaggtctgaagaagacacatcgcgcgatalcatgtgcctgcgaacacagcatcctgtttag	2373
QY	2342	ctgtgtcaatctgaagcctcatctcctctctgtgtgagcgtctgcctgtagtgtcatcct	2401
Db	2374	ctgtgtcaatctgaagcctcatctcctctctgtgtgagcgtctgcctgtagtgtcatcct	2433
QY	2402	gaagcttaaggaaacccgtgcgcctcaatgatatccagcggtgtttctctccgtctcgt	2461
Db	2434	gaagcttaaggaaacccgtgcgcctcaatgatatccagcggtgtttctctccgtctcgt	2493
QY	2462	gttttcgtctgtgatacaatctctcgcagtgcttccgtatgacacacatctctccaaagcaaa	2521
Db	2494	gttttcgtctgtgatacaatctctcgcagtgcttccgtatgacacacatctctccaaagcaaa	2553
QY	2522	cctgtgcacacagcctcgtctgggggacatcatctacttaacgcctgtacactgcctacagtcctgtg	2551
Db	2554	cctgtgcacacagcctcgtctgggggacatcatctacttaacgcctgtacactgcctacagtcctgtg	2613
QY	2582	tgctgcacgtgacagacatacgtctgcgccttccacatcaagaactctagcgcgtcgtctcc	2641
Db	2614	tgctgcacgtgacagacatacgtctgcgccttccacatcaagaactctagcgcgtcgtctcc	2673
QY	2642	tgctgcctttcgttggtctgtgccttgatcttgccttgccttttgaggagcaggcatctgagct	2701
Db	2674	tgctgcctttcgttggtctgtgccttgatcttgccttgccttttgaggagcaggcatctgagct	2733
QY	2702	gcaagtggaacaaacccgttttgagagtcctgttgaggagaagatgccttcaatctcacacattc	2761
Db	2734	gcaagtggaacaaacccgttttgagagtcctgttgaggagaagatgccttcaatctcacacattc	2793
QY	2762	gattcccaatgtatcgtctttgatcaccttccctatcgtgggtgaatgaccttgatcatctgggc	2821
Db	2794	gattcccaatgtatcgtctttgatcaccttccctatcgtgggtgaatgaccttgatcatctgggc	2853
QY	2822	tgctcttcccaagccagatacggaaatccccaagccctgtgtatttcccttgacaccaagtcccta	2881
Db	2854	tgctcttcccaagccagatacggaaatccccaagccctgtgtatttcccttgacaccaagtcccta	2913
QY	2882	ctgtgtcttgcgagaaatgatatgagaagaagcacaacccgtgttccaaacccaagaaatgctc	2941
Db	2914	ctgtgtcttgcgagaaatgatatgagaagaagcacaacccgtgttccaaacccaagaaatgctc	2973
QY	2942	agaaatctgcatactgagagagaaaccaaccacttgaagctgtggcgtgtccatctcgaacct	3001
Db	2974	agaaatctgcatactgagagagaaaccaaccacttgaagctgtggcgtgtccatctcgaacct	3033
QY	3002	ggttaaaagctctacccagatactggaatgaaggtggtctgtcgaatgagcctctgcagcatatttta	3061
Db	3034	ggttaaaagctctacccagatactggaatgaaggtggtctgtcgaatgagcctctgcagcatatttta	3093
QY	3062	tgaggggccagatcacctcctctccttggtgcacacatggaacggtggagaggaagacacacatgtc	3121
Db	3094	tgaggggccagatcacctcctctccttggtgcacacatggaacggtggagaggaagacacacatgtc	3153

OY 6422 ctatagtgaggaacaaacgaacgtctctacagccatggtcttgatcgcggtctcc 6481
 |||||
 Db 6454 ctatagtgaggaacaaacgaacgtctctacagccatggtcttgatcgcggtctcc 6513
 |||||
 OY 6482 tgtgtgtctctgtatgtacccacacagcagatgtatcccaaaagcccggtctctgtg 6541
 |||||
 Db 6514 tgtgtgtctctgtatgtacccacacagcagatgtatcccaaaagcccggtctctgtg 6573
 |||||
 OY 6542 gaattgtgccttaagtgtgttgcagagagggagatcagtaagtcttatactatagat 6601
 |||||
 Db 6574 gaattgtgccttaagtgtgttgcagagagggagatcagtaagtcttatactatagat 6633
 |||||
 OY 6602 ggaagaatgtgaagctctcttgcaatgagatgtacatcttgaaaggttcaggtg 6661
 |||||
 Db 6634 ggaagaatgtgaagctctcttgcaatgagatgtacatcttgaaaggttcaggtg 6663
 |||||
 OY 6662 ccttgcaggtgtccagcactcaaaaataggttctgagatgttatacaatagtgtacg 6721
 |||||
 Db 6694 ccttgcaggtgtccagcactcaaaaataggttctgagatgttatacaatagtgtacg 6753
 |||||
 OY 6722 aatagcaggtgtccaccccgagctgtgaagctgtccagatcttcttgactgtcatctc 6781
 |||||
 Db 6754 aatagcaggtgtccaccccgagctgtgaagctgtccagatcttcttgactgtcatctc 6813
 |||||
 OY 6782 tgggaagtgtcttaaaaggaacacccggaacatgtctacatcacagcttccatctcatt 6841
 |||||
 Db 6814 tgggaagtgtcttaaaaggaacacccggaacatgtctacatcacagcttccatctcatt 6873
 |||||
 OY 6842 atctctctgcgcaggaatattcaacatctctccacagacaaaagcgactccacataga 6901
 |||||
 Db 6874 atctctctgcgcaggaatattcaacatctctccacagacaaaagcgactccacataga 6933
 |||||
 OY 6902 agactactctgttctctcagacacacacttgaccagatatttgtgaacttgcacagagaca 6961
 |||||
 Db 6934 agactactctgttctctcagacacacacttgaccagatatttgtgaacttgcacagagaca 6993
 |||||
 OY 6962 aagtatgatgacacacttaaaagacactctcaatcacacaaaacacagacagtagtggagct 7021
 |||||
 Db 6994 aagtatgatgacacacttaaaagacactctcaatcacacaaaacacagacagtagtggagct 7053
 |||||
 OY 7022 tgcagttctcacatcttctctacaggaatgtagaaggtgaagaagctatgtatgaagaat 7081
 |||||
 Db 7054 tgcagttctcacatcttctctacaggaatgtagaaggtgaagaagctatgtatgaagaat 7113
 |||||
 OY 7082 cctgttctaaaggggtgtgtctgaagaagtaagaagtaactgacttcccttgacatgtga 7141
 |||||
 Db 7114 cctgttctaaaggggtgtgtctgaagaagtaagaagtaactgacttcccttgacatgtga 7173
 |||||
 OY 7142 agtgtgtggagaaagagccagaagttgagtgtggaagaagtaaaactggaactgtact 7201
 |||||
 Db 7174 agtgtgtggagaaagagccagaagttgagtgtggaagaagtaaaactggaactgtact 7233
 |||||
 OY 7202 gatactattcaatgtcaatgtcaatltcaatgtcaatgtcaatltcaatgtcaatgtcaat 7261
 |||||
 Db 7234 gatactattcaatgtcaatgtcaatltcaatgtcaatgtcaatltcaatgtcaatgtcaat 7293
 |||||
 OY 7262 tgcctttagcctatgtctgtatgtctgtcaagtgtgaagaacttgaatttgaatttga 7321
 |||||
 Db 7294 tgcctttagcctatgtctgtatgtctgtcaagtgtgaagaacttgaatttgaatttga 7353
 |||||
 OY 7322 cctatacctatgtgaacacttatgtgaagccaaatgtgacatgtggttgaactcacac 7381
 |||||
 Db 7354 cctatacctatgtgaacacttatgtgaagccaaatgtgacatgtggttgaactcacac 7413
 |||||
 OY 7382 tttttttttttttgtctgtgtatctcatatgtgggtgtgcaacaatltcaatgaat 7441
 |||||
 Db 7414 tttttttttttttgtctgtgtatctcatatgtgggtgtgcaacaatltcaatgaat 7473
 |||||
 OY 7442 aatcagtcagcaggttatgtatcaaaatcaaaaggtatgtacatctctcattcaatag 7501
 |||||
 Db 7474 aatcagtcagcaggttatgtatcaaaatcaaaaggtatgtacatctctcattcaatag 7533
 |||||

OY 7502 ccaltgcacatgccagagagatgtttcccggtgacacatcacttgcctgcaatgtagtgt 7561
 |||||
 Db 7534 ccaltgcacatgccagagagatgtttcccggtgacacatcacttgcctgcaatgtagtgt 7593
 |||||
 OY 7562 ccagagttaatgtgccaaagttttcagaagaatttgaagaaccaatgtgtgtcaatgtca 7621
 |||||
 Db 7594 ccagagttaatgtgccaaagttttcagaagaatttgaagaaccaatgtgtgtcaatgtca 7653
 |||||
 OY 7622 ctttttggaagctgtctgtctcagagctctatcaaatgtgaattgaatttgaagaatgt 7681
 |||||
 Db 7654 ctttttggaagctgtctgtctcagagctctatcaaatgtgaattgaatttgaagaatgt 7713
 |||||
 OY 7682 tgcacatgcgtgtcaacatctctgttgccttgcctctgaatgaatgttctgtgtgagta 7741
 |||||
 Db 7714 tgcacatgcgtgtcaacatctctgttgccttgcctctgaatgaatgttctgtgtgagta 7773
 |||||
 OY 7742 acatgtcaacaaaatgtgtgtgtctctgaagcagcggaaacttgcattgttatatgt 7801
 |||||
 Db 7774 acatgtcaacaaaatgtgtgtgtctctgaagcagcggaaacttgcattgttatatgt 7833
 |||||
 OY 7802 tctatgtcttcagagccatgtgtctacaggtgtacttcttataagacttcaatataacta 7861
 |||||
 Db 7834 tctatgtcttcagagccatgtgtctacaggtgtacttcttataagacttcaatataacta 7893
 |||||
 OY 7862 gatccctgtgaagagcgaagaatcacaacagcacaactgtgtgtgtcgaactgtgaagc 7921
 |||||
 Db 7894 gatccctgtgaagagcgaagaatcacaacagcacaactgtgtgtgtcgaactgtgaagc 7953
 |||||
 OY 7922 caaggaatggatlaaagagatgtgtgtgtcaaaactgaaggaaagcctgtgtccattgtgc 7981
 |||||
 Db 7954 caaggaatggatlaaagagatgtgtgtgtcaaaactgaaggaaagcctgtgtccattgtgc 8013
 |||||
 OY 7982 ctgactgtctgtcaaaatgtgtacacgtgcactcaaatgtttatctgcacaaagtgatt 8041
 |||||
 Db 8014 ctgactgtctgtcaaaatgtgtacacgtgcactcaaatgtttatctgcacaaagtgatt 8073
 |||||
 OY 8042 attctgtccttcttgaatlaatcctagaaaaatgaagaatgtgaattgtatttgcacaaaa 8101
 |||||
 Db 8074 attctgtccttcttgaatlaatcctagaaaaatgaagaatgtgaattgtatttgcacaaaa 8133
 |||||
 OY 8102 tgtttgaacttcttaatgttaattgtgaatttgaatttgaatttgaatttgaatttgaattt 8161
 |||||
 Db 8134 tgtttgaacttcttaatgttaattgtgaatttgaatttgaatttgaatttgaatttgaattt 8193
 |||||
 OY 8162 agaatggcctcttgtgaagccctgtgtgtatagaagatgtgacacacacacacacatt 8221
 |||||
 Db 8194 agaatggcctcttgtgaagccctgtgtgtatagaagatgtgacacacacacacacatt 8253
 |||||
 OY 8222 ttatttctatgtgaattgtgacatcagtaagtaagtaagtaagtaagtaagtaagtaag 8281
 |||||
 Db 8254 ttatttctatgtgaattgtgacatcagtaagtaagtaagtaagtaagtaagtaagtaag 8313
 |||||
 OY 8282 gtcaagatcctatgtacatlatatgtagtttcttccagatcattatagatccttaac 8341
 |||||
 Db 8314 gtcaagatcctatgtacatlatatgtagtttcttccagatcattatagatccttaac 8373
 |||||
 OY 8342 tcaacttcaatcaaatatt 8401
 |||||
 Db 8374 tcaacttcaatcaaatatt 8433
 |||||
 OY 8402 gtaaaagactagagagatataatgtatcagtaacacttccgtgtcattgttatcaactca 8461
 |||||
 Db 8434 gtaaaagactagagagatataatgtatcagtaacacttccgtgtcattgttatcaactca 8493
 |||||
 OY 8462 ctggtttcaacaatataggt 8521
 |||||
 Db 8494 ctggtttcaacaatataggt 8553
 |||||
 OY 8522 ggccttt 8581
 |||||
 Db 8554 ggccttt 8613
 |||||
 OY 8582 agtttaacaatgaattcttcaacagggaaacagctagcttgaaaaactgtgtgaaaaac 8641
 |||||


```

Db      8614  agtttaacaatgaatcttcaacaggaacagctagcttgaacatgtcgtgaacac 8673
Qy      8642  acaactgtgtttagtcatttagtaccttcaataatgtgcttgtagtattgatac 8701
Db      8674  acaactgtgtttagtcatttagtaccttcaataatgtgcttgtagtattgatac 8733
Qy      8702  cccattaaatcagcagctcctcaaatcttcaatcctcaatcactagtcagaanaaat 8761
Db      8734  cccattaaatcagcagctcctcaaatcttcaatcctcaatcactagtcagaanaaat 8793
Qy      8762  aaaaaacaataatcttccatagtgagcatttttcagagcttttcaaccagcttatt 8821
Db      8794  aaaaaacaataatcttccatagtgagcatttttcagagcttttcaaccagcttatt 8853
Qy      8822  ttctagtcagtaaacatttgaanaatactgttcaactaactaactgttaactgtctt 8881
Db      8854  ttctagtcagtaaacatttgaanaatactgttcaactaactaactgttaactgtctt 8913
Qy      8882  gagagaaagaaaaaataatgagagaaactatgttggggaagttcaagtgatcttcaata 8941
Db      8914  gagagaaagaaaaaataatgagagaaactatgttggggaagttcaagtgatcttcaata 8973
Qy      8942  tcaatctaaccttcttccacttttccaataattgaaataatcaacgctgaagagc 9001
Db      8974  tcaatctaaccttcttccacttttccaataattgaaataatcaacgctgaagagc 9033
Qy      9002  ttcaagattcaaatatacttctctataatttttaaatlttaacagaaatataataaccac 9061
Db      9034  ttcaagattcaaatatacttctctataatttttaaatlttaacagaaatataataaccac 9093
Qy      9062  tgcctgaaaaagaaaaaataatgtttagaagttaagccaatattgattttaaatata 9121
Db      9094  tgcctgaaaaagaaaaaataatgtttagaagttaagccaatattgattttaaatata 9153
Qy      9122  agtaataagagcatttccaataactagtgatagtcacgttgcatttacaatatac 9181
Db      9154  agtaataagagcatttccaataactagtgatagtcacgttgcatttacaatatac 9213
Qy      9182  tcaaaaaatacagaattatagaataatcttcccaatttataatatttcaaaaatacaga 9241
Db      9214  tcaaaaaatacagaattatagaataatcttcccaatttataatatttcaaaaatacaga 9273
Qy      9242  tatgttctcatttcttcttcaaaaatgttatctcaattctctatagtaactctgag 9301
Db      9274  tatgttctcatttcttcttcaaaaatgttatctcaattctctatagtaactctgag 9333
Qy      9302  caactccttactcgtctcctcgtatccaagccatattttaaaaaatacaaaagcact 9361
Db      9334  caactccttactcgtctcctcgtatccaagccatattttaaaaaatacaaaagcact 9393
Qy      9362  gtgaactatttgaagaacacagacatttaatacagattgaagaagcctctctgag 9421
Db      9394  gtgaactatttgaagaacacagacatttaatacagattgaagaagcctctctgag 9453
Qy      9422  ctgaacaaactctatagttatactctcaatctcaatctggttaccctttaaaatagtaa 9481
Db      9454  ctgaacaaactctatagttatactctcaatctcaatctggttaccctttaaaatagtaa 9513
Qy      9482  ttttttaacttctcgtgtgaacctaattgtgtagaanaatttttaaccaactatactc 9541
Db      9514  ttttttaacttctcgtgtgaacctaattgtgtagaanaatttttaaccaactatactc 9573
Qy      9542  aatcaagcaaaatttctgtatatctcctgtggaatgatactatgtagtttgaagaatcc 9601
Db      9574  aatcaagcaaaatttctgtatatctcctgtggaatgatactatgtagtttgaagaatcc 9633
Qy      9602  tcaaaatacgttcaaaaattctcgtcttgcattcttgaggacacctgaagaactttat 9661
Db      9634  tcaaaatacgttcaaaaattctcgtcttgcattcttgaggacacctgaagaactttat 9693
Qy      9662  taacaactgtgaatagagaatacagaagaanaataaagccctctatacataaatggc 9721

```

```

Db      9694  taacaactgtgaataatgagaataacagaagaanaataaagccctctataataaatggc 9753
Qy      9722  cagcaacttcaatgtttaaaaaaacacacacacacacacacacacacacacacacacac 9781
Db      9754  cagcaacttcaatgtttaaaaaaacacacacacacacacacacacacacacacacacac 9813
Qy      9782  ctgaagaacaaatgtcttgaactataatgttgcacacacacacacacacacacacacac 9841
Db      9814  ctgaagaacaaatgtcttgaactataatgttgcacacacacacacacacacacacacac 9873
Qy      9842  tcaatgactaaagcatttgcgtgttcttctctgttgmgnatataatgaagaata 9901
Db      9874  tcaatgactaaagcatttgcgtgttcttctctgttgmgnatataatgaagaata 9933
Qy      9902  tttcccaaaagacacatgtcctatgaatacctgaaccccttgatattgaaacataatctg 9961
Db      9934  tttcccaaaagacacatgtcctatgaatacctgaaccccttgatattgaaacataatctg 9993
Qy      9962  gacccttggtattatctactagaataatgataactcgnagaataatgtcttaattctt 10021
Db      9994  gacccttggtattatctactagaataatgataactcgnagaataatgtcttaattctt 10053
Qy      10022  caaatgtgtacatcccccctaaagttctatltccaaagatttaagcttgcattcc 10081
Db      10054  caaatgtgtacatcccccctaaagttctatltccaaagatttaagcttgcattcc 10113
Qy      10082  ttctataccctaagaatgaagcgttlttgtgctcttgttcaatcattgcccctcattcc 10141
Db      10114  ttctataccctaagaatgaagcgttlttgtgctcttgttcaatcattgcccctcattcc 10173
Qy      10142  aagcactttagcgtgtcgttaatgagatcattttttagcgggaatctgaagaatgca 10201
Db      10174  aagcactttagcgtgtcgttaatgagatcattttttagcgggaatctgaagaatgca 10233
Qy      10202  aaactagacaaagtttcaacaacagatctcaagttaaatcaatttcaatlaaaggaa 10261
Db      10234  aaactagacaaagtttcaacaacagatctcaagttaaatcaatttcaatlaaaggaa 10293
Qy      10262  aagaaaaaaaatttctgtatgtcaataacttataatgaatataaatgcatattctat 10321
Db      10294  aagaaaaaaaatttctgtatgtcaataacttataatgaatataaatgcatattctat 10353
Qy      10322  gtgttaataataatgagtaacaaataaagcgttgacgttctgtttaaaaaaataaaaaa 10381
Db      10354  gtgttaataataatgagtaacaaataaagcgttgacgttctgtttaaaaaaataaaaaa 10413
Qy      10382  aaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaa 10441
Db      10414  aaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaa 10473
Qy      10442  a 10442
Db      10474  a 10474

RESULT 5
AAF24707
ID AAF24707 standard; DNA; 10474 BP.
XX
XX AAF24707;
XX
XX AC
XX
XX DT 20-APR-2001 (first entry)
XX
XX DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
XX KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
XX
XX KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
XX
XX KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
XX
XX KW atherosclerosis; cholesterol transport; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers

```


Db	1414	taagctcttccgcattatcttgaaagctctgaagccgctgctgttgvggaagctct	1477
Qy	1442	gfatacactgacactccagcccaagcgaggtcaatgctgtaggtgtaacaagacttca	1501
Db	1474	gtataaacctgacactccagcccaagcgaggtcaatgctgtaggtgtaacaagacttca	1533
Qy	1502	ggagcgggtggtgtccatctgtagctcggaagagatgtgggaagaaactaagcccaagctcg	1561
Db	1534	ggaactggtgtgttccatgtatctcggaagagatgtgggaagaaactaagcccaagctcg	1593
Qy	1562	gaactlcatggaagaaacagcccaagaaatggaactgtctcggaatgtctgttgacaagcgagga	1621
Db	1594	gaactlcatggaagaaacagcccaagaaatggaactgtctcggaatgtctgttgacaagcgagga	1653
Qy	1622	caatgacaacttttgggaacagcgagttggatggtcttagatgtgacaagcccaagaaatcgt	1681
Db	1654	caatgacaacttttgggaacagcgagttggatggtcttagatgtgacaagcccaagaaatcgt	1713
Qy	1682	ggcggttttggccaagaccccaagagatgtctccagctccaagaatggtctgttlaaccccg	1744
Db	1714	ggcggttttggccaagaccccaagagatgtctccagctccaagaatggtctgttlaaccccg	1776
Qy	1742	ggagagaagcttcaaagagactaaacaaaggcaatccgagacatactcccgcttcatggagtg	1801
Db	1774	ggagagaagcttcaaagagactaaacaaaggcaatccgagacatactcccgcttcatggagtg	1833
Qy	1802	ttccaactggaacagctcagaaacccatagaaacaagaatgtctgtctcatcaacaagctcat	1861
Db	1834	ttccaactggaacagctcagaaacccatagaaacaagaatgtctgtctcatcaacaagctcat	1893
Qy	1862	ggagctgtctgtagtagagagaatgtctgtggtlatgtgttcaacggagatattccaaag	1921
Db	1894	ggagctgtctgtagtagagagaatgtctgtggtlatgtgttcaacggagatattccaaag	1953
Qy	1922	cgagcattagctgtgcccatactatgtccaagtatacgaatccgaaatgagacattgacaatgtgga	1981
Db	1954	cgagcattagctgtgcccatactatgtccaagtatacgaatccgaaatgagacattgacaatgtgga	2013
Qy	1982	ggagacaataataaatacgaagtagtgtaactgtggaacccgtgctcccgagctggaaccccttga	2041
Db	2014	ggagacaataataaatacgaagtagtgtaactgtggaacccgtgctcccgagctggaaccccttga	2073
Qy	2042	ggacactgtagtagtctcgvgggggggtcttcgctacttgcaagatgtgtgtgtagagagaacat	2101
Db	2074	ggacactgtagtagtctcgvgggggggtcttcgctacttgcaagatgtgtgtgtagagagaacat	2133
Qy	2102	catcaggggtgctgtgcagggacacccggaagaanaatgtgtgtctatatgacaacagatgtcccta	2161
Db	2134	catcaggggtgctgtgcagggacacccggaagaanaatgtgtgtgtctatatgacaacagatgtcccta	2193
Qy	2162	tcactgttagtgtagtagaacatcttctctgcygggtgtagtagacggtgtaatgtccctcttcat	2221
Db	2194	tcactgttagtgtagtagaacatcttctctgcygggtgtagtagacggtgtaatgtccctcttcat	2253
Qy	2222	gaagctgagccgtggaatttaaccacgtgtgtgtagatcatcaaggggcatcgtgtatggaagga	2281
Db	2254	gaagctgagccgtggaatttaaccacgtgtgtgtagatcatcaaggggcatcgtgtatggaagga	2313
Qy	2282	ggacagcgctggaagaagacaaatgtagatcatatggtgctcggaacaacagatcaatctgttttag	2341
Db	2314	ggacagcgctggaagaagacaaatgtagatcatatggtgctcggaacaacagatcaatctgttttag	2373
Qy	2342	ctgtgttaattagtagactcatcttccctctctgttgtagcgctgtagctgtgaatgtgtcatcct	2401
Db	2374	ctgtgttaattagtagactcatcttccctctctgttgtagcgctgtagctgtgaatgtgtcatcct	2433
Qy	2402	gaagttaggaacactgtgtgcctctacaagtgatcccgagctgtgtgttgcttccctccgtcgt	2461
Db	2434	gaagttaggaacactgtgtgcctctacaagtgatcccgagctgtgtgtgttgcttccctccgtcgt	2493
Qy	2462	gtttgctgtgtgtgacaactccgtcagtagtcttccctgtagtagacactcttctcaagagccaa	2521

Dh	2494	gltctgctgtgtgtgacaacatccgtcagtgcttccttgatlaagacaactctcttcacagagccaa	2553
Qy	2522	ccctgagacagacgcctgtgtgggggacatcaactcaactcaacgcctgtacgcctccatagctctgtg	2581
Dh	2554	ccctgagacagacgcctgtgtgggggacatcaactcaactcaacgcctgtacgcctccatagctctgtg	2613
Qy	2582	tgtgtgacatgtgcagagactacgtgtgggcttcaacatcacaagatcttcgtactagccctgtctctcc	2641
Dh	2614	tgtgtgacatgtgcagagactacgtgtgggcttcaacatcacaagatcttcgtactagccctgtctctcc	2673
Qy	2642	tgtgtgctttgttgctttgtgcctgtgagtaactttgccccttttgagagaaacaggtatggaggt	2701
Dh	2674	tgtgtgctttgttgctttgtgcctgtgagtaactttgccccttttgagagaaacaggtatggaggt	2733
Qy	2702	gcagttgtgagcaaacctgttlttgagagtcctgtgtgagagaaabtggtctcaactcaactcc	2761
Dh	2734	gcagttgtgagcaaacctgttlttgagagtcctgtgtgagagaaabtggtctcaactcaactcc	2793
Qy	2762	gacatccatgagatgcctgtttgacaccttcctctctgtgggttgatgagacctgtgtatattgagac	2821
Dh	2794	gacatccatgagatgcctgtttgacaccttcctctctgtgggttgatgagacctgtgtatattgagac	2853
Qy	2822	tgtctcttcacaggtccagatgacagaaatctccacagacctgtgatatcttcctgtgacacaaatcccta	2881
Dh	2854	tgtctcttcacaggtccagatgacagaaatctccacagacctgtgatatcttcctgtgacacaaatcccta	2913
Qy	2882	ctgtgtcttgcagagagaagtgtatgtagaagagccacacctgtgttccaacagaaagaaatgtct	2941
Dh	2914	ctgtgtcttgcagagagaagtgtatgtagaagagccacacctgtgttccaacagaaagaaatgtct	2973
Qy	2942	agaaaatctgcatagtgagagagagaaacccaactctgtgaagctgtgggcgtgtccattccagaacct	3001
Dh	2974	agaaaatctgcatagtgagagagagaaacccaactctgtgaagctgtgggcgtgtccattccagaacct	3033
Qy	3002	ggttaaaagtctacccagagatgtgagatltgaaggtgtgcctgtcagatgtggcctgtgcacitgaatttta	3061
Dh	3034	ggttaaaagtctacccagagatgtgagatltgaaggtgtgcctgtcagatgtggcctgtgcacitgaatttta	3093
Qy	3062	tgaagggcacagatctcaactcctctctctgtgggcacaaatgtgagagcgggagaaagacacacatgtct	3121
Dh	3094	tgaagggcacagatctcaactcctctctctgtgggcacaaatgtgagagcgggagaaagacacacatgtct	3153
Qy	3122	aactcctgcacgggtgtgttccccccgcagactcgtggcagccgcctcaactcaactcctgtggaaaaagacat	3181
Dh	3154	aactcctgcacgggtgtgttccccccgcagactcgtggcagccgcctcaactcaactcctgtggaaaaagacat	3213
Qy	3182	tgcgtctgaagatgtgagacacatctccgcagaaacctgtggggtgtcttccccagacataacgtgcct	3241
Dh	3214	tgcgtctgaagatgtgagacacatctccgcagaaacctgtggggtgtcttccccagacataacgtgcct	3273
Qy	3242	gttttgacatgtctgacctgtctgcgaagaacacatctgtgtctcatgtgcctgcctgtgaagaaggtcttc	3301
Dh	3274	gttttgacatgtctgacctgtctgcgaagaacacatctgtgtctcatgtgcctgcctgtgaagaaggtcttc	3333
Qy	3302	tgaagaaagacgtgtgaagcccgagatgtgaagacagatctgacctgtgagatgtgtgtttgtgcataaag	3361
Dh	3334	tgaagaaagacgtgtgaagcccgagatgtgaagacagatctgacctgtgagatgtgtgtttgtgcataaag	3393
Qy	3362	caagctgtgaagaagccaanaacaaagacagactgtccaagtgtgaatgtgacagaaagacatctgtgtgc	3421
Dh	3394	caagctgtgaagaagccaanaacaaagacagactgtccaagtgtgaatgtgacagaaagacatctgtgtgc	3453
Qy	3422	cttggccttgtctgcggggagatctaaagttgtcaatctctgtgatgaacccaacagctgtgtgtga	3481
Dh	3454	cttggccttgtctgcggggagatctaaagttgtcaatctctgtgatgaacccaacagctgtgtgtga	3513
Qy	3482	cccttaactcccgaggggagaaatgtggaagctgtgtctgtgaataatccagaaagcccgacacat	3541
Dh	3514	cccttaactcccgaggggagaaatgtggaagctgtgtctgtgaataatccagaaagcccgacacat	3573
Qy	3542	tattctcctctaacacacacatgtgatagtgaagccggaagctcctctgtggggagacagagattgcatcat	3601
Dh	3574	tattctcctctaacacacacatgtgatagtgaagccggaagctcctctgtggggagacagagattgcatcat	3633

Db 5794 aaacccagcagatggtcgtgacccctggaaaggttggggaatcgcgttctgtccaccatt 5853
QY 5822 atcttggagcttgggtggagaaaccccttcgcacatgacgttggaggggtgtgtctt 5881
Db 5854 atcttggagcttgggtggagaaaccccttcgcacatgacgttggaggggtgtgtctt 5913
QY 5882 cctcatctgcttctgtatccagtaacagattcttcacatcagccagacctgtlaaata 5941
Db 5914 cctcatctgcttctgtatccagtaacagattcttcacatcagccagacctgtlaaata 5973
QY 5942 gctatctcctctgacatgataatgaagatggtgagcgaggaagacagaaattcttga 6001
Db 5974 gctatctcctctgacatgataatgaagatggtgagcgaggaagacagaaattcttga 6033
QY 6002 tgggtggagccagaaatgacattcttagaaatcaagaggttggacgaagatalatagaagaa 6061
Db 6034 tgggtggagccagaaatgacattcttagaaatcaagaggttggacgaagatalatagaagaa 6093
QY 6062 ggggaagccctggttggacagatttgcgtgggcatctcctcgtgtgagtgttgggt 6121
Db 6094 ggggaagccctggttggacagatttgcgtgggcatctcctcgtgtgagtgttgggt 6153
QY 6122 cctgggagttaatggggttggaaatcaltcaacttcaagatgttacaaggaataccac 6181
Db 6154 cctgggagttaatggggttggaaatcaltcaacttcaagatgttacaaggaataccac 6213
QY 6182 tgttaccagagagagatgcttctcttaaaaaaataatgatacttaacaacatcagaat 6241
Db 6214 tgttaccagagagagatgcttctcttaaaaaaataatgatacttaacaacatcagaat 6273
QY 6242 acatcagaataatggctactgacctcagtttgaatgacatcacaagacgttggactggag 6301
Db 6274 acatcagaataatggctactgacctcagtttgaatgacatcacaagacgttggactggag 6333
QY 6302 agaacacgttggagttcttctgaccttggagagagatccacagaaagaaatgttggcaagt 6361
Db 6334 agaacacgttggagttcttctgaccttggagagagatccacagaaagaaatgttggcaagt 6393
QY 6362 tgggtggagctgacatccgaaactgggacctgtgaagtttggagaaataatgactgtaa 6421
Db 6394 tgggtggagctgacatccgaaactgggacctgtgaagtttggagaaataatgactgtaa 6453
QY 6422 ctatagtggagacacaacacgcaagctctctacagacatggtcttgcgcggtccac 6481
Db 6454 ctatagtggagacacaacacgcaagctctctacagacatggtcttgcgcggtccac 6513
QY 6482 tgtgtgttcttctgataacccacacagacatgatacccaagcccggttcttctgt 6541
Db 6514 tgtgtgttcttctgataacccacacagacatgatacccaagcccggttcttctgt 6573
QY 6542 gaattgtgacctagttgttcaagaaggagatcagtagtgcatacctccatagat 6601
Db 6574 gaattgtgacctagttgttcaagaaggagatcagtagtgcatacctccatagat 6633
QY 6602 ggaagaatgtgaagccttctgacatgagatgacatcagtcgaatgagaagttcaagt 6661
Db 6634 ggaagaatgtgaagccttctgacatgagatgacatcagtcgaatgagaagttcaagt 6693
QY 6662 ccttggcagtgatccacatctaaataatagtttggagttggttatacaatggtttag 6721
Db 6694 ccttggcagtgatccacatctaaataatagtttggagttggttatacaatggtttag 6753
QY 6722 aatagcaggttccaaacccggaacctgaagcgtlccaggaattcttctgtgactgtatcc 6781
Db 6754 aatagcaggttccaaacccggaacctgaagcgtlccaggaattcttctgtgactgtatcc 6813
QY 6782 tgggaagtgttcttaaaaaaagacacggagacatgtctacacatccagcttccattcat 6841
Db 6814 tgggaagtgttcttaaaaaaagacacggagacatgtctacacatccagcttccattcat 6873
QY 6842 atcttctcggcagagatatcagatcctctccagaaacaaagcgactccacataga 6901
|||||

Db 6874 atcttctcggcagagatatcagatcctctccagaaacaaagcgactccacataga 6933
QY 6902 agactactctgttctcagacaacacatctgacaaatatttggacttgcgaagacca 6961
Db 6934 agactactctgttctcagacaacacatctgacaaatatttggacttgcgaagacca 6993
QY 6962 aagtgatgatacgaacttaaaagacctcatttacaacaaaaacagacagtagtgagct 7021
Db 6994 aagtgatgatacgaacttaaaagacctcatttacaacaaaaacagacagtagtgagct 7053
QY 7022 tgcagttctcaacatcttctcagaagatgagaaggttgaagaagacatgataaagat 7081
Db 7054 tgcagttctcaacatcttctcagaagatgagaaggttgaagaagacatgataaagat 7113
QY 7082 cctgttcaacgggttgcgtgaagaatgaagagagactagacttctccttgcacatgtga 7141
Db 7114 cctgttcaacgggttgcgtgaagaatgaagagagactagacttctccttgcacatgtga 7173
QY 7142 agtgttggagaaagagccagaaggtgatgtgggaagaaatgatactgatactgact 7201
Db 7174 agtgttggagaaagagccagaaggtgatgtgggaagaaatgatactgatactgact 7233
QY 7202 gatactatcaatgacatgacatcaltcaatgacatgacaaatctcattacagggcag 7261
Db 7234 gatactatcaatgacatgacatcaltcaatgacatgacaaatctcattacagggcag 7293
QY 7262 tgccttggtaagctatgtctgtatggtctcgaagtgaagaacttgaattgtttta 7321
Db 7294 tgccttggtaagctatgtctgtatggtctcgaagtgaagaacttgaattgtttta 7353
QY 7322 cctataactatgtgaactcattatggaacccaatgacatgaggttggaaactcac 7381
Db 7354 cctataactatgtgaactcattatggaacccaatgacatgaggttggaaactcac 7413
QY 7382 ttttttttttttctgtctgtgtatctcattcgaattgggggttgcacaaatcacaagt 7441
Db 7414 ttttttttttttctgtctgtgtatctcattcgaattgggggttgcacaaatcacaagt 7473
QY 7442 aatcatggccagagattatgatacaaaatcagaaggaatgaaatccatccatcaag 7501
Db 7474 aatcatggccagagattatgatacaaaatcagaaggaatgaaatccatccatcaag 7533
QY 7502 ccatgtccatggccagagactgtttcccggtgacacatccatgtcgtgcaatgagtgt 7561
Db 7534 ccatgtccatggccagagactgtttcccggtgacacatccatgtcgtgcaatgagtgt 7593
QY 7562 ccagagattatgagccaaagtttctcagaagatttgaagacaaatgtgtgtcatgtca 7621
Db 7594 ccagagattatgagccaaagtttctcagaagatttgaagacaaatgtgtgtcatgtca 7653
QY 7622 ctttgtgaagcgtgctgtcagagatctatacaaatgaaatagttgacagaaatg 7681
Db 7654 ctttgtgaagcgtgctgtcagagatctatacaaatgaaatagttgacagaaatg 7713
QY 7682 tgcacatgctgttcaacatcctgttgaatcctctgtataagctgttctgtgtgacgtga 7741
Db 7714 tgcacatgctgttcaacatcctgttgaatcctctgtataagctgttctgtgtgacgtga 7773
QY 7742 acatgtcaacaaaatgttgggtgtctcctcaggaacgggaacttggatctgtatatt 7801
Db 7774 acatgtcaacaaaatgttgggtgtctcctcaggaacgggaacttggatctgtatatt 7833
QY 7802 tccatgtctcgaagcattgggtctacaggttcatcctctatgagacttcaataactta 7861
Db 7834 tccatgtctcgaagcattgggtctacaggttcatcctctatgagacttcaataactta 7893
QY 7862 gatcctgttaagaggaagaagaatcaacagccaactgtcgtgagcgtgtaagc 7921
Db 7894 gatcctgttaagaggaagaagaatcaacagccaactgtcgtgagcgtgtaagc 7953
QY 7922 caggagcattgaggaagagatgtgtgttcaaacctcagggaagcgtgtccattgttc 7981
Db 7954 caggagcattgaggaagagatgtgtgttcaaacctcagggaagcgtgtgtccattgttc 8013
|||||

QY 7982 ctgactgtctctaacatggttaacatgcctccaagatgtttatctgcacaaagtgtatt 8041
DB 8014 ctgactgtctctaacatggttaacatgcctccaagatgtttatctgcacaaagtgtatt 8073
QY 8042 attctgtgcttttgaatcaatctagaanaaagaaagatgaggtgtatcttgcacaaa 8101
DB 8074 attctgtgcttttgaatcaatctagaanaaagaaagatgaggtgtatcttgcacaaa 8133
QY 8102 tgttttacttttaagtgtatgtttgaatttaagtctctatgaactctgaactcctt 8161
DB 8134 tgttttacttttaagtgtatgtttgaatttaagtctctatgaactctgaactcctt 8193
QY 8162 agaatgacctcttgcagaaacctgtgtatagagagatgagccacccacactatt 8221
DB 8194 agaatgacctcttgcagaaacctgtgtatagagagatgagccacccacactatt 8253
QY 8222 ttaattcttaagtgtatgcatalcagtcagtagtgcctagaanaagcaatgtatg 8281
DB 8254 ttaattcttaagtgtatgcatalcagtcagtagtgcctagaanaagcaatgtatg 8313
QY 8282 gttaagatctcagacatatattttgagttcttccagatcaatttgatattccttaac 8341
DB 8314 gttaagatctcagacatatattttgagttcttccagatcaatttgatattccttaac 8373
QY 8342 tcaactcaatcaataatattttgagtgatgctgtagcgtgaagaagatgatagtac 8401
DB 8374 tcaactcaatcaataatattttgagtgatgctgtagcgtgaagaagatgatagtac 8433
QY 8402 gtataagactagagagatataatagtcctcagtaacactcctgtgcatalgtatcagctca 8461
DB 8434 gtataagactagagagatataatagtcctcagtaacactcctgtgcatalgtatcagctca 8493
QY 8462 ctgtgtttacaataatagtgctgtctgtgtgtgtatgagagccactgtcaacaatattggca 8521
DB 8494 ctgtgtttacaataatagtgctgtctgtgtgtgtatgagagccactgtcaacaatattggca 8553
QY 8522 gacctttttttttttttttttatctgcacaatgtcaaaagccaagaagatataaggtcaca 8581
DB 8554 gacctttttttttttttttttatctgcacaatgtcaaaagccaagaagatataaggtcaca 8613
QY 8582 agtttaacaatgaatctctcaacagggaaacagctagctgtgaaactgtcgtgaaac 8641
DB 8614 agtttaacaatgaatctctcaacagggaaacagctagctgtgaaactgtcgtgaaac 8673
QY 8642 acaactgtgtttatagtgatattgtaacctcaataatattgacctgtgcagatatgtatgc 8701
DB 8674 acaactgtgtttatagtgatattgtaacctcaataatattgacctgtgcagatatgtatgc 8733
QY 8702 cccatttaaatctgacagctcacaatttttcaactctcaactcaactcaactcaactcaact 8761
DB 8734 cccatttaaatctgacagctcacaatttttcaactctcaactcaactcaactcaactcaact 8793
QY 8762 aaaaacaacaatactcataltgagagcatcttgcagagtttctcaaccagacttatt 8821
DB 8794 aaaaacaacaatactcataltgagagcatcttgcagagtttctcaaccagacttatt 8853
QY 8822 ttctagtcagtaaacattgtttaaataactcgttcaacttaactactgttaactgtctt 8881
DB 8854 ttctagtcagtaaacattgtttaaataactcgttcaacttaactactgttaactgtctt 8913
QY 8882 gagagaaagaaaataatgagagaaactgtgttgaggaggtccaagtgtcttcaata 8941
DB 8914 gagagaaagaaaataatgagagaaactgtgttgaggaggtccaagtgtcttcaata 8973
QY 8942 tcaatttaactcttccacttttccaaaaattgaaatataacgttaaaagtgttaagac 9001
DB 8974 tcaatttaactcttccacttttccaaaaattgaaatataacgttaaaagtgttaagac 9033
QY 9002 ttcaagattcaaatattcttctatataatttttaaatatcaagaatatataataccac 9061
DB 9034 ttcaagattcaaatattcttctatataatttttaaatatcaagaatatataataccac 9093

QY 9062 tgcgtgaaaaaagaaaaatgattgttttagaaglttaagtcacatattgatttaataata 9121
DB 9094 tgcgtgaaaaaagaaaaatgattgttttagaaglttaagtcacatattgatttaataata 9153
QY 9122 agtaatgagcatatttccataactagtgatagtgtgatgtgtgcaatttttagatct 9181
DB 9154 agtaatgagcatatttccataactagtgatagtgtgatgtgtgcaatttttagatct 9213
QY 9182 tcaaaaatacagaatttataagaataattcccccatttaataatttccaanaacaaagt 9241
DB 9214 tcaaaaatacagaatttataagaataattcccccatttaataatttccaanaacaaagt 9273
QY 9242 tatgtttcccttaatttcaaaaacoglatctcaatttccattataglaaactatagag 9301
DB 9274 tatgtttcccttaatttcaaaaacoglatctcaatttccattataglaaactatagag 9333
QY 9302 caactccttactcgttccctctgatttccaagccatattttaaanaatcaaaagagact 9361
DB 9334 caactccttactcgttccctctgatttccaagccatattttaaanaatcaaaagagact 9393
QY 9362 gtgaactatttgaagaacaacagcatatttaatacagattgaaagagacctctgag 9421
DB 9394 gtgaactatttgaagaacaacagcatatttaatacagattgaaagagacctctgag 9453
QY 9422 ctgaaacaatcctatagttataacalcctcaatcaactgtgttaccctttaaataagtaa 9481
DB 9454 ctgaaacaatcctatagttataacalcctcaatcaactgtgttaccctttaaataagtaa 9513
QY 9482 ttttttaacttctcgtgtgtaaacctaatgtgtgtgagaatttttaccactatctac 9541
DB 9514 ttttttaacttctcgtgtgtaaacctaatgtgtgtgagaatttttaccactatctac 9573
QY 9542 aatcaagcaaaattcctblataattccctgtgaagtgtaacctatgtgattccaagaattc 9601
DB 9574 aatcaagcaaaattcctblataattccctgtgaagtgtaacctatgtgattccaagaattc 9633
QY 9602 tcaaaaatacgtttcaaaaattctgtccttgcacacttggagacacctcaagaactat 9661
DB 9634 tcaaaaatacgtttcaaaaattctgtccttgcacacttggagacacctcaagaactat 9693
QY 9662 taacaactgtgtaattgagaaatacagaagaataataaagccctctataataatggc 9721
DB 9694 taacaactgtgtaattgagaaatacagaagaataataaagccctctataataatggc 9753
QY 9722 cagcaaatcttaattttaaanaaaccaaacctcaacactatgtatttcaattctgta 9781
DB 9754 cagcaaatcttaattttaaanaaaccaaacctcaacactatgtatttcaattctgta 9813
QY 9782 ctgaaagcaaatgcttctgtacatttaaatgtgtgacacalcattcaactgtagtaa 9841
DB 9814 ctgaaagcaaatgcttctgtacatttaaatgtgtgacacalcattcaactgtagtaa 9873
QY 9842 tcaattgaactaaagcaattgtcgtgttttctctctgtgngtgnatataatcaggttaata 9901
DB 9874 tcaattgaactaaagcaattgtcgtgttttctctctgtgngtgnatataatcaggttaata 9933
QY 9902 ttttccaagagccatgtgtcatalgtcaatgaaccccttgatattgagacatttaattg 9961
DB 9934 ttttccaagagccatgtgtcatalgtcaatgaaccccttgatattgagacatttaattg 9993
QY 9962 gaccttggatattactactagaataatgttaactgtagaataatgtcttaattctt 10021
DB 9994 gaccttggatattactactagaataatgttaactgtagaataatgtcttaattctt 10053
QY 10022 caaaatgtgtcatccccccttaanaangtctatttccaataaggaatttagctgttatccc 10081
DB 10054 caaaatgtgtcatccccccttaanaangtctatttccaataaggaatttagctgttatccc 10113
QY 10082 ttcttaatacctaaagatgaagctgtttgtgtctctgttgcatacatgtgcccctatccc 10141
DB 10114 ttcttaatacctaaagatgaagctgtttgtgtctctgttgcatacatgtgcccctatccc 10173
QY 10142 aagcaattacgctgtctglaatggagctatatttgcaactggaatctatgagaattgca 10201

```

Db 10174 aagccttaccgctgctgtaatgagatcttcttgcactggaatatctgaattgca 10233
QY 10202 aaactagacaaagtctcacacagattctcaagttaataatcatttaaaagga 10261
Db 10234 aaactagacaaagtctcacacagattctcaagttaataatcatttaaaagga 10293
QY 10262 aagaaaaaaatttctgtaatgcaatacttataatgaattaaatgcatlctat 10321
Db 10294 aagaaaaaaatttctgtaatgcaatacttataatgaattaaatgcatlctat 10353
QY 10322 gttgtaataatgagtcacaaataaagctgacagttctgtttaaataaa 10381
Db 10354 gttgtaataatgagtcacaaataaagctgacagttctgtttaaataaa 10413
QY 10382 aaaaaaaataaaataaaataaaataaaataaaataaaataaa 10441
Db 10414 aaaaaaaataaaataaaataaaataaaataaaataaaataaa 10473
QY 10442 a 10442
Db 10474 a 10474

```

RESULT 6
AAF24708 standard; DNA; 10474 BP.

AAF24708:

20-APR-2001 (first entry)

Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.

Human: adenosine triphosphate binding cassette protein 1; ABC1;
apolipoprotein mediated mobilisation; cholesterol; Tangier disease;
chromosome 9q22-9q31; heart disease; hypercholesterolemia;
atherosclerosis; cholesterol transport; ss.

Homo sapiens.

Location/Qualifiers
Key 323..7108
FT CDS /*tag= a
FT /product= "defective ABC1 polypeptide"

MO200078971-A2.

28-DEC-2000.

16-JUN-2000; 2000MO-US16591.

18-JUN-1999; 99US-0140264.

14-SEP-1999; 99US-0153872.

19-NOV-1999; 99US-0166573.

(CVTH-) CV THERAPEUTICS INC.

(UNIV) UNIV WASHINGTON.

Lawn RM, Wade D, Oram JF, Garvin M;

WPI; 2001-137811/14.

P-PSDB; AAB31367.

Adenosine triphosphate (ATP) binding cassette protein (ABC) 1

and other disorders associated with hypercholesterolemia and

atherosclerosis -

Claim 30; Page 165-172; 211pp; English.

The present sequence encodes a human adenosine triphosphate (ATP)

binding cassette protein (ABC) 1 polypeptide, and is isolated from

```

CC a Tangier disease patient. ABC1 resides in cell membranes and utilizes
CC ATP hydrolysis to transport a wide variety of substrates across the
CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC Tangier disease, a genetic disorder characterised by abnormal
CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC 9q22-9q31. The ABC1 genes and proteins are useful for developing
CC pharmaceutical agents for the treatment of heart disease and other
CC disorders associated with hypercholesterolemia and atherosclerosis. The
CC genes are useful for developing screening assays to screen for compounds
CC that regulate the expression of genes associated with cholesterol
CC transport. The genes and proteins are also useful for are also useful
CC as diagnostic indicators of cardiovascular disease and other disorders
CC associated with hypercholesterolemia.
CC
XX
SQ Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;

Query Match 99.9%; Score 10429; DB 22; Length 10474;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10436; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 gccggagcccgagagcagagccgacccctctctccggctgcgagcgagcg 61
Db 34 ggcacgagcgcgacgagcgcgagccgacccctctctccggctgcgagcgagcg 93
QY 62 gagctcgcgcacacacagagcgcgttctcaggcgcttgcctgttttcccg 121
Db 94 gagctcgcgcacacacagagcgcgttctcaggcgcttgcctgttttcccg 153
QY 122 ttctgtttcccccctcccgagagcgttgcaggggtgaggaagagacgaaca 181
Db 154 ttctgtttcccccctcccgagagcgttgcaggggtgaggaagagacgaaca 213
QY 182 caaaagtgaacacagttatgacacagcagcgctccctgtgtgagcttgcgcgt 241
Db 214 caaaagtgaacacagttatgacacagcagcgctccctgtgtgagcttgcgcgt 273
QY 242 gccctcagaggtcccgagcagcagcgctggcgctgctgagggagacagctgtg 301
Db 274 gccctcagaggtcccgagcagcagcgctggcgctgctgagggagacagctgtg 333
QY 302 gccctcagaggttgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 361
Db 334 gccctcagaggttgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 393
QY 362 gctgttactggaagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 421
Db 394 gctgttactggaagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 453
QY 422 gagctacccacccctatgacacacagatgacatgacatgacatgacatgacatg 481
Db 454 gagctacccacccctatgacacacagatgacatgacatgacatgacatgacatg 513
QY 482 aggaacacttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 541
Db 514 aggaacacttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 573
QY 542 cccgactcctggggaggtcccgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 601
Db 574 cccgactcctggggaggtcccgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 633
QY 602 cctgttctcagatgctgagagctctcttcttcttcttcttcttcttcttcttctt 661
Db 634 cctgttctcagatgctgagagctctcttcttcttcttcttcttcttcttcttctt 693
QY 662 catgcaaaagttctgagacattacagcagatcaagaatccagctcaactgtgaagt 721
Db 694 catgcaaaagttctgagacattacagcagatcaagaatccagctcaactgtgaagt 753
QY 722 tcaagattctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 781
Db 754 tcaagattctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 813

```


OY 762 cccaagtactctgtgacaaagatgctgaggtgctgatactctccacaagattttt 841
|||||
Db 814 cccaagtactctgtgacaaagatgctgaggtgctgatactctccacaagattttt 873
OY 842 gcaaggtcacttaatttgacaagtctgtgcaatgataccaatccaagaatgata 901
|||||
Db 874 gcaaggtcacttaatttgacaagtctgtgcaatgataccaatccaagaatgata 933
OY 902 tcaacttgttaccacaagaagtcttctgagcttctgtgcttaccacaagaagaatctgtgc 961
|||||
Db 934 tcaacttgttaccacaagaagtcttctgagcttctgtgcttaccacaagaagaatctgtgc 993
OY 962 agcagaagcagtaactcgttcccaatgagacatccctgaagccaatccctgtgagactataa 1021
|||||
Db 994 agcagaagcagtaactcgttcccaatgagacatccctgaagccaatccctgtgagactataa 1053
OY 1022 ccttaccatctccctcccgagcaagagctgtgctgaagccaacaacatctgtctgacatag 1081
|||||
Db 1054 ccttaccatctccctcccgagcaagagctgtgctgaagccaacaacatctgtctgacatag 1113
OY 1082 tcttggactctgagcccgagagctgttccagacatgagaagctgagatgacatgacagagga 1141
|||||
Db 1114 tcttggactctgagcccgagagctgttccagacatgagaagctgagatgacatgacagagga 1173
OY 1142 ggtgatgttcttgaccaaattggaacagctccaagctctccacccaatctacacagctgt 1201
|||||
Db 1174 ggtgatgttcttgaccaaattggaacagctccaagctctccacccaatctacacagctgt 1233
OY 1202 gctcgtatgtctgtcgagcatcccgagagggagctgtgaagatccaagcttccacatg 1261
|||||
Db 1234 gctcgtatgtctgtcgagcatcccgagagggagctgtgaagatccaagcttccacatg 1293
OY 1262 gfatgagagcaacaactacaagaagccctcttggagggcaatgagcactgtgagagatgctga 1321
|||||
Db 1294 gfatgagagcaacaactacaagaagccctcttggagggcaatgagcactgtgagagatgctga 1353
OY 1322 aaactcttatgacaactcctacaactccttactcgaactatgttgaatgaagaatttggagctc 1381
|||||
Db 1354 aaactcttatgacaactcctacaactccttactcgaactatgttgaatgaagaatttggagctc 1413
OY 1382 taatcctcttcccgcatatcttgaaagctctgaaagcagctgtcgttctgggaagatcct 1441
|||||
Db 1414 taatcctcttcccgcatatcttgaaagctctgaaagcagctgtcgttctgggaagatcct 1473
OY 1442 gatacaccttgacaactccagccaagaaggtcactgtgaggtgagaaacagacttcca 1501
|||||
Db 1474 gatacaccttgacaactccagccaagaaggtcactgtgaggtgagaaacagacttcca 1533
OY 1502 ggaactggtgctgttccatgactctgaaaggaactgtgagaggaactcagccccaagatctg 1561
|||||
Db 1534 ggaactggtgctgttccatgactctgaaaggaactgtgagaggaactcagccccaagatctg 1593
OY 1562 gaccttcatgagagaacagccaagaanaatggaactgttccggaatgctgttggacagcagga 1621
|||||
Db 1594 gaccttcatgagagaacagccaagaanaatggaactgttccggaatgctgttggacagcagga 1653
OY 1622 caatgagccacttgggaacagagatgagatgagttgaagttggaagcccaagacatcgt 1681
|||||
Db 1654 caatgagccacttgggaacagagatgagatgagttgaagttggaagcccaagacatcgt 1713
OY 1682 ggcgttttggccaagacccaagagagatgtccagtccagtaaatggttctgtgtacacgtg 1741
|||||
Db 1714 ggcgttttggccaagacccaagagagatgtccagtccagtaaatggttctgtgtacacgtg 1773
OY 1742 gagagaagcttccaagagactaaacaggaatcccgagacatactcgtttcatatgaggtg 1801
|||||
Db 1774 gagagaagcttccaagagactaaacaggaatcccgagacatactcgtttcatatgaggtg 1833
OY 1802 tgttaaccttaaacagctagaaccataagacaagaagctgtgctcatcaacaagtctcat 1861
|||||
Db 1834 tgttaaccttaaacagctagaaccataagacaagaagctgtgctcatcaacaagtctcat 1893

OY 1862 ggaactgtgatgagagaagatctctgggctgtgatactgttcaactggaatactccag 1921
|||||
Db 1894 ggaactgtgatgagagaagatctctgggctgtgatactgttcaactggaatactccag 1953
OY 1922 caagatgagctgccccatcaatgtccaagtacagaalccgaatgagaattgaaatgtgga 1981
|||||
Db 1954 caagatgagctgccccatcaatgtccaagtacagaalccgaatgagaattgaaatgtgga 2013
OY 1982 gaggacaataaataatcaagatgagatgagctggagccctggcctcgagctgaccccttga 2041
|||||
Db 2014 gaggacaataaataatcaagatgagatgagctggagccctggcctcgagctgaccccttga 2073
OY 2042 ggaactggtgactctgtggggggcttccgctacttgcaggaatgtgtgagaggaat 2101
|||||
Db 2074 ggaactggtgactctgtggggggcttccgctacttgcaggaatgtgtgagaggaat 2133
OY 2102 catcaggtgtctgacgggacccgagaagaaaactggtgtatataatgcaaaagtgcctta 2161
|||||
Db 2134 catcaggtgtctgacgggacccgagaagaaaactggtgtatataatgcaaaagtgcctta 2193
OY 2162 tccctgttaagcttgaatgacatcttctcgagggtgataagccggtcaatgtgccccttcat 2221
|||||
Db 2194 tccctgttaagcttgaatgacatcttctcgagggtgataagccggtcaatgtgccccttcat 2253
OY 2222 gacgctggccttgagatttactcaatgagctgtgatacatcaaggacatgataagaaga 2281
|||||
Db 2254 gacgctggccttgagatttactcaatgagctgtgatacatcaaggacatgataagaaga 2313
OY 2282 ggcacggtctgaagaagacacatgagcatatagagctgtgacacaagcaatctcgtgttag 2341
|||||
Db 2314 ggcacggtctgaagaagacacatgagcatatagagctgtgacacaagcaatctcgtgttag 2373
OY 2342 ctggttcatatgatacccatctccctctctgttgaagcgttgcctgtatgtgtacatc 2401
|||||
Db 2374 ctggttcatatgatacccatctccctctctgttgaagcgttgcctgtatgtgtacatc 2433
OY 2402 gaagttaggaacaactgtgcccctacagtgatcccaagcgtgtgttcttctccgtctcgt 2461
|||||
Db 2434 gaagttaggaacaactgtgcccctacagtgatcccaagcgtgtgttcttctccgtctcgt 2493
OY 2462 gtttgtgtgtgatacaatccctgacgtgtcttctgaattgagcaactctctccagaagcaa 2521
|||||
Db 2494 gtttgtgtgtgatacaatccctgacgtgtcttctgaattgagcaactctctccagaagcaa 2553
OY 2522 ccttgagcagacctgttgggggcatcatctactcaagctgtacactgtccctagctcgtg 2581
|||||
Db 2554 ccttgagcagacctgttgggggcatcatctactcaagctgtacactgtccctagctcgtg 2613
OY 2582 tgttgacatgagcagactacgtgtggttccactcaagaatcttctgtagcgtgtctcc 2641
|||||
Db 2614 tgttgacatgagcagactacgtgtggttccactcaagaatcttctgtagcgtgtctcc 2673
OY 2642 tgttgacttgtggttggctgtgagtaacttgccttcttgaagagcagggcatgtgagt 2701
|||||
Db 2674 tgttgacttgtggttggctgtgagtaacttgccttcttgaagagcagggcatgtgagt 2733
OY 2702 gcaatgggacaacctgttggagaatcctgttggagaagaatggtcttcaatctccacactc 2761
|||||
Db 2734 gcaatgggacaacctgttggagaatcctgttggagaagaatggtcttcaatctccacactc 2793
OY 2762 gatctccatgatacttcttggacacactcctctcatatgggtgagatgatactgaaagc 2821
|||||
Db 2794 gatctccatgatacttcttggacacactcctctcatatgggtgagatgatactgaaagc 2853
OY 2822 tgtcttccagcagtlacggaattcccaagccctgtatatttctctgcaccaagtctta 2881
|||||
Db 2854 tgtcttccagcagtlacggaattcccaagccctgtatatttctctgcaccaagtctta 2913
OY 2882 ctggttggcgaagaaatgataagagaagccaactgttcttccaacggaagaatgtc 2941
|||||
Db 2914 ctggttggcgaagaaatgataagagaagccaactgttcttccaacggaagaatgtc 2973
OY 2942 agaatctgcatgagagagaagacccaactggaagctggcggtgtcatcagaacct 3001

Db 2974 agaatctgcatgagaggaacccaccacttgaaagctgggacgtgttcatttcagaacct 3033
QY 3002 ggttaaaagctacccgagatggaatgaaggtgctgtcgaatggcctggacatgaatttta 3061
Db 3034 ggttaaaagctacccgagatggaatgaaggtgctgtcgaatggcctggacatgaatttta 3093
QY 3062 tggagagcaaatcactctctctctggccacaaatggagaggggagagacacacacatgttc 3121
Db 3094 tggagagcaaatcactctctctctggccacaaatggagaggggagagacacacacatgttc 3153
QY 3122 aatctgacccgggtgttccccccgacccctcggccacccgacatcatccttggaagaacat 3181
Db 3154 aatctgacccgggtgttccccccgacccctcggccacccgacatcatccttggaagaacat 3213
QY 3182 tgccttgagatgagacacatcccgagagacacttgggggtctgtccccagacataacgttct 3241
Db 3214 tgccttgagatgagacacatcccgagagacacttgggggtctgtccccagacataacgttct 3273
QY 3242 gtttgacatgctgactgttcgaaagacacatctgtctatactgcccgttgaaagggcttc 3301
Db 3274 gtttgacatgctgactgttcgaaagacacatctgtctatactgcccgttgaaagggcttc 3333
QY 3302 tggagagcaatgagagagcgagagatggaagagatggccttgatgttggttgcataag 3361
Db 3334 tggagagcaatgagagagcgagagatggaagagatggccttgatgttggttgcataag 3393
QY 3362 caagctgaaagcaaaacaaagcagctgtcaggtggaatgagagagaaagctatactgttgc 3421
Db 3394 caagctgaaagcaaaacaaagcagctgtcaggtggaatgagagagaaagctatactgttgc 3453
QY 3422 ctgtgacctgttcgggggagatctaaggtgtcattcttgatgaaacacacagctgtgtga 3481
Db 3454 ctgtgacctgttcgggggagatctaaggtgtcattcttgatgaaacacacagctgtgtga 3513
QY 3482 ccccttaactcccgagagaaatatggaagctgtgtctgtaataataccgacagccgacat 3541
Db 3514 ccccttaactcccgagagaaatatggaagctgtgtctgtaataataccgacagccgacat 3573
QY 3542 tattctctacacacacatgtaagcgagacgtctctgggggagacagatggccatcat 3601
Db 3574 tattctctacacacacatgtaagcgagacgtctctgggggagacagatggccatcat 3633
QY 3602 cttcccatgggaagctgtgtctgtgtggtctctccctgttctctgaaacacacgttggagc 3661
Db 3634 cttcccatgggaagctgtgtctgtgtggtctctccctgttctctgaaacacacgttggagc 3693
QY 3662 aggtactaacctgacactgtgtcaagaagaatgtgaaatccctccctcaagttcttcagaaa 3721
Db 3694 aggtactaacctgacactgtgtcaagaagaatgtgaaatccctccctcaagttcttcagaaa 3753
QY 3722 cagtgatgacactgtgtcaataccttgaaaagagacagtggttcttcagagcaatltctga 3781
Db 3754 cagtgatgacactgtgtcaataccttgaaaagagacagtggttcttcagagcaatltctga 3813
QY 3782 tgcctggctggcgagcgagacatgagagatgacacgtgacacatctgatatgtctctgtatctc 3841
Db 3814 tgcctggctggcgagcgagacatgagagatgacacgtgacacatctgatatgtctctgtatctc 3873
QY 3842 caacctcaacgaagaatgtgtctgtaagccggctgtgtgaaagacataagagcagacat 3901
Db 3874 caacctcaacgaagaatgtgtctgtaagccggctgtgtgaaagacataagagcagacat 3933
QY 3902 gacctatgtgtgacacataatgaagctgtctaaagagagagcctttgtgaaactcttcaatga 3961
Db 3934 gacctatgtgtgacacataatgaagctgtctaaagagagagcctttgtgaaactcttcaatga 3993
QY 3962 gattgatgacccgctctcagacccctggcattcttaagttatgagacatccagagagaccc 4021
Db 3994 gattgatgacccgctctcagacccctggcattcttaagttatgagacatccagagagaccc 4053
QY 4022 ggaagaataatctctcaaggtgcccgaagaagatgggtgtgagatcgtgagacctcagatgg 4081
Db 4054 ggaagaataatctctcaaggtgcccgaagaagatgggtgtgagatcgtgagacctcagatgg 4113
QY 4082 taacttgcagaagaagacagacagcggtctctgggggacagacagctgtcttgc 4141
Db 4114 taacttgcagaagaagacagacagcggtctctgggggacagacagctgtcttgc 4173
QY 4142 gttcaatgaagaatgctgtctgataccaatgatactgacataagacacagatccagaga 4201
Db 4174 gttcaatgaagaatgctgtctgataccaatgatactgacataagacacagatccagaga 4233
QY 4202 gacagactgtctcagatggatgagatggcaaggggtccctaccaggtgaaagagctggaact 4261
Db 4234 gacagactgtctcagatggatgagatggcaaggggtccctaccaggtgaaagagctggaact 4293
QY 4262 tacacagacaaagtgttgccctttgttgaaagagactgataatgtccagacagagctg 4321
Db 4294 tacacagacaaagtgttgccctttgttgaaagagactgataatgtccagacagagctg 4353
QY 4322 gaaaggttttttctcagaatgtgtctgccaagctgtgtgtctgtcgtacatgtccctgtgt 4381
Db 4354 gaaaggttttttctcagaatgtgtctgccaagctgtgtgtgtctgtcgtacatgtccctgtgt 4413
QY 4382 cagctgtatcgttgcacccctttggcaagtaaccacagccttgaaactcaagccctgata 4441
Db 4414 cagctgtatcgttgcacccctttggcaagtaaccacagccttgaaactcaagccctgata 4473
QY 4442 caagaaacagttacacatgttctcagcaatgatactctctgagagacacggaaacctgtgaact 4501
Db 4474 caagaaacagttacacatgttctcagcaatgatactctctgagagacacggaaacctgtgaact 4533
QY 4502 ctlaaagccctcccaaaagacccctgtgtcggagacccgtgtatgaaagaaacacat 4561
Db 4534 ctlaaagccctcccaaaagacccctgtgtcggagacccgtgtatgaaagaaacacat 4593
QY 4562 cccaagacagccctgtccagagcagggagagagatggaaacatgtcccaagctcccaagac 4621
Db 4594 cccaagacagccctgtccagagcagggagagagatggaaacatgtcccaagctcccaagac 4653
QY 4622 catcatgacactcttccagaatgagagatggaaatgacaaagacacacacacacacacacacac 4681
Db 4654 catcatgacactcttccagaatgagagatggaaatgacaaagacacacacacacacacacacac 4713
QY 4682 gttgaagcagcacaataatcagaagaatgtctgtctgtctccccaagggcgagggggt 4741
Db 4714 gttgaagcagcacaataatcagaagaatgtctgtctgtctccccaagggcgagggggt 4773
QY 4742 gctctctcccaagaagaagaac 4801
Db 4774 gctctctcccaagaagaagaac 4833
QY 4802 catctcgaatctgtgtgaagcgtatgtcagatcatagcccaaaagcttaagaagaca 4861
Db 4834 catctcgaatctgtgtgaagcgtatgtcagatcatagcccaaaagcttaagaagaca 4893
QY 4862 gatctgggtgaatgaattgaatgaatggcgttctccctgggtgtctgaataactcaagc 4921
Db 4894 gatctgggtgaatgaattgaatgaatggcgttctccctgggtgtctgaataactcaagc 4953
QY 4922 acttctccgaatcagaagatgataatgatacacaacaaatgaagaagaacacactaaact 4981
Db 4954 acttctccgaatcagaagatgataatgatacacaacaaatgaagaagaacacactaaact 5013
QY 4982 ggcacagacagttctgacatcgaatltctcaacagcttgggaaagattatgacagagct 5041
Db 5014 ggcacagacagttctgacatcgaatltctcaacagcttgggaaagattatgacagagct 5073
QY 5042 ggaacccagaataatgtcaaggtgtgttcaataaagaagctgtgcatcaatcagctc 5101
Db 5074 ggaacccagaataatgtcaaggtgtgttcaataaagaagctgtgcatcaatcagctc 5133
QY 5102 ttctctgaaatgcatcaacaatgtcatctccgggccaacctgtgcaaaaggagagaaaccc 5161
Db 5134 ttctctgaaatgcatcaacaatgtcatctccgggccaacctgtgcaaaaggagagaaaccc 5193

QY 5162 tagccatagtgaattactgcttccatcatccctcgaatctccacagcagctctc 5221
|||||
Db 5194 tagccatagtgaattactgcttccatcatccctcgaatctccacagcagctctc 5253
QY 5222 agagcgtgctctgatcacacatcaatgagtgatctctgctgcatctgctgctc 5281
|||||
Db 5254 agagcgtgctctgatcacacatcaatgagtgatctctgctgcatctgctgctc 5313
QY 5282 aatgctctctgctccacagcagcttctgctgctgctgctgctgctgctgct 5341
5314 aatgctctctgctccacagcagcttctgctgctgctgctgctgctgctgct 5373
QY 5342 aaaaaccgcgcaggttcatagtgagtgagtgagtgagtgagtgagtgagtgag 5401
5374 aaaaaccgcgcaggttcatagtgagtgagtgagtgagtgagtgagtgagtgag 5433
QY 5402 ctggagatagtgcaatagtgctgctcctgccaacgtgcatatcatctgctc 5461
5434 ctggagatagtgcaatagtgctgctcctgccaacgtgcatatcatctgctc 5493
QY 5462 ccagcagaagctccatagtgctgctcctcacaacgtgctgctgctgctgct 5521
5494 ccagcagaagctccatagtgctgctcctcacaacgtgctgctgctgctgct 5553
QY 5522 gtagtggtgctgcaatcaacacgttcatagtcacacagcctcttctgctgct 5581
5554 gtagtggtgctgcaatcaacacgttcatagtcacacagcctcttctgctgct 5613
QY 5582 caacagcctatgctgctgctcctcacaacgtgctgctgctgctgctgctgct 5641
5614 caacagcctatgctgctgctcctcacaacgtgctgctgctgctgctgctgct 5673
QY 5642 caacttctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 5701
5674 caacttctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 5733
QY 5702 gtcgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 5761
5734 gtcgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 5793
QY 5762 aaacagcagcaatgctgctgctgctgctgctgctgctgctgctgctgct 5821
5794 aaacagcagcaatgctgctgctgctgctgctgctgctgctgctgctgct 5853
QY 5822 atcttggagcttggctgctgctgctgctgctgctgctgctgctgctgct 5881
5854 atcttggagcttggctgctgctgctgctgctgctgctgctgctgctgct 5913
QY 5882 ccccatattgctgctgctgctgctgctgctgctgctgctgctgctgctgct 5941
5914 ccccatattgctgctgctgctgctgctgctgctgctgctgctgctgctgct 5973
QY 5942 gctatcctcctgctgctgctgctgctgctgctgctgctgctgctgctgct 6001
5974 gctatcctcctgctgctgctgctgctgctgctgctgctgctgctgctgct 6033
QY 6002 tggctgagcgcagaaatgacatcttagaaatcaagaggttgagcaaaatataagagaa 6061
6034 tggctgagcgcagaaatgacatcttagaaatcaagaggttgagcaaaatataagagaa 6093
QY 6062 ggcgaagcgcgtgctgctgctgctgctgctgctgctgctgctgctgctgct 6121
6094 ggcgaagcgcgtgctgctgctgctgctgctgctgctgctgctgctgctgct 6153
QY 6122 cctggaggttaatgctgctgctgctgctgctgctgctgctgctgctgctgct 6181
6154 cctggaggttaatgctgctgctgctgctgctgctgctgctgctgctgctgct 6213
QY 6182 ttttaccagagagagcttctcttccaaataatagatattatccaaatccataagt 6241
6214 ttttaccagagagagcttctcttccaaataatagatattatccaaatccataagt 6273

QY 6242 acatcagacatagtgctgctgctgctgctgctgctgctgctgctgctgctgct 6301
6274 acatcagacatagtgctgctgctgctgctgctgctgctgctgctgctgctgct 6333
QY 6302 agaacagctgaggttcttgccttctgagagagctcccaagaaagatgagaggt 6361
6334 agaacagctgaggttcttgccttctgagagagctcccaagaaagatgagaggt 6393
QY 6362 tggctgagcgcaggttccggaacgtgctgctgctgctgctgctgctgctgct 6421
6394 tggctgagcgcaggttccggaacgtgctgctgctgctgctgctgctgctgct 6453
QY 6422 ctatagtgagcgcagaaacagcctctctacagcagctgctgctgctgctgct 6481
6454 ctatagtgagcgcagaaacagcctctctacagcagctgctgctgctgctgct 6513
QY 6482 tggctgcttctgctgctgctgctgctgctgctgctgctgctgctgctgct 6541
6514 tggctgcttctgctgctgctgctgctgctgctgctgctgctgctgctgct 6573
QY 6542 gaattgctccttaagtgctgctgctgctgctgctgctgctgctgctgctgct 6601
6574 gaattgctccttaagtgctgctgctgctgctgctgctgctgctgctgctgct 6633
QY 6602 ggaagaaatgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6661
6634 ggaagaaatgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6693
QY 6662 ccttggcagctgctgctgctgctgctgctgctgctgctgctgctgctgct 6721
6694 ccttggcagctgctgctgctgctgctgctgctgctgctgctgctgctgct 6753
QY 6722 aatagcaggtgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6781
6754 aatagcaggtgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6813
QY 6782 tggaggtgttctaaagaaacacccggaacatgctgctgctgctgctgct 6841
6814 tggaggtgttctaaagaaacacccggaacatgctgctgctgctgctgctgct 6873
QY 6842 atcttctctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6901
6874 atcttctctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6933
QY 6902 agactacgtgttctcagacacacgtgctgctgctgctgctgctgctgct 6961
6934 agactacgtgttctcagacacacgtgctgctgctgctgctgctgctgct 6993
QY 6962 aagtgtatgacacacttaaaagacctctcatlacacaaaaacagacagtagtgagct 7021
6994 aagtgtatgacacacttaaaagacctctcatlacacaaaaacagacagtagtgagct 7053
QY 7022 tgcagttctcaaatcttcttctcagagatgagatgagaaagctatgataagaaat 7081
7054 tgcagttctcaaatcttcttctcagagatgagatgagaaagctatgataagaaat 7113
QY 7082 cctgttcatagcgggtgctgctgctgctgctgctgctgctgctgctgctgct 7141
7114 cctgttcatagcgggtgctgctgctgctgctgctgctgctgctgctgctgct 7173
QY 7142 agtgtgtgagaaagagccagaggttgaatgctgctgctgctgctgctgct 7201
7174 agtgtgtgagaaagagccagaggttgaatgctgctgctgctgctgctgct 7233
QY 7202 gatactattcaatgctgctgctgctgctgctgctgctgctgctgctgctgct 7261
7234 gatactattcaatgctgctgctgctgctgctgctgctgctgctgctgctgct 7293
QY 7262 tgcctttagcctatgtctgttctgctgctgctgctgctgctgctgctgctgct 7321
7294 tgcctttagcctatgtctgttctgctgctgctgctgctgctgctgctgctgct 7353
QY 7322 cctatacctatgtgaaactctatlatgaaaccaaagacalaggttgaactcacac 7381

```
Db 7354 cctaaactatgtgaactctatctatgtgaacccaaatgacataatggtttgaactcaac 7413
OY 7382 ttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt 7441
Db 7414 ttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt 7473
OY 7442 aatcagtcagagcgttttttttttttttttttttttttttttttttttttttttttttt 7501
Db 7474 aatcagtcagagcgttttttttttttttttttttttttttttttttttttttttttttt 7533
OY 7502 ccatgtccatgtcccaagagactgtttcccggtgacacatccatgtctgtccatgtgtg 7561
Db 7534 ccatgtccatgtcccaagagactgtttcccggtgacacatccatgtctgtccatgtgtg 7593
OY 7562 ccaaggtttattagttgcgaagttttcgaagaagtttgaagccatgtgtgttcacgtcca 7621
Db 7594 ccaaggtttattagttgcgaagttttcgaagaagtttgaagccatgtgtgttcacgtcca 7653
OY 7622 cttttgtgaaagctgtctgtccagagctcctcaacatgttaattcagttacagaaatgg 7681
Db 7654 cttttgtgaaagctgtctgtccagagctcctcaacatgttaattcagttacagaaatgg 7713
OY 7682 tgcacatgtgtgctaaacatccctgtcttgaatccctctgataagctgttctgtgtgcaatg 7741
Db 7714 tgcacatgtgtgctaaacatccctgtcttgaatccctctgataagctgttctgtgtgcaatg 7773
OY 7742 acatgcaacaaatagttgtgtgtctctctgacagaggaactgtgtccattgttatattg 7801
Db 7774 acatgcaacaaatagttgtgtgtctctctgacagaggaactgtgtccattgttatattg 7833
OY 7802 tccatgtctcagagcagaggtgtcctcaaggtccatccatgtatagactcttaataactta 7861
Db 7834 tccatgtctcagagcagaggtgtcctcaaggtccatccatgtatagactcttaataactta 7893
OY 7862 gatccctgttaagagagcnaaagaatcaacacagccaaactgtcgggctgtgaagctgtgaagc 7921
Db 7894 gatccctgttaagagagcnaaagaatcaacacagccaaactgtcgggctgtgaagctgtgaagc 7953
OY 7922 caggagcattggatlaaagaattgttcgttcaaaccttaggagaacgtgtgcccattgttc 7981
Db 7954 caggagcattggatlaaagaattgttcgttcaaaccttaggagaacgtgtgcccattgttc 8013
OY 7982 ctgacgtctgtcacaatgtgtacacatgcacatcgaagatgtttatctgacacaagtgtatt 8041
Db 8014 ctgacgtctgtcacaatgtgtacacatgcacatcgaagatgtttatctgacacaagtgtatt 8073
OY 8042 attctcgtcttttttttttttttttttttttttttttttttttttttttttttttttttt 8101
Db 8074 attctcgtcttttttttttttttttttttttttttttttttttttttttttttttttttt 8133
OY 8102 tgtttgtacttttlaattgttattttgaatttgaatttgaatttgaatttgaatttgaatttga 8161
Db 8134 tgtttgtacttttlaattgttattttgaatttgaatttgaatttgaatttgaatttgaatttga 8193
OY 8162 agaattgacctcttctgtagaacctctgtgtatagaagagatgtgacctgtccccaatttt 8221
Db 8194 agaattgacctcttctgtagaacctctgtgtatagaagagatgtgacctgtccccaatttt 8253
OY 8222 ttattttcttaagttaagtttgcacatagatgaactagtgccctagaagaacaatgttatg 8281
Db 8254 ttattttcttaagttaagtttgcacatagatgaactagtgccctagaagaacaatgttatg 8313
OY 8282 gtccagatctcatalgacatlatatttttttttttttttttttttttttttttttttttttt 8341
Db 8314 gtccagatctcatalgacatlatatttttttttttttttttttttttttttttttttttttt 8373
OY 8342 tcaacttaacatcaataatatttttttttttttttttttttttttttttttttttttttttt 8401
Db 8374 tcaacttaacatcaataatatttttttttttttttttttttttttttttttttttttttttt 8433
OY 8402 gtataaagactagagatatlaaagttccagctacacccgtgtgcaagtattcagctca 8461
Db 8434 gtataaagactagagatatlaaagttccagctacacccgtgtgcaagtattcagctca 8493
OY 8462 ctgttttacaatatagattgttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 8521
Db 8494 ctgttttacaatatagattgttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 8553
OY 8522 gtccttttttttttttttttttttttttttttttttttttttttttttttttttttttt 8581
Db 8554 gtccttttttttttttttttttttttttttttttttttttttttttttttttttttttt 8613
OY 8582 agtttaacatgaattcttccacaggaagaaacagcttaagctgtgaaactgtgtgaaac 8641
Db 8614 agtttaacatgaattcttccacaggaagaaacagcttaagctgtgaaactgtgtgaaac 8673
OY 8642 acaactgtgtttatgtgcaatttagtaaccttcaaatattgtgtgtgtgtgtgtgtgtgtgt 8701
Db 8674 acaactgtgtttatgtgcaatttagtaaccttcaaatattgtgtgtgtgtgtgtgtgtgtgt 8733
OY 8702 cccatttaactgtcagagctcctcaaattttcaatcttcaatcttcaatcttcaatcttcaat 8761
Db 8734 cccatttaactgtcagagctcctcaaattttcaatcttcaatcttcaatcttcaatcttcaat 8793
OY 8762 aaaaacacacaaactcctcatalgtgagcaatttcagagtttctcaacccaatcttatt 8821
Db 8794 aaaaacacacaaactcctcatalgtgagcaatttcagagtttctcaacccaatcttatt 8853
OY 8822 ttctagtcagtaacatlttgttaaaaactgtttcaacttaacttaactgttcaactgtctt 8881
Db 8854 ttctagtcagtaacatlttgttaaaaactgtttcaacttaacttaactgttcaactgtctt 8913
OY 8882 gaagagaaagaaataatagagaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 8941
Db 8914 gaagagaaagaaataatagagaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 8973
OY 8942 tcaacttaactcttccacttttccaaaatttgaataatgaacgtgaaggtgaagac 9001
Db 8974 tcaacttaactcttccacttttccaaaatttgaataatgaacgtgaaggtgaagac 9033
OY 9002 ttcaagatttcaaatatttcttcaatttttcaatttttcaatttttcaatttttcaatttttca 9061
Db 9034 ttcaagatttcaaatatttcttcaatttttcaatttttcaatttttcaatttttcaatttttca 9093
OY 9062 tgcgtgaaagaaataatagatgttttgaagaattgaagttcaataatgtatttcaataata 9121
Db 9094 tgcgtgaaagaaataatagatgttttgaagaattgaagttcaataatgtatttcaataata 9153
OY 9122 agtaatgaagcattttcccaataactagtgatagtgatgtgtgtgtgtgtgtgtgtgtgt 9181
Db 9154 agtaatgaagcattttcccaataactagtgatagtgatgtgtgtgtgtgtgtgtgtgtgt 9213
OY 9182 tcaaaaatacagaatttcaagataatttccctcaatttcaatttcaatttcaatttcaatttca 9241
Db 9214 tcaaaaatacagaatttcaagataatttccctcaatttcaatttcaatttcaatttcaatttca 9273
OY 9242 tatgtttcccaatttactaaatcogfatcctaaatcctcaattataglaaglaag 9301
Db 9274 tatgtttcccaatttactaaatcogfatcctaaatcctcaattataglaaglaag 9333
OY 9302 caacttccattctgtgttccctgtgttttcaagggcaatttcaaaaatacaaaaggcact 9361
Db 9334 caacttccattctgtgttccctgtgttttcaagggcaatttcaaaaatacaaaaggcact 9393
OY 9362 gtgaactatttgaagaacacagcaatttlaatacgaattgaagaagcccttctgtgaag 9421
Db 9394 gtgaactatttgaagaacacagcaatttlaatacgaattgaagaagcccttctgtgaag 9453
OY 9422 ctgaagaacacatcatagttatcatcttcaatcaatcaatcaatcaatcaatcaatcaatca 9481
Db 9454 ctgaagaacacatcatagttatcatcttcaatcaatcaatcaatcaatcaatcaatcaatca 9513
OY 9482 tttttttacatttccctgtgttaaacctaatgtgtgtgaagaatttttaccactctatactc 9541
Db 9514 tttttttacatttccctgtgttaaacctaatgtgtgtgaagaatttttaccactctatactc 9573
```

OY	9542	aatcaagcaaaatttcctgtaatactccgtaggaatgtaactatgtaattgcaaatcc	9601
Db	9574	aattcaagcaaaatttcctgtaatactccgtaggaatgtaactatgtaattgcaaatcc	9633
OY	9602	tcaaatatcgtgtcctcaaaaatttcctgctttgtaactctttgggaacctcagaataattat	9661
Db	9634	tcaaatatcgtgtcctcaaaaatttcctgctttgtaactctttgggaacctcagaataattat	9693
OY	9662	taacacatgtgaatatgagaaatcacagaagaataataagccctctatacataaatgcc	9721
Db	9694	taacacatgtgaatatgagaaatcacagaagaataataagccctctatacataaatgcc	9753
OY	9722	cagcacatctcatgtgttaaaaaacacacaaacctccacactacgtgtatttcattatctgta	9781
Db	9754	cagcacatctcatgtgttaaaaaacacacaaacctccacactacgtgtatttcattatctgta	9813
OY	9782	ctgaagaacaaattgctttgtaactataaattgtgcacatcatctatcatcgtatagttaa	9841
Db	9814	ctgaagaacaaattgctttgtaactataaattgtgcacatcatctatcatcgtatagttaa	9873
OY	9842	tcaatgtaataagccaattgcgtggttttctctctgtggtgtnatataatagtaaatata	9901
Db	9874	tcaatgtaataagccaattgcgtggttttctctctgtggtgtnatataatagtaaatata	9933
OY	9902	ttttccaaagagcagatgtgtcaatgaatcacgaacctttgatattgaagacataatttg	9961
Db	9934	ttttccaaagagcagatgtgtcaatgaatcacgaacctttgatattgaagacataatttg	9993
OY	9962	gaccttggtatatactataagaataatgtaataactgmgagaatattgctctaattcttt	10021
Db	9994	gaccttggtatatactataagaataatgtaataactgmgagaatattgctctaattcttt	10053
OY	10022	caaaaatgtgtacatccccccttaaaaangtctctattccataaagattatgcttgtatccc	10081
Db	10054	caaaaatgtgtacatccccccttaaaaangtctctattccataaagattatgcttgtatccc	10113
OY	10082	ttcttaaaccttaagaatgaagctgtttttgtgctctttgtttcattcattgtggccttaacc	10141
Db	10114	ttcttaaaccttaagaatgaagctgtttttgtgctctttgtttcattcattgtggccttaacc	10173
OY	10142	aagcactttacgctgtctgtaatggtgatactatttttgactcgtgaatactgtagaattgca	10201
Db	10174	aagcactttacgctgtctgtaatggtgatactatttttgactcgtgaatactgtagaattgca	10233
OY	10202	aaactagacaaaagtttcacacacagatttctaaagttaatactatttcattaaagaagaaa	10261
Db	10234	aaactagacaaaagtttcacacacagatttctaaagttaatactatttcattaaagaagaaa	10293
OY	10262	aagaaaaaaaattttgatgtcctaacttaacttaagaagatttaaagtcatatttctat	10321
Db	10294	aagaaaaaaaattttgatgtcctaacttaacttaagaagatttaaagtcatatttctat	10355
OY	10322	gtgttaatatatgagtccaacaataaagctgtgtgacgtttctgtttaaaaaaaaataaa	10381
Db	10354	gtgttaatatatgagtccaacaataaagctgtgtgacgtttctgtttaaaaaaaaataaa	10413
OY	10382	aa	10441
Db	10414	aa	10473
OY	10442	a 10442	
Db	10474	a 10474	

RESULT	7
AA506121	
ID	AA506121 standard; cDNA; 9854 BP
XX	
AC	AA506121;
XX	
DT	12-SEP-2001 (first entry)

[illegible]

Db 248 tgcctccagaggtcccgagccacacgctgagggtgctgctgaggaatggtctgtc 307
QY 301 ggcctcagctgaggtgctgctgtggaagaacctcattcagaagaacacacatgctc 360
Db 308 ggcctcagctgaggtgctgctgtggaagaacctcattcagaagaacacacatgctc 367
QY 361 agctgtactcaggaagtgctgctgctctattatcttcctgacccctgctgctgcgc 420
Db 368 agctgtactcaggaagtgctgctgctctattatcttcctgacccctgctgctgcgc 427
QY 421 tgaagtaacccactatgacacacatgaaatgacatttcccaataaagccatctgc 480
Db 428 tgaagtaacccactatgacacacatgaaatgacatttcccaataaagccatctgc 487
QY 481 caggaacactcctctgtgctcaggggattatctgttaatgcacaaacccctgttccgt 540
Db 488 caggaacactcctctgtgctcaggggattatctgttaatgcacaaacccctgttccgt 547
QY 541 accgagctcctgggagagctcccgaggtgttggaacttaacatcatctgtgctc 600
Db 548 accgagctcctgggagagctcccgaggtgttggaacttaacatcatctgtgctc 607
QY 601 ggcctgtctcagatgctcggagagctcttcttatacagccagaaagacacagatgaag 660
Db 608 ggcctgtctcagatgctcggagagctcttcttatacagccagaaagacacagatgaag 667
QY 661 acatgcgcaaatgtctgagagacattcagagatcagaatccaatccaacttgaagc 720
Db 668 acatgcgcaaatgtctgagagacattcagagatcagaatccaatccaacttgaagc 727
QY 721 ttaagaatttcctggtggaacaatgaaacctctctgtgttccatatacaacctctcc 780
Db 728 ttaagaatttcctggtggaacaatgaaacctctctgtgttccatatacaacctctcc 787
QY 781 tcccaaatgtactgtggaacaatgctgagggctgaatgcatctccacaagtatttt 840
Db 788 tcccaaatgtactgtggaacaatgctgagggctgaatgcatctccacaagtatttt 847
QY 841 tgcgaagctacccagattacatttgacaagctgtgcaatgcatataaataatagaagata 900
Db 848 tgcgaagctacccagattacatttgacaagctgtgcaatgcatataaataatagaagata 907
QY 901 ttaaaacttgctgacacgaagatttctgagcttgtgagctacccaaggaagaaactgctg 960
Db 908 ttaaaacttgctgacacgaagatttctgagcttgtgagctacccaaggaagaaactgctg 967
QY 961 cagcagagcagagctactgcttccacaatgacatcctgaaagccaatcccgaaacactaa 1020
Db 968 cagcagagcagagctactgcttccacaatgacatcctgaaagccaatcccgaaacactaa 1027
QY 1021 aactcaatccctctcccgaggaagagctgtgctgaagccacaacaaacattgttcata 1080
Db 1028 aactcaatccctctcccgaggaagagctgtgctgaagccacaacaaacattgttcata 1087
QY 1081 gttctggagctcggcccgagagctgttcaagcatgagaagctggaatgacatgacagag 1140
Db 1088 gttctggagctcggcccgagagctgttcaagcatgagaagctggaatgacatgacagag 1147
QY 1141 agctgtatgttctgacacatgttaacagctccagctcccccacacacacacacacagctg 1200
Db 1148 agctgtatgttctgacacatgttaacagctccagctcccccacacacacacacacagctg 1207
QY 1201 tgtctgtatgtctgaggggcatcccgaggaaggggagcttgaagatcaagtctcaact 1260
Db 1208 tgtctgtatgtctgaggggcatcccgaggaaggggagcttgaagatcaagtctcaact 1267
QY 1261 ggtataggaac 1320
Db 1268 ggtataggaac 1327
QY 1321 aaacctctatgacacactacacactctactgacatattgattgaagaattggaagt 1380
Db 1328 aaacctctatgacacactacacactctactgacatattgattgaagaattggaagt 1387
QY 1381 ctagtccctcttcccgacatctatctggaagagctcgtgctgttggaagatcc 1440
Db 1388 ctagtccctcttcccgacatctatctggaagagctcgtgctgttggaagatcc 1447
QY 1441 tgtataacctgacacactccagacacacacacacacacacacacacacacacacacacac 1500
Db 1448 tgtataacctgacacactccagacacacacacacacacacacacacacacacacacacac 1507
QY 1501 aggaactgctgtgttccatgacatcgtgaagagcatggaaggaactcaagcccaagatct 1560
Db 1508 aggaactgctgtgttccatgacatcgtgaagagcatggaaggaactcaagcccaagatct 1567
QY 1561 ggaacttcatggaagacacagccagaaatggaactgttccagatgctgttgagacagag 1620
Db 1568 ggaacttcatggaagacacagccagaaatggaactgttccagatgctgttgagacagag 1627
QY 1621 acaatgacacactttgggaacacagcagtggaatggaatggaacacacacacacacac 1680
Db 1628 acaatgacacactttgggaacacagcagtggaatggaatggaacacacacacacacac 1687
QY 1681 tggcgtttttgccaagacacacagagatgctcagatccaatgaatgctgtgtgacact 1740
Db 1688 tggcgtttttgccaagacacacagagatgctcagatccaatgaatgctgtgtgacact 1747
QY 1741 ggaaggaagcttcaacagagacacacagcgaatcccgacacacacacacacacacac 1800
Db 1748 ggaaggaagcttcaacagagacacacagcgaatcccgacacacacacacacacacac 1807
QY 1801 gttcaacactgaacacagctagaacacacacacacacacacacacacacacacacacac 1860
Db 1808 gttcaacactgaacacagctagaacacacacacacacacacacacacacacacacacac 1867
QY 1861 tggagctgctgagatgagagagagatctgagctgtgattgttcaactggaattactcag 1920
Db 1868 tggagctgctgagatgagagagagatctgagctgtgattgttcaactggaattactcag 1927
QY 1921 gcaagattgagctgcccccatatgtcaagatcaagatccagatgagatgagatgagatg 1980
Db 1928 gcaagattgagctgcccccatatgtcaagatcaagatccagatgagatgagatgagatg 1987
QY 1981 agaggaac 2040
Db 1988 agaggaac 2047
QY 2041 aggaatgcggttaagctcgggggggcttgcctacttcgagagatggttggaagagca 2100
Db 2048 aggaatgcggttaagctcgggggggcttgcctacttcgagagatggttggaagagca 2107
QY 2101 tcatcagaggtgctgacgggaccccgagaaacacacacacacacacacacacacacacac 2160
Db 2108 tcatcagaggtgctgacgggaccccgagaaacacacacacacacacacacacacacac 2167
QY 2161 atccctgttaagcttgatgacatcttctcggggtggtgagacccggttaatgcccccttca 2220
Db 2168 atccctgttaagcttgatgacatcttctcggggtggtgagacccggttaatgcccccttca 2227
QY 2221 tgaagctgctgctgattacacagctggtgacatccaaggggagatggttatgagaag 2280
Db 2228 tgaagctgctgctgattacacagctggtgacatccaaggggagatggttatgagaag 2287
QY 2281 agcagcggctgaaagagacacatgagacatctgagctgagacacacacacacacacacac 2340
Db 2288 agcagcggctgaaagagacacatgagacatctgagctgagacacacacacacacacacac 2347
QY 2341 gctggttcaatagtagcctcaatcttctctgttgaacgctgagcgtgagtgatcc 2400
Db 2348 gctggttcaatagtagcctcaatcttctctgttgaacgctgagcgtgagtgatcc 2407
QY 2401 tgaagttaggaac 2460
Db 2408 tgaagttaggaac 2467

Db 4628 ccaaccaagagacccctccccaagaatggaagcagcaatgacgaacccctccacgcatgccc 4687
QY 4681 agtgaagcagcagaataatcaagaagatgctgcctgtgtctcccccaggcgagggggc 4740
Db 4688 agtgaagcagcagaataatcaagaagatgctgcctgtgtctcccccaggcgagggggc 4747
QY 4741 tgcctctccacaagaagaacaaacacgctgcagatccctccagacctgcagagaagaa 4800
Db 4748 tgcctctccacaagaagaacaaacacgctgcagatccctccagacctgcagagaagaa 4807
QY 4801 acattcgagatctgtgtaagaacgfatgtgcagatcatagccaaagcttaagaaca 4860
Db 4808 acattcgagatctgtgtaagaacgfatgtgcagatcatagccaaagcttaagaaca 4867
QY 4861 agatcgtgtgtaagatgattagatagcggtcttccctgggtgtaagtaataactaag 4920
Db 4868 agatcgtgtgtaagatgattagatagcggtcttccctgggtgtaagtaataactaag 4927
QY 4921 cactctccgagtcagaaagattatgatactgcaacaagaatgaaagaaacactaagc 4980
Db 4928 cactctccgagtcagaaagattatgatactgcaacaagaatgaaagaaacactaagc 4987
QY 4981 tggcacaagacagcttcgcagatcagatcttccacaagccttgggaagatattatagagac 5040
Db 4988 tggcacaagacagcttcgcagatcagatcttccacaagccttgggaagatattatagagac 5047
QY 5041 tggacaccagaataatgataagtgatggttcaatacaagagcgctgcagatcaagct 5100
Db 5048 tggacaccagaataatgataagtgatggttcaatacaagagcgctgcagatcaagct 5107
QY 5101 cttctctgaatgtcatcaacaatgcatctccggcgccaacgctgcacaagggagagaaac 5160
Db 5108 cttctctgaatgtcatcaacaatgcatctccggcgccaacgctgcacaagggagagaaac 5167
QY 5161 ctgagccattatggaattactgcttcaatcatcccttgaaactccacaagcagagctct 5220
Db 5168 ctgagccattatggaattactgcttcaatcatcccttgaaactccacaagcagagctct 5227
QY 5221 cagaggtggtctctgatacacaatcagtgatgtctctgtgctcatctgtatctcttg 5280
Db 5228 cagaggtggtctctgatacacaatcagtgatgtctctgtgctcatctgtatctcttg 5287
QY 5281 caatgtcctctgtccagcagcagcttgctcatctccctgataccagagcggtgcaagaa 5340
Db 5288 caatgtcctctgtccagcagcagcttgctcatctccctgataccagagcggtgcaagaa 5347
QY 5341 caaaacacgctgcatcatcagtgaggtgaagctgtcatctactgtgctctcaatttg 5400
Db 5348 caaaacacgctgcatcatcagtgaggtgaagctgtcatctactgtgctctcaatttg 5407
QY 5401 tctgggatatgtgcaatctacgtgtccctgcagacatggtgcatcatctcatctgct 5460
Db 5408 tctgggatatgtgcaatctacgtgtccctgcagacatggtgcatcatctcatctgct 5467
QY 5461 tccagcagaagctctctgtgctccccaacatctgcctgtgtagcctctactttgc 5520
Db 5468 tccagcagaagctctctgtgctccccaacatctgcctgtgtagcctctactttgc 5527
QY 5521 tgratgtgtgtgcaatcacacccctcatgtaccagcccttgggttcaagaatcccca 5580
Db 5528 tgratgtgtgtgcaatcacacccctcatgtaccagcccttgggttcaagaatcccca 5587
QY 5581 gcaagcctatgtgtgtccacacgctgtgaacctcttcaatggcatatgtgcagcggtg 5640
Db 5588 gcaagcctatgtgtgtccacacgctgtgaacctcttcaatggcatatgtgcagcggtg 5647
QY 5641 caaccttgtgtgcagcgctgtccacgacaataagctgataataatcaatgatactcgtga 5700
Db 5648 caaccttgtgtgcagcgctgtccacgacaataagctgataataatcaatgatactcgtga 5707
QY 5701 agtcgctgtctgtgactcccaacatttgcctgtgagcagggctcagcagcatggtga 5760
Db 5708 agtcgctgtctgtgactcccaacatttgcctgtgagcaggggtcagcagatggtga 5767
QY 5761 aaaacagagcaatgtgctgatactgcctgcgaagaagtttggggagaatcgcttctgtcacat 5820
Db 5768 aaaacagagcaatgtgctgatactgcctgcgaagaagtttggggagaatcgcttctgtcacat 5827
QY 5821 tatcttggacttggctgggaacgaacccctctccgcataagcgctgtgaaggggtgtctct 5880
Db 5828 tatcttggacttggctgggaacgaacccctctccgcataagcgctgtgaaggggtgtctct 5887
QY 5881 tccatactacttctgttccagctacagatctcttcatagggcccaagacctttaatgcaa 5940
Db 5888 tccatactacttctgttccagctacagatctcttcatagggcccaagacctttaatgcaa 5947
QY 5941 agctatctctcttgaatgataagagaatgaagatgtgaagcggggaagacagaagaaattcttg 6000
Db 5948 agctatctctcttgaatgataagagaatgaagatgtgaagcggggaagacagaagaaattcttg 6007
QY 6001 atggtgagggcagagaatgacatcttaagaatcaagagatgacagaatataatagaaga 6060
Db 6008 atggtgagggcagagaatgacatcttaagaatcaagagatgacagaatataatagaaga 6067
QY 6061 agcgaagcctgctgttgaacgagatttgcgtggtgacatccctccgtgtgagtgcttgagc 6120
Db 6068 agcgaagcctgctgttgaacgagatttgcgtggtgacatccctccgtgtgagtgcttgagc 6127
QY 6121 tccctggaggttaatgaggtgctggaaaaatcaacttcaagaatgtaacagagatacca 6180
Db 6128 tccctggaggttaatgaggtgctggaaaaatcaacttcaagaatgtaacagagatacca 6187
QY 6181 ctgttaccagaagagatgctcttcccttaacaaaatagatcttcaacaatccatagaag 6240
Db 6188 ctgttaccagaagagatgctcttcccttaacaaaatagatcttcaacaatccatagaag 6247
QY 6241 taacatcagaacaatggtgctactgcctccagcttgaatgcaatcaacagagctgttgacgtgga 6300
Db 6248 taacatcagaacaatggtgctactgcctccagcttgaatgcaatcaacagagctgttgacgtgga 6307
QY 6301 gagaacagctgagatgctcttcccttggagagagatccccaagagaagaatttgcagag 6360
Db 6308 gagaacagctgagatgctcttcccttggagagagatccccaagagaagaatttgcagag 6367
QY 6361 ttggtgaatggggtgcaatcgcgaactgggctcgtgtgaagtatgagaagaataatgctgtga 6420
Db 6368 ttggtgaatggggtgcaatcgcgaactgggctcgtgtgaagtatgagaagaataatgctgtga 6427
QY 6421 actatagtgagggcaacaaacgcgaagctctctacagccatgtgcttgcgcgggctc 6480
Db 6428 actatagtgagggcaacaaacgcgaagctctctacagccatgtgcttgcgcgggctc 6487
QY 6481 ctgtgtgttctctgatatcccccacacagcagatcgatcccaagcccggtgtctgt 6540
Db 6488 ctgtgtgttctctgatatcccccacacagcagatcgatcccaagcccggtgtctgt 6547
QY 6541 ggaattgtgcccataagtggttgaagaagccacacagtgatcccaagcccggtgtctgt 6600
Db 6548 ggaattgtgcccataagtggttgaagaagccacacagtgatcccaagcccggtgtctgt 6607
QY 6601 tggagaagtgtggaagccttgcacatgatatgatacagtgatcaatgtaaggttcaagt 6660
Db 6608 tggagaagtgtggaagccttgcacatgatatgatacagtgatcaatgtaaggttcaagt 6667
QY 6661 gctctggcagctgctcagacatctaaataatggttggagatgtgtatatacatggtgtac 6720
Db 6668 gctctggcagctgctcagacatctaaataatggttggagatgtgtatatacatggtgtac 6727
QY 6721 gaataagcaggttccaaacccggaaccttgagcctgtccaggaattcttggacttgacatc 6780
Db 6728 gaataagcaggttccaaacccggaaccttgagcctgtccaggaattcttggacttgacatc 6787
QY 6781 ctggaagtgttcttaagaagaagaacacggaacatgcatcaatccagctcattccat 6840
Db 6788 ctggaagtgttcttaagaagaagaacacggaacatgcatcaatccagctcattccat 6847

QY	6841	tattctctgtgccagatattcagcatccctctccagagcaaaagcgatccacatag	6500
Db	6848	tattctctgtgccagatattcagcatccctctccagagcaaaagcgatccacatag	6507
QY	6901	aagactactgtttcttcagacaacaacttggaccaagtattttgtgaactttggccaagacc	6560
Db	6908	aagactactgtttcttcagacaacaacttggaccaagtattttgtgaactttggccaagacc	6567
QY	6961	aaagtgtgtatgtccacttaaaagacctctcatcacaaaaacagacagtagtagacg	7020
Db	6968	aaagtgtgtatgtccacttaaaagacctctcatcacaaaaacagacagtagtagacg	7027
QY	7021	ttgcagttctcacatctttcttaccagatgtagaagaagtgaagaagactatgtatgaagaa	7080
Db	7028	ttgcagttctcacatctttcttaccagatgtagaagaagtgaagaagactatgtatgaagaa	7087
QY	7081	ttccgtttcaacgggtgtgctgtgaagtagaaggcgaaacttagactttccctttgcacacatgt	7140
Db	7088	ttccgtttcaacgggtgtgctgtgaagtagaaggcgaaacttagactttccctttgcacacatgt	7147
QY	7141	aagctgttggaagaaagagccaggaagcttgatgttgaggagaagatgaacttgcatactgtac	7200
Db	7148	aagctgttggaagaaagagccaggaagcttgatgttgaggagaagatgaacttgcatactgtac	7207
QY	7201	tgatactattcaatgtccaatgtccaatltccaatgtcaaaacaaatltccattacaggggca	7260
Db	7208	tgatactattcaatgtccaatgtccaatltccaatgtcaaaacaaatltccattacaggggca	7267
QY	7261	gtgcctttgtagcctatgtctgttatgagctcttcacagtgaagaagacttgaatttaattttt	7320
Db	7268	gtgcctttgtagcctatgtctgttatgagctcttcacagtgaagaagacttgaatttaattttt	7327
QY	7321	accataaccatgtggaaccctctatcttggaaccccaatgtgaacataggttttgaactcca	7380
Db	7328	accataaccatgtggaaccctctatcttggaaccccaatgtgaacataggttttgaactcca	7387
QY	7381	ctttttttttttttgttccctgtgtactcccatcttggggtgtgcaacaataatcatcaag	7440
Db	7388	ctttttttttttttgttccctgtgtactcccatcttggggtgtgcaacaataatcatcaag	7447
QY	7441	taatacatggccagagatatttgttccaataatccaagaagtatgcatactccatcaactaa	7500
Db	7448	taatacatggccagagatatttgttccaataatccaagaagtatgcatactccatcaactaa	7507
QY	7501	gccatgccaatgccagagagactgtttcccggtgtacaacatcccatgtcgtgccaatgagtt	7560
Db	7508	gccatgccaatgccagagagactgtttcccggtgtacaacatcccatgtcgtgccaatgagtt	7567
QY	7561	gccagagttatagtgccaaagttttccaagaagtttgaagccaatggtgtgtacatgtctc	7620
Db	7568	gccagagttatagtgccaaagttttccaagaagtttgaagccaatggtgtgtacatgtctc	7627
QY	7621	acttttggaaaagctgtctgtcccgacaggtctacaacatcttgaaatctgaagttgaacgaatg	7680
Db	7628	acttttggaaaagctgtctgtcccgacaggtctacaacatcttgaaatctgaagttgaacgaatg	7687
QY	7681	gtgcacatgctgtgtcaacatccctgtttgaattccctctgataagactgttctgtgtgcagt	7740
Db	7688	gtgcacatgctgtgtcaacatccctgtttgaattccctctgataagactgttctgtgtgcagt	7747
QY	7741	aacatgtcaacaaaaatgttgggtgtctctctagggccagggaaacttgttccatgttatatt	7800
Db	7748	aacatgtcaacaaaaatgttgggtgtctctctagggccagggaaacttgttccatgttatatt	7807
QY	7801	gtccctatgcttcggagccaatgtgtctacaggtcatccttatgagactcttaataatactt	7860
Db	7808	gtccctatgcttcggagccaatgtgtgtctacaggtcatccttatgagactcttaataatactt	7867
QY	7861	agatctctgttaagagccaagaatccaacagccaactgctgtgggctgtgcaagctgtctgaag	7920
Db	7868	agatctctgttaagagccaagaatccaacagccaactgctgtgggctgtgcaagctgtctgaag	7927

QY	7921	ccaggcagatggatgaagaagattgqgtlccaacccagggaagcctggtgccatttgc	7980
Db	7928	ccaggcatgggattaaagagattgycgtlccaacccagggaagcctggtgccatttgc	7987
QY	7981	cctacgctgcgcaaaatgatacctgatacctccaagtgattatctgaaccaagtta	8040
Db	7988	ccgaactgcgcgcaaaatgatacctgatacctccaagtgattatctgaaccaagtgat	8047
QY	8041	tattctgcgtcttggatataatctcgaagaatgaaagatgagtgattttgaca	8100
Db	8048	tattctgcgtcttggatataatctcgaagaatgaaagatgagtgatttttgc	8107
QY	8101	atgtttgacctttaaattgatttggaaatttaagtctcctacgtgaccttgaaccc	8160
Db	8108	atgtttgacctttaaattgatttggaaatttaagtctcctacgtgaccttgaaccc	8167
QY	8161	tagaatgcccccttgtagaaccccttggtatagagagatagtgccactgccccat	8220
Db	8168	tagaatgcccccttgtagaaccccttggtatagagagatagtgccactgccccat	8227
QY	8221	tttatcttctatgtaagatttgcaatcaagtcagtcagtgccatgaagaatgtag	8280
Db	8228	tttatcttctatgtaagatttgcaatcaagtcagtcagtgccatgaagaatgtag	8287
QY	8281	ggtcagagctccagacattataattgagtttcctccaacatttagatatacctta	8340
Db	8288	ggtcagagctccagacattataattgagtttcctccaacatttagatatacctta	8347
QY	8341	cctacattatcaatcaaatattttttgagtgtagtcgttagctgaagaagatagta	8400
Db	8348	cctacattatcaatcaaatattttttgagtgtagtcgttagctgaagaagatagta	8407
QY	8401	cgtataaagacagagagattttaagttcgaataccttccttgccagtttaccgct	8460
Db	8408	cgtataaagacagagagattttaagttcgaataccttccttgccagtttaccgct	8467
QY	8461	actgtgttacaacaatagtggtctctgtgtgtgtgtaagagcccaactgtataac	8520
Db	8468	actgtgttacaacaatagtggtctctgtgtgtgtgtaagagcccaactgtataac	8527
QY	8521	agcccttttttttttttttttaattgcaacaatgcaaaacgaagaagtataaggt	8580
Db	8528	agcc- ttttttttttttttttttaattgcaacaatgcaaaacgaagaagtataaggt	8586
QY	8581	aagtttaacaatgatatcttccaacagagaaacagctagctctgaaactgtgtgaa	8640
Db	8587	aagtttaacaatgatatcttccaacagagaaacagctagctctgaaactgtgtgaa	8646
QY	8641	cacaactgtgttttatgagcatttagtaacctccaataatgtgctttgcagatat	8700
Db	8647	cacaactgtgttttatgagcatttagtaacctccaataatgtgctttgcagatat	8706
QY	8701	ccccattaaatctgacagttccaaatttttccatcttcaacacagtcagcaaga	8760
Db	8707	ccccattaaatctgacagttccaaatttttccatcttcaacacagtcagcaaga	8766
QY	8761	taaaaaacaacaatactccaatagtgagcattttccagagtttccaaccagctta	8820
Db	8767	taaaaaacaacaatactccaatagtgagcattttccagagtttccaaccagctta	8826
QY	8821	ttttctagtcgaagaaatgtttaaataactgtttccaactcaactacgttaactgt	8880
Db	8827	ttttctagtcgaagaaatgtttaaataactgtttccaactcaactacgttaactgt	8886
QY	8881	tgaagaaagaagaataatgagaaactatgtttgaggagttcaagtatcttcca	8940
Db	8887	tgaagaaagaagaataatgagaaactatgtttgaggagttcaagtatcttcca	8946
QY	8941	atcattactaacctttctcactttttccaatattgaaataacgtataaagtgta	9000
Db	8947	atcattactaacctttctcactttttccaatattgaaataacgtataaagtgta	9006
QY	9001	cttcaacttcaaatatacttctataattttttaaatttaccgaatataataacca	9060

```

Db 9007 cttcaacattcaataacccttcacatttcaattcaacgaatataataccca 9066
Oy 9061 ctgctgaataaagaaaaatgattgtttagaagttaagaatcatattgatttaaat 9120
Db 9067 ctgctgaataaagaaaaatgattgtttagaagttaagaatcatattgatttaaat 9126
Oy 9121 aagtaataagagcatattcccaataactagatagatgacatgcttgcaattcaaglatc 9180
Db 9127 aagtaataagagcatattcccaataactagatagatgacatgcttgcaattcaaglatc 9186
Oy 9181 ttcaaaaatacagaattttaagaataattccoccatataattttcaaatcaagaag 9240
Db 9187 ttcaaaaatacagaattttaagaataattccoccatataattttcaaatcaagaag 9246
Oy 9241 ttatggttcccatatttctactaataacgtatctccaattcttcataatagtaaatcctatga 9300
Db 9247 ttatggttcccatatttctactaataacgtatctccaattcttcataatagtaaatcctatga 9306
Oy 9301 gcaactccctactcgttcctcctgatttcaaggccataatttaaaaaatcaaaagcac 9360
Db 9307 gcaactccctactcgttcctcctgatttcaaggccataatttaaaaaatcaaaagcac 9366
Oy 9361 tgtgaactatttgaagaacacagacatttaataacagattgaagaagccctctctgaa 9420
Db 9367 tgtgaactatttgaagaacacacacatttataacagattgaagaagccctctctgaa 9426
Oy 9421 gctgaagaacacatctatagatatacatcttcataactcgtgttactcctttaaatga 9480
Db 9427 gctgaagaacacatctatagatatacatcttcataactcgtgttactcctttaaatga 9486
Oy 9481 attttacatttccctcgtgaacataatgttgtagaattttaccacactatct 9540
Db 9487 attttacatttccctcgtgaacataatgttgtagaattttaccacactatct 9546
Oy 9541 caatcaagaacaaattctgtatattccctcgtgaatgtlaactatgttgagattcagaat 9600
Db 9547 caatcaagaacaaattctgtatattccctcgtgaatgtlaactatgttgagattcagaat 9606
Oy 9601 cctcaaatcagctgttcaaaaatttctgcttgcacatttggaacactcagaacacta 9660
Db 9607 cctcaaatcagctgttcaaaaatttctgcttgcacatttggaacactcagaacacta 9666
Oy 9661 ttaacaactgtgaatatagaataacagagaataataaagccctctatacataatgc 9720
Db 9667 ttaacaactgtgaatatagaataacagagaataataaagccctctatacataatgc 9726
Oy 9721 ccagcacaattcattgttaaaaaaacacacacactcacactactgtattcattatctgt 9780
Db 9727 ccagcacaattcattgttaaaaaaacacacacactcacactactgtattcattatctgt 9786
Oy 9781 actgaagaacaaatgcttctgtgacttaaatgttgacatcatcatca 9830
Db 9787 actgaagaacaaatgcttctgtgacttaaatgttgacatcatcatca 9836

```

```

RESULT      8
ID AAS06120 standard; cDNA; 9741 BP.
AC AAS06120;
DE 12-SEP-2001 (first entry)
XX Human ABC1 DNA sequence #1.
XX Human ABC1 gene; atherosclerosis; reverse transport; cholesterol;
KW cardiovascular; neurological; Tangier disease; LCAT deficiency;
KW lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
OS Homo sapiens.
XX Key Location/Qualifiers
FH

```

```

FT CDS 185..6967
FT /tag= a
FT /product= "Human ABC1 protein"
Mo200130848-A2.
03-MAY-2001.
26-OCT-2000; 2000WO-EPI0886.
26-OCT-1999; 99EP-0402668.
01-MAR-2000; 2000US-0186260.
PA (AVET ) AVENTIS PHARMA SA.
XX Deneffe P, Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L;
PI Lemoine C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;
PI Dean M;
XX WPI: 2001-316327/33.
DR P-PSDB: AAU02176.
PT New human ABC1 nucleic acids and polypeptides for treating
PT atherosclerosis, malaria and diabetes -
XX Claim 1; Page 204-208; 368pp; English.
XX The sequence represents the coding sequence #1 of human ABC1. The
XX nucleic acid sequence, primers and probes derived from the ABC1 sequence,
XX and polypeptides and vectors are useful for the prevention of
XX atherosclerosis, in a subject affected by a dysfunction in the reverse
XX transport of cholesterol. The polypeptide encoded by the ABC1 gene is
XX useful for screening for an active ingredient for the prevention or
XX treatment of a disease resulting from dysfunction in the reverse
XX transport of cholesterol. The nucleic acids and polypeptides are also
XX useful for treating and preventing cardiovascular and neurological
XX pathologies, and other diseases e.g. Tangier disease, lecithin-
XX cholesterol (LCAT) deficiency, malaria and diabetes.
SQ Sequence 9741 BP; 2650 A; 2180 C; 2290 G; 2620 T; 1 other;
Query Match 92.6%; Score 9672.8; DB 22; Length 9741;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 9705; Conservative 0; Mismatches 18; Indels 2; Gaps 2;
Oy 106 ctgtttttcccggttctgttttccctctccggaagctgtcaagggtaga 165
Db 1 ctgtttttcccggttctgttttccctctccggaagctgtcaagggtaga 60
Oy 166 gaaagagagcgaacacaaaggggaagtaatgacagccagggcgctcctgt 225
Db 61 gaaagagagcgaacacaaaggggaagtaatgacagccagggcgctcctgt 119
Oy 226 gtgagctctgcccgtccttccagggctccgagcacaagctgtgctgtgctgag 285
Db 120 gtgagctctgcccgtccttccagggctccgagcacaagctgtgctgtgctgag 179
Oy 286 ggaacatgctgttggcctcagctgaggttgcctgtgtggaagacactcacttcaaga 345
Db 180 ggaacatgctgttggcctcagctgaggttgcctgtgtggaagacactcacttcaaga 239
Oy 346 gaagacaacatgacgttacttgaagtgagcgcgcgtctattatctcccgatcc 405
Db 240 gaagacaacatgacgttacttgaagtgagcgcgcgtctattatctcccgatcc 299
Oy 406 tgaatctgttgcgtgaactacacacatgaagaacaaatgaatgcatatttccaata 465
Db 300 tgaatctgttgcgtgaactacacacatgaagaacaaatgaatgcatatttccaata 359
Oy 466 aagcatgcccctctgaggaacacattccttgggttcaagggtatctgtatgccaca 525
Db 360 aagcatgcccctctgaggaacacattccttgggttcaagggtatctgtatgccaca 419

```

QY 526 accccgtttccgttaaccggaactccctggggaagctcccggaattgtttgaaacttaaca 585
|||||
Db 420 acccgtttccgttaaccggaactccctggggaagctcccggaattgtttgaaacttaaca 479
QY 586 aatcattgtgtcgcgcgttctcagatgcgcgagagctctcttatcaaccagaag 645
|||||
Db 480 aatcattgtgtcgcgcgttctcagatgcgcgagagctctcttatcaaccagaag 539
QY 646 acacagacatgaaagacatgacgcaaaagtctgaaacattacagacagatcaagaatcca 705
|||||
Db 540 acacagacatgaaagacatgacgcaaaagtctgaaacattacagacagatcaagaatcca 599
QY 706 gctcaacttgaagcttcaagatttccgtgtgagacaataaactcttctgtgttccat 765
|||||
Db 600 gctcaacttgaagcttcaagatttccgtgtgagacaataaactcttctgtgttccat 659
QY 766 atcacaaactctctccccaagaagtctactgtgacaagaatgctggaaggtctgtatcc 825
|||||
Db 660 atcacaaactctctccccaagaagtctactgtgacaagaatgctggaaggtctgtatcc 719
QY 826 tcccaagaattatttgcagaagctaccagttacattgacaagctctgtgcaatgataca 885
|||||
Db 720 tcccaagaattatttgcagaagctaccagttacattgacaagctctgtgcaatgataca 779
QY 886 aatcagaagaatgataatcaactgtgtgacaagaagtttctgaagcttctgtgcttaacca 945
|||||
Db 780 aatcagaagaatgataatcaactgtgtgacaagaagtttctgaagcttctgtgcttaacca 839
QY 946 aggaagaactgtgtgcagaagagcgagtaattcgttccacaatgacatcccgaaagccaa 1005
|||||
Db 840 aggaagaactgtgtgcagaagagcgagtaattcgttccacaatgacatcccgaaagccaa 899
QY 1006 tccctggaagaactaaactctacatctcccttcccgagaagaagctggtctgaaagccaa 1065
|||||
Db 900 tccctggaagaactaaactctacatctcccttcccgagaagaagctggtctgaaagccaa 959
QY 1066 aaacattgtgcatactctgtgagacctgtgcccagaagctgttccacatgaaagcttga 1125
960 aaacattgtgcatactctgtgagacctgtgcccagaagctgttccacatgaaagcttga 1019
QY 1126 gtgacaatgcgaagaggtgatagttctgcacaatgataagcttccagctccctccacc 1185
|||||
Db 1020 gtgacaatgcgaagaggtgatagttctgcacaatgataagcttccagctccctccacc 1079
QY 1186 aaatcacaagagctgtgtcgtatgtctgtgagacatcccgagaagggaggggtcttaaa 1245
|||||
Db 1080 aaatcacaagagctgtgtcgtatgtctgtgagacatcccgagaagggaggggtcttaaa 1139
QY 1246 tcaagctctcaactgtgatagagaacaacaactaaagccctcttctgaggaatgagca 1305
1140 tcaagctctcaactgtgatagagaacaacaactaaagccctcttctgaggaatgagca 1199
QY 1306 ctgagaagaatgcttgaacactctatgacaactcaacactcttactgcaatgatttga 1365
1200 ctgagaagaatgcttgaacactctatgacaactcaacactcttactgcaatgatttga 1259
QY 1366 tgaagaatttggaagctgaagctcttcccgacattatcggaaagcttctgaaagccgttc 1425
1260 tgaagaatttggaagctgaagctcttcccgacattatcggaaagcttctgaaagccgttc 1319
QY 1426 tcttctggaagaatcctgtatataccttgacaactcacaagcagaagctatgctgaaag 1485
1320 tcttctggaagaatcctgtatataccttgacaactcacaagcagaagctatgctgaaag 1379
QY 1486 tgaacaagaactcctcagaagaactgtgttccatgatactgaaagcatgttggagaagac 1545
1380 tgaacaagaactcctcagaagaactgtgttccatgatactgaaagcatgttggagaagac 1439
QY 1546 tcaagcccaagatctgacaactcatgagagaacagccaagaatgagccctgttccgaatgc 1605
1440 tcaagcccaagatctgacaactcatgagagaacagccaagaatgagccctgttccgaatgc 1499
QY 1606 tgttgcagacagagacatgacacatttggagacagcagttgatagtcttaagta 1665
1500 tgttgcagacagagagacatgacacatttggagacagcagttgatagtcttaagta 1559
QY 1666 cagcccaagacatcgttgcgttcttggccaagcaccagaagatgtccagttcaagta 1725
1560 cagcccaagacatcgttgcgttcttggccaagcaccagaagatgtccagttcaagta 1619
QY 1726 gttctgtgttaaccttgagaagaacatttcaacgagataacccaagcattccggaccat 1785
1620 gttctgtgttaaccttgagaagaacatttcaacgagataacccaagcattccggaccat 1679
QY 1786 ctgccttcatgagatgttcaacctgaaacagctagaaacccatagcaacagaagtctgac 1845
1680 ctgccttcatgagatgttcaacctgaaacagctagaaacccatagcaacagaagtctgac 1739
Db 1740 tcatcaacaagtctcagatgagctgtgagagaagttctgtggtctgtatgttca 1799
QY 1846 tcatcaacaagtctcagatgagctgtgagagaagttctgtggtctgtatgttca 1905
1740 tcatcaacaagtctcagatgagctgtgagagaagttctgtggtctgtatgttca 1799
QY 1906 ctggaattacttccagagcagcattgagctgcccacatgataagtataagaatccgaatg 1965
1800 ctggaattacttccagagcagcattgagctgcccacatgataagtataagaatccgaatg 1859
Db 1860 acattgacaatgtgagagagacaataaataaatacaagatggttacttggaccctgtcttc 1919
QY 2026 gaagctgaccccttgaagacatgcgtatgcgtctgtgggggcttccgacttgcagaatg 2085
1920 gaagctgaccccttgaagacatgcgtatgcgtctgtgggggcttccgacttgcagaatg 1979
QY 2086 tgtgtgagacagacaaatcatcaggtgtgctgaggggacccagaaagaaactgttctata 2145
1980 tgtgtgagacagacaaatcatcaggtgtgctgaggggacccagaaagaaactgttctata 2039
Db 2146 tgcacaagaatgcctataccctgttactgttgaatgacatcttctgcgggtgatagcaggt 2205
2040 tgcacaagaatgcctataccctgttactgttgaatgacatcttctgcgggtgatagcaggt 2099
QY 2206 caatgccccttcttcatgacgctgtgctgtgatttaactgaatgtgcgttgaatcaaggca 2265
2100 caatgccccttcttcatgacgctgtgctgtgatttaactgaatgtgcgttgaatcaaggca 2159
Db 2266 tctgtatgagaagaggaacagctgaaagagacatctcgatcatgtgaccttgaaca 2325
2160 tctgtatgagaagaggaacagctgaaagagacatctcgatcatgtgaccttgaaca 2219
QY 2326 gcatactcgtgtttagctgttcatltagttagcctatcctctctctgttgaagcgtgac 2385
2220 gcatactcgtgtttagctgttcatltagttagcctatcctctctctgttgaagcgtgac 2279
Db 2386 tgtctgtgtgtaactctgaaagttaagaaactgtgtccctaaagtatccagcgtgtgt 2445
2280 tgtctgtgtgtaactctgaaagttaagaaactgtgtccctaaagtatccagcgtgtgt 2339
QY 2446 tttgttctcgtgcgtgttgt 2505
2340 tttgttctcgtgcgtgttgt 2399
QY 2506 tcttctccagagcaaacctgagcagcctgttggggcatcatcatctactccagctgtacc 2565
2400 tcttctccagagcaaacctgagcagcctgttggggcatcatctactccagctgtacc 2459
Db 2566 tgccttaagctcctgt 2625
2460 tgccttaagctcctgt 2519
QY 2626 ctgagctgtgtctcctgt 2685
2520 ctgagctgtgtctcctgt 2579
QY 2686 agcagggcatgtgagatgagatgagacaactgttctgagagcttccgttggagaagatgct 2745

Db 2580 ||||| agcaggagatttgagtgagcagtgaggacaacccgtttgagagtlccgttggaagaaatgagct 2639
QY 2746 tcaattcacaacctgcatactcacaatgatactgtttgacaccttcctctatagggtatga 2805
Db 2640 tcaattcacaacctgcatactcacaatgatactgtttgacaccttcctctatagggtatga 2699
QY 2806 cctgttacaattgagctgtcttcccaaggcagtaaggaaatcccaaggccctgtatlttc 2865
Db 2700 cctgttacaattgagctgtcttcccaaggcagtaaggaaatcccaaggccctgtatlttc 2759
QY 2866 ctgtcaccaaatctcactgtgttttgagaggaagaatgataaggagaagcaccctgtttcca 2925
Db 2760 ctgtcaccaaatctcactgtgttttgagaggaagaatgataaggagaagcaccctgtttcca 2819
QY 2926 accagaagagaaatgtcagaatactgcataaggagagaaaccaaccttgaagctgagcg 2985
Db 2820 accagaagagaaatgtcagaatactgcataaggagagaaaccaaccttgaagctgagcg 2879
QY 2986 tgttcattcagaaccctgtgtaaaagctcacaggagatggatgaaagtgtgtctcagtgcc 3045
Db 2880 tgttcattcagaaccctgtgtaaaagctcacaggagatggatgaaagtgtgtctcagtgcc 2939
QY 3046 tggcactgaatttttatagaaggccaagatcacctcctcctcgtgggccaacaatggagcgagga 3105
Db 2940 tggcactgaatttttatagaaggccaagatcacctcctcctcgtgggccaacaatggagcgagga 2999
QY 3106 agacagacacacatgtcacaatccctgacgggtgttccccccgacctcgggacacggcctaca 3165
Db 3000 agacagacacacatgtcacaatccctgacgggtgttccccccgacctcgggacacggcctaca 3059
QY 3166 tccctgggaaaaagacattcgccttgagagtgagacacatcccgccggcagaaccttgagggtctgtc 3225
Db 3060 tccctgggaaaaagacattcgccttgagagtgagacacatcccgccggcagaaccttgagggtctgtc 3119
QY 3226 cccagacataacgttgcttgcagatagtcagctgcagaaagacacatctgtttctatgccc 3285
Db 3120 cccagacataacgttgcttgcagatagtcagctgcagaaagacacatctgtttctatgccc 3179
QY 3286 gcttgtaaaaggctctcctgcagaagaacgttgaaagccgagatgagagcagatgagccctgagatg 3345
Db 3180 gcttgtaaaaggctctcctgcagaagaacgttgaaagccgagatgagagcagatgagccctgagatg 3239
QY 3346 ttggtttgcatcacaagcaagcctgaaagcacaagccagcgtctcaaggttgagatcaga 3405
Db 3240 ttggtttgcatcacaagcaagcctgaaagcacaagccagcgtctcaaggttgagatcaga 3299
QY 3406 gaaagctactctgtgaccttgaccttgctcgaggagatctaagttgtlcatctgagatgaac 3465
Db 3300 gaaagctactctgtgaccttgaccttgctcgaggagatctaagttgtlcatctgagatgaac 3359
QY 3466 ccaacagctgtgtgagaccttactcccgagagggaatatgagagcgtcgtgtgaataaac 3525
Db 3360 ccaacagctgtgtgagaccttactcccgagagggaatatgagagcgtcgtgtgaataaac 3419
QY 3526 gacaagccgacacatattctctctacacacacacatgagatgaaagcgagcttcctggggg 3585
Db 3420 gacaagccgacacatattctctctacacacacacatgagatgaaagcgagcttcctggggg 3479
QY 3586 acaaggttgcatcattcccatggggaagctgtgctgtgtgggctccctcgtttctga 3645
Db 3480 acaaggttgcatcattcccatggggaagctgtgctgtgtgggctccctcgtttctga 3539
QY 3646 agaaacagctcgggaaacagctactacactgacacttgcttgaagaagaatgtggaatctctcc 3705
Db 3540 agaaacagctcgggaaacagctactacactgacacttgcttgaagaagaatgtggaatctctcc 3599
QY 3706 tcaagttctgcagaagaacagtagtagcactgtgtcatcactgaaagaaagagagcagtgctt 3765
Db 3600 tcaagttctgcagaagaacagtagtagcactgtgtcatcactgaaagaaagagagcagtgctt 3659
QY 3766 ctaagagcaattctgactgtgaccttgaggcagacatagagatgacacgctgacacatcg 3825
|||||

Db 3660 ctcaagagcagttctgatagtctgacctgggcaagcaccatgaaagtgacacgctgacacatcg 3719
QY 3826 atgtctctgatactcccaacctcacaagaacagcatgttctgaagcccgctgtgtgaaag 3885
Db 3720 atgtctctgatactcccaacctcacaagaacagcatgttctgaagcccgctgtgtgaaag 3779
QY 3886 acaatagagcagatgacactatgtctgcacatagaaagctgtcataagaaagagcccttg 3945
Db 3780 acaatagagcagatgacactatgtctgcacatagaaagctgtcataagaaagagagcccttg 3839
QY 3946 tggaaactcttaataagatgtgataagccgctctcagacctgggacattctcagatagca 4005
Db 3840 tggaaactcttaataagatgtgataagccgctctcagacctgggacattctcagatagca 3899
QY 4006 tctcagagacagacccctggaagaataatctcccaaaagtgtgcgaagaagatgaggttgatg 4065
Db 3900 tctcagagacagacccctggaagaataatctcccaaaagtgtgcgaagaagatgaggttgatg 3959
QY 4066 ctgagacctcagaatgatactgtccagcagaagacgaagcgggctctcggggacaagc 4125
Db 3960 ctgagacctcagaatgatactgtccagcagaagacgaagcgggctctcggggacaagc 4019
QY 4126 agagctgtcttcggccgttccactgtaagaatgatagtctgtcatccaaatgatactcagatag 4185
Db 4020 agagctgtcttcggccgttccactgtaagaatgatagtctgtcatccaaatgatactcagatag 4079
QY 4186 acccagaatcacaagagacagactgtctcagtgagatgagatgagcaaaaggtccctacagag 4245
Db 4080 acccagaatcacaagagacagactgtctcagtgagatgagatgagcaaaaggtccctacagag 4139
QY 4246 tgaagagctggaataattcacaagcacaagcttgtgagcccttttggagaagactgtctaa 4305
Db 4140 tgaagagctggaataattcacaagcacaagcttgtgagcccttttggagaagactgtctaa 4199
QY 4306 tggcagacagagctggaagaagattttgtgcacaaatgtctgcacaaatgtctgttct 4365
Db 4200 tggcagacagagctggaagaagattttgtgcacaaatgtctgcacaaatgtctgttct 4259
QY 4366 gcatgtgacctgtgttcaagctgatactgtgcaacctttggcaagtaaccaagcctgtgaac 4425
Db 4260 gcatgtgacctgtgttcaagctgatactgtgcaacctttggcaagtaaccaagcctgtgaac 4319
QY 4426 ttcagcccttgagtgatgacaagcaagatcacattgtgacaagatgactctcctaagaca 4485
Db 4320 ttcagcccttgagtgatgacaagcaagatcacattgtgacaagatgactctcctaagaca 4379
QY 4486 cgggaacccctggaactcttaaaagccctcacaagaaagacccctgtctcgggacccgctgta 4545
Db 4380 cgggaacccctggaactcttaaaagccctcacaagaaagacccctgtctcgggacccgctgta 4439
QY 4546 tggagagaaacccaatcccaagacagccctgcagagcaggaggaaagatgagacacatg 4605
Db 4440 tggagagaaacccaatcccaagacagccctgcagagcaggaggaaagatgagacacatg 4499
QY 4606 ccccaagttcccaagacacatcagagcccttcacagaaatgagaaatgagacacacac 4665
Db 4500 ccccaagttcccaagacacatcagagcccttcacagaaatgagaaatgagacacacac 4559
QY 4666 cttaacctgcagatgcagtgatgacagcgacaacaaatcacaagaatgctgctgtgtgtccc 4725
Db 4560 cttaacctgcagatgcagtgatgacagcgacaacaaatcacaagaatgctgctgtgtgtccc 4619
QY 4726 cagggcaggggggctgctcctccacaagaagaacaaacacacgcagatatactctcag 4785
Db 4620 cagggcaggggggctgctcctccacaagaagaacaaacacacgcagatatactctcag 4679
QY 4786 acctgacaagaaacacatctcagatattctgtgaaagcgtatgtgcagatcatalagcca 4845
Db 4680 acctgacaagaaacacatctcagatattctgtgaaagcgtatgtgcagatcatalagcca 4739
QY 4846 aaagcttaagaagaagaatcgggtgagatgagatttaagatgagggcttccctgtgtg 4905
Db 4740 aaagcttaagaagaagaatcgggtgagatgagatttaagatgagggcttccctgtgtg 4799
|||||


```
Db 6960 gcatgtatgaagaalcccttccatagcgggtgctgaagaatgaagagactgacatt 7019
QY 7126 cctttgacacatgtgaagtgttggaagaaagccagaagtgtgttggaagaagta 7185
Db 7020 cctttgacacatgtgaagtgttggaagaaagccagaagtgtgttggaagaagta 7079
QY 7186 aactggaactgtacgtacatctcaatgcaatgcaatgcaatgcaatgcaatgcaat 7245
Db 7080 aactggaactgtacgtacatctcaatgcaatgcaatgcaatgcaatgcaatgcaat 7139
QY 7246 tccatcaagggcagtgcttctgtgacatgtctgtgacatgtctgtgacatgtctgt 7305
Db 7140 tccatcaagggcagtgcttctgtgacatgtctgtgacatgtctgtgacatgtctgt 7199
QY 7306 tgaattagtttttaccatacctatgtgaacactatbatggaacccaatggaacata 7365
Db 7200 tgaattagtttttaccatacctatgtgaacactatbatggaacccaatggaacata 7259
QY 7366 ggggttgaactcaacttttttttttttttttttttttttttttttttttttttttt 7425
Db 7260 ggggttgaactcaacttttttttttttttttttttttttttttttttttttttttt 7319
QY 7426 caataatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatca 7485
Db 7320 caataatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatca 7379
QY 7486 atccatcttaactcaagcagatgcagccagagactggttcccggtgacacacacatt 7545
Db 7380 atccatcttaactcaagcagatgcagccagagactggttcccggtgacacacacatt 7439
QY 7546 gctggaatagtgctgcagagatgatactgccaagtcttccagaagtgttaagaacca 7605
Db 7440 gctggaatagtgctgcagagatgatactgccaagtcttccagaagtgttaagaacca 7499
QY 7606 tgggtgtgctacgtcacttctgtgaagcgtcgtccagagactcctcaacatggaata 7665
Db 7500 tgggtgtgctacgtcacttctgtgaagcgtcgtccagagactcctcaacatggaata 7559
QY 7666 tccagttgacagaaatgctgcacatgcgtgcaacatcctgtgacttccctcgtgaagc 7725
Db 7560 tccagttgacagaaatgctgcacatgcgtgcaacatcctgtgacttccctcgtgaagc 7619
QY 7726 tgttctggtgagcaatgcaatgcaaaaaatgtgggtgtcctcgaagccaggaacttgg 7785
Db 7620 tgttctggtgagcaatgcaatgcaaaaaatgtgggtgtcctcgaagccaggaacttgg 7679
QY 7786 ttcacattgtatatacttccatgctcgaagcagatggtctacaagggtaccccttaagaa 7845
Db 7680 ttcacattgtatatacttccatgctcgaagcagatggtctacaagggtaccccttaagaa 7739
QY 7846 ctcttaataatacttgaatcctgtgaagagcaagaatcaacagcaaacgcgtcgggac 7905
Db 7740 ctcttaataatacttgaatcctgtgaagagcaagaatcaacagcaaacgcgtcgggac 7799
QY 7906 tgaagctgtcgaagcagcagatggtgataagagattgtcgtcgtcaaaccttaaggag 7965
Db 7800 tgaagctgtcgaagcagcagatggtgataagagattgtcgtcgtcaaaccttaaggag 7859
QY 7966 ccgtgtccacattgtcctcactgctcgtcaacatggtacacgcatcctaagaattttat 8025
Db 7860 ccgtgtccacattgtcctcactgctcgtcaacatggtacacgcatcctaagaattttat 7919
QY 8026 ctgacaagaatgataatctcgtcgttcttgaatcaatcctagaanaatgaaatgaaatg 8085
Db 7920 ctgacaagaatgataatctcgtcgttcttgaatcaatcctagaanaatgaaatgaaatg 7979
QY 8086 tctatttgaacaaaatgttgaacttttaattgaattgaattgaattgaattgaattgaatt 8145
Db 7980 tgaatttgaacaaaatgttgaacttttaattgaattgaattgaattgaattgaattgaatt 8039
QY 8146 tgaacttgaactcctagaatgaccttctgtagaacccgtggtatagaagagatggc 8205
|||||

Db 8040 tgaacttgaactcctagaatgaccttctgtagaacccgtggtatagaagagatggc 8099
QY 8206 cactgcccacatttttttttttttttttttttttttttttttttttttttttttttttt 8265
Db 8100 cactgcccacatttttttttttttttttttttttttttttttttttttttttttttttt 8159
QY 8266 agaaagcaatgtgataagcagatcctcaatgacatataattgagttccttcaagcatt 8325
Db 8160 agaaagcaatgtgataagcagatcctcaatgacatataattgagttccttcaagcatt 8219
QY 8326 taggatacttcaatcctcaatcctcaatcctcaatcctcaatcctcaatcctcaatcct 8385
Db 8220 taggatacttcaatcctcaatcctcaatcctcaatcctcaatcctcaatcctcaatcct 8279
QY 8386 aagagatgtaacgtacataagcagatgaagataatgaatcctcaatcctcgtg 8445
Db 8280 aagagatgtaacgtacataagcagatgaagataatgaatcctcaatcctcgtg 8339
QY 8446 catgttatacgtcactcgtgttacaataataggtgtgtgtgtgtgtgtgtgtgtgtgtgt 8505
Db 8340 catgttatacgtcactcgtgttacaataataggtgtgtgtgtgtgtgtgtgtgtgtgtgt 8399
QY 8506 gtaacaatattgggagccttttttttttttttttttttttttttttttttttttttttt 8565
Db 8400 gtaacaatattgggagccttttttttttttttttttttttttttttttttttttttttt 8458
QY 8566 aagataaagggtcacaagttaacaatgaatccttcaacaggggaaacagctagtga 8625
Db 8459 aagataaagggtcacaagttaacaatgaatccttcaacaggggaaacagctagtga 8518
QY 8626 aaactgtcgaaaaaacacacttgtttatgagcattagtaacctcaataatgtgctt 8685
Db 8519 aaactgtcgaaaaaacacacttgtttatgagcattagtaacctcaataatgtgctt 8578
QY 8686 tgcagataatggatacccatlaaatcctgacagctcacaatttttcaatccttcaatcac 8745
Db 8579 tgcagataatggatacccatlaaatcctgacagctcacaatttttcaatccttcaatcac 8638
QY 8746 tagtcaagaataataataaacaataataataataataataataataataataataataata 8805
Db 8639 tagtcaagaataataataaacaataataataataataataataataataataataataata 8698
QY 8806 taaccagcttatttttttctagtcagtaaacattgtgaanaaatcgtttcactaact 8865
Db 8699 taaccagcttatttttttctagtcagtaaacattgtgaanaaatcgtttcactaact 8758
QY 8866 taactgttaactgtttgaggaagaaagaaataatagagaagacattgtttgggaggttc 8925
Db 8759 taactgttaactgtttgaggaagaaagaaataatagagaagacattgtttgggaggttc 8818
QY 8926 aagtgatccttcaatcactaactcctcacttccacttcccaaatltgaatlaaac 8985
Db 8819 aagtgatccttcaatcactaactcctcacttccacttcccaaatltgaatlaaac 8878
QY 8986 gctaaaggtgtgaagacttcaagattcaaatatcttctataatlttttaaatlttacaga 9045
Db 8879 gctaaaggtgtgaagacttcaagattcaaatatcttctataatlttttaaatlttacaga 8938
QY 9046 atattataaacccacgtcgtgaanaagaaagaaatgtgttttgaaggttaagaaat 9105
Db 8939 atattataaacccacgtcgtgaanaagaaagaaatgtgttttgaaggttaagaaat 8998
QY 9106 atgattttaataataagtaagagcatatttccaaatagatagatagatagatagatagat 9165
Db 8999 atgattttaataataagtaagagcatatttccaaatagatagatagatagatagatagat 9058
QY 9166 gcaatttaacgtatcttcaaaaataacagaattatagaataatlttccctcatttaaat 9225
Db 9059 gcaatttaacgtatcttcaaaaataacagaattatagaataatlttccctcatttaaat 9118
QY 9226 ttctcaaatcaagaatgtgttccctcatttcaacaaatcgtatcctcaatcctcat 9285
Db 9119 ttctcaaatcaagaatgtgttccctcatttcaacaaatcgtatcctcaatcctcat 9178
```


Db	2881	gaqcgsggaagagaccacatgtcaatccctgacccgggtgttccccccgacctgggca	2940
QY	3157	ccgcctacaatcctgggaaaaagacatcgctcgatgagacacatccggcagaaacctgg	3216
Db	2941	ccgcctacatactcctgggaaaaagacatcgctcgatgagacacatccggcagaaacctgg	3000
QY	3217	gggtcgtcccgacataacgctgctgttgagatgctgactgtcgaagaacacatctgt	3276
Db	3001	gggtcgtcccgacataacgctgctgttgagatgctgactgtcgaagaacacatctgt	3060
QY	3277	tcatacgcccgcttgaaaaagggctctctgaaagcaacgtagaaggcggagatgagacagatg	3336
Db	3061	tcatacgcccgcttgaaaaagggctctctgaaagcaacgtagaaggcggagatgagacagatg	3120
QY	3337	ccctggatgtgtgttgcctatcaagcaagctgaaaaaacaagcagctgtcaagtg	3396
Db	3121	ccctggatgtgtgttgcctatcaagcaagctgaaaaaacaagcagctgtcaagtg	3180
QY	3397	gaatcgagaagaagctatctgtgacctggaccttgcggggagatctaagttgtcatc	3456
Db	3181	gaatcgagaagaagctatctgtgacctggaccttgcggggagatctaagttgtcatc	3240
QY	3457	tgatgtaacccaacagctggtgtggaaccttactccgcaggggaaatagggagctgtgc	3516
Db	3241	tgatgtaacccaacagctggtgtggaaccttactccgcaggggaaatagggagctgtgc	3300
QY	3517	tgaataccggaagaagccgcgcacattatctctcaacacacacatggaatgaagcggag	3576
Db	3301	tgaataccggaagaagccgcgcacattatctctcaacacacacatggaatgaagcggag	3360
QY	3577	tcctgggggagacagatgccaatcatctccatctgggaagctgtgctgtgtgggctctcc	3636
Db	3361	tcctgggggagacagatgccaatcatctccatctgggaagctgtgctgtgtgggctctcc	3420
QY	3637	tgcttctgaagaacacagctgaggaaacagctactactgacctggttcaagaagaatgtg	3696
Db	3421	tgcttctgaagaacacagctgaggaaacagctactactgacctggttcaagaagaatgtg	3480
QY	3697	aatctccctcaagttccctcgacgaagaacagtagaactgttcaatccttgaaaaaggg	3756
Db	3481	aatctccctcaagttccctcgacgaagaacagtagaactgttcaatccttgaaaaaggg	3540
QY	3757	acagtgttctcagaagcagttctgaatgtctggccttggcagcgacatgaaagtgaacagc	3816
Db	3541	acagtgttctcagaagcagttctgaatgtctggccttggcagcgacatgaaagtgaacagc	3600
QY	3817	tgaacatgagtgctctgctatcttccaaacctcataggaacatgtgtctgaagccggc	3876
Db	3601	tgaacatgagtgctctgctatcttccaaacctcataggaacatgtgtctgaagccggc	3660
QY	3877	tggtagaagacataaggagatagctgaacctatgtgctgcataatgaagctctaagagg	3936
Db	3661	tggtagaagacataaggagatagctgaacctatgtgctgcataatgaagctctaagagg	3720
QY	3937	gagccttgtggaaactcttcaatgagatgagtcagccgctctcagaacctgggcatctca	3996
Db	3721	gagccttgtggaaactcttcaatgagatgagtcagccgctctcagaacctgggcatctca	3780
QY	3997	gttatggcatctcagagacgagccctgggaagaataatctccaagtgaggccgaagaagtg	4056
Db	3781	gttatggcatctcagagacgagccctgggaagaataatctccaagtgaggccgaagaagtg	3840
QY	4057	gggtgagatgctgagacctaagatgtaactgtgcagcagaacgaagaacggcgccctcg	4116
Db	3841	gggtgagatgctgagacctaagatgtaactgtgcagcagaacgaagaacggcgccctcg	3900
QY	4117	gggaacacagagctgttcttgcgcgttccactggaagatgagtgctgtgataccaaatgatt	4176
Db	3901	gggaacacagagctgttcttgcgcgttccactggaagatgagtgctgtgataccaaatgatt	3960
QY	4177	ctgacatagaccagaacatccagagagacagacttgctcagtgagatgagtgcaaaaggt	4236
Db	3961	ctgacatagaccagaacatccagagagacagacttgctcagtgagatgagtgcaaaaggt	4020

QY	4237	cctacacaggtagaaagctggaacacttacacagcaacagttgtgaccttgttgaga	4296
Db	4021	cctacacaggtagaaagctggaacacttacacagcaacagttgtgaccttgttgaga	4080
QY	4297	gactgtaattgccaagacggagcttggaagaagatttltgtctcagatgtgtcttcagctg	4356
Db	4081	gactgtaattgccaagacggagcttggaagaagatttltgtctcagatgtgtcttcagctg	4140
QY	4357	tgcttgcctgcatgacctgtgttctcagcctgtagatcggtgcaacaccttggcaatcccc	4416
Db	4141	tgcttgcctgcatgacctgtgttctcagcctgtagatcggtgcaacaccttggcaatcccc	4200
QY	4417	gcttggaaactcagccctgtagatgtagaagcaacagatgacacattgtcgaatgtgctc	4476
Db	4201	gcttggaaactcagccctgtagatgtagaagcaacagatgacacattgtcgaatgtgctc	4260
QY	4477	ctgaggaacacgggaacaccttggaactcttaagcgccctcaccaagacacctggttcggga	4536
Db	4261	ctgaggaacacgggaacaccttggaactcttaagcgccctcaccaagacacctggttcggga	4320
QY	4537	cccgctgtagaaggaagaacccaatccacagacagccctgcagcgagggaggaagat	4596
Db	4321	cccgctgtagaaggaagaacccaatccacagacagccctgcagcgagggaggaagat	4380
QY	4597	ggaccacatgcccagcttccccagacacatcatggaactctctccgaalggaaactggaca	4656
Db	4381	ggaccacatgcccagcttccccagacacatcatggaactctctccgaalggaaactggaca	4440
QY	4657	tgcagaacacctcaacctgcatgacagtgtagcagcgacgaacaaatcaagaagaatgctcctg	4716
Db	4441	tgcagaacacctcaacctgcatgacagtgtagcagcgacgaacaaatcaagaagaatgctcctg	4500
QY	4717	tggttcccccaaggcgagggggctgctcctccacacaaagaaaaacaaacacgtcagata	4776
Db	4501	tggttcccccaaggcgagggggctgctcctccacacaaagaaaaacaaacacgtcagata	4560
QY	4777	tccttcagagacctgacaggaagaacacatctcgatattctgtggaagacgtatgtcaga	4836
Db	4561	tccttcagagacctgacaggaagaacacatctcgatattctgtggaagacgtatgtcaga	4620
QY	4837	tcatagcacaaagcttlaaagaacacagatcctgggtgaaatgagtttaagtggcgctt	4896
Db	4621	tcatagcacaaagcttlaaagaacacagatcctgggtgaaatgagtttaagtggcgctt	4680
QY	4897	ccctgggtgtcagtaatactcaagcacttccctccagatcgaagaatgaatgatgtccatca	4956
Db	4681	ccctgggtgtcagtaatactcaagcacttccctccagatcgaagaatgaatgatgtccatca	4740
QY	4957	aacaaatgaaagaacacctaagaactgagcgaagacagttctgacatgcatcttcaaca	5016
Db	4741	aacaaatgaaagaacacctaagaactgagcgaagacagttctgacatgcatcttcaaca	4800
QY	5017	gcttgggaagatltatgacagactggacacccagaataatgtccaaggtgtgttcaata	5076
Db	4801	gcttgggaagatltatgacagactggacacccagaataatgtccaaggtgtgttcaata	4860
QY	5077	acaaaggctgtgcatgaatcagcttcttcttgaaatgtcatcaacaatgcatcttccggg	5136
Db	4861	acaaaggctgtgcatgaatcagcttcttcttgaaatgtcatcaacaatgcatcttccggg	4920
QY	5137	ccaaactgcaaaaagggaagaaacctagccattatggaattatgtcttcaatcatcccc	5196
Db	4921	ccaaactgcaaaaagggaagaaacctagccattatggaattatgtcttcaatcatcccc	4980
QY	5197	tgaatctcacaagcagcagctctcagaggttgctctgtagaccacatcagtgatgtcc	5256
Db	4981	tgaatctcacaagcagcagctctcagaggttgctctgtagaccacatcagtgatgtcc	5040
QY	5257	ttgtgtccatctgtgtcatcttgcgaatgtgccttgcacagcagaccttgttcgatctcc	5316
Db	5041	ttgtgtccatctgtgtcatcttgcgaatgtgccttgcacagcagaccttgttcgatctcc	5100

QY 5317 tgatccagagcggtcagcaaaacacactgagttcaatgagtgagtcgtg 5376
|||||
Db 5101 tgatccagagcggtcagcaaaacacactgagttcaatgagtgagtcgtg 5160
5377 tcatcaacggcctctaatcttgctgagatgtgcaatgagttgctctgcaac 5436
|||||
Db 5161 tcaatcaacggcctctaatcttgctgagatgtgcaatgagttgctctgcaac 5220
5437 tgatcatlcatlcatctgtcttccagcaaaagtcctatgtgttctctccaaatctgc 5496
|||||
Db 5221 tggatcatlcatlcatctgtcttccagcaaaagtcctatgtgttctctccaaatctgc 5280
5497 ctgtgtcagcccttcaactttgtgtatgtgtgtcacaacactctcagttacccag 5556
|||||
QY 5281 ctgtgtcagcccttcaactttgtgtatgtgtgtcacaacactctcagttacccag 5340
5557 cctcctttgtgtcacaagatcccccagcacagcctatgtgtgtcacaacagcgtaaacctc 5616
|||||
Db 5341 cctcctttgtgtcacaagatcccccagcacagcctatgtgtgtcacaacagcgtaaacctc 5400
5617 tcatgtgcattaaatggcagcggtgccaacttgtgtcagagctgtgtcaccgacaataagc 5676
|||||
Db 5401 tcatgtgcattaaatggcagcggtgccaacttgtgtcagagctgtgtcaccgacaataagc 5460
5677 tgaataataataatgatatctgaatctcggtgttctgtatcttccacacttttgccttg 5736
|||||
QY 5461 tgataataataataatgatatctgaatctcggtgttctgtatcttccacacttttgccttg 5520
5737 gacagagcgctcatalcgcacatgttgaaaaacagcaaatgtgcgtgaatgtccctggaaaagtttg 5796
|||||
Db 5521 gacagagcgcgccatcgatcgtatgtgaaaaacagcaaatgtgcgtgaatgtccctggaaaagtttg 5580
5797 gggagaaatcgcttgtgtcacaatctatcttggagactgtgtggagcaaaactcttgcca 5856
|||||
Db 5581 gggagaaatcgcttgtgtcacaatctatcttggagactgtgtggagcaaaactcttgcca 5640
5857 tggccggtggagaggggtgtgttcttccatctatctgtccgacccagtaacatcttcca 5916
|||||
Db 5641 tggccggtggagaggggtgtgttcttccatctatctgttccgacccagtaacatcttcca 5700
5917 tcaagggccagacctgttaaatgtcaaaagctatcctcctgtgaatgtatgaatgtatgtga 5976
|||||
Db 5701 tcaagggccagacctgttaaatgtcaaaagctatcctcctgtgaatgtatgaatgtatgtga 5760
5977 ggcgggaaaacagagaaatcttctgtatgtgtgagggccaagaaatgtacattgaataacaa 6036
|||||
Db 5761 ggcgggaaaacagagaaatcttctgtatgtgtgagggccaagaaatgtacattgaataacaa 5820
6037 agttgacgaagatatagaaaggaagcggaagcctgtgtgtgaacagatlttgctggcca 6096
|||||
Db 5821 agttgacgaagatatagaaaggaagcggaagcctgtgtgtgaacagatlttgctggcca 5880
6097 ttcctcctgtgtgagtgcttctgtgggtcctggaggttaatggggtgtgaataatcaact 6156
|||||
Db 5881 ttcctcctgtgtgagtgcttctgtgggtcctggaggttaatggggtgtgaataatcaact 5940
6157 tcaagatgttaaacagagagatacaccctgttaccagagagagatgtcttctcctaacaataa 6216
|||||
Db 5941 tcaagatgtgttaaacagagagatacaccctgttaccagagagagatgtcttctcctaacaataa 6000
6217 gtaactatcaaaaatccatgaagttacatcagaacatgtgagctactgacctcagttgatg 6276
|||||
Db 6001 gtaactatcaaaaatccatgaagttacatcagaacatgtgagctactgacctcagttgatg 6060
6277 ccatcaacagagctgtgtactcgggaggaacacgttgaggtcttcttgccttltgagagag 6120
|||||
QY 6061 ccatcaacagagctgtgtactcgggaggaacacgttgaggtcttcttgccttltgagagag 6120
6337 tcccaagaaagaaagttgtgcaaggtltgtgtatgtgtgcattcggaaaactgtgctgtga 6396
|||||
Db 6121 tcccaagaaagaaagttgtgcaaggtltgtgtatgtgtgcattcggaaaactgtgctgtga 6180
6397 agtatggagaaaataatgtctgtgtatctatagtgtgagggcaaaaacgcaagctctctacag 6456

Db 6181 agtatggagaaaataatgtctgtgtatctatagtgtgagggcaaaaacgcaagctctctacag 6240
6457 ccatgtgcttltgatctgcgggctcctctgtgtgttctctgtatgaacccacagcgatgg 6516
|||||
Db 6241 ccatgtgcttltgatctgcgggctcctctgtgtgttctctgtatgaacccacagcgatgg 6300
6517 atcccaagggccggcggttctgtgtgaaatgtgtgcccgaagtgtgtgaagaaggagagat 6576
|||||
Db 6301 atcccaagggccggcggttctgtgtgaaatgtgtgcccgaagtgtgtgaagaaggagagat 6360
6577 cagtaatgtcacaatcatalagtaatgaagaatgtgaagctcttgcactatagatgtgcaa 6636
|||||
Db 6361 cagtaatgtcacaatcatalagtaatgaagaatgtgaagctcttgcactatagatgtgcaa 6420
6421 tcatgttcaatggaaaggtgttcaggtgccttggcaggtgtccagcatctaaaaataagtttg 6480
6637 tcatgttcaatggaaaggtgttcaggtgccttggcaggtgtccagcatctaaaaataagtttg 6696
|||||
QY 6481 gagatgttatacataatgtgttacgaatagcaggtcccaacccgagactgaagctgtcc 6756
6697 gagatgttatacataatgtgttacgaatagcaggtcccaacccgagactgaagctgtcc 6540
6481 gagatgttatacataatgtgttacgaatagcaggtcccaacccgagactgaagctgtcc 6540
6757 aggatltcttggacttgcatttctctgtgaaggtgttcttaaaagagaacacccgacaatgc 6816
|||||
Db 6541 aggatltcttggacttgcatttctctgtgaaggtgttcttaaaagagaacacccgacaatgc 6600
6817 tacaatcacagcttccatctcattatcttctctgcggcagatattgaatcctctccc 6876
|||||
Db 6601 tacaatcacagcttccatctcattatcttctctgcggcagatattgaatcctctccc 6660
6877 agagcaaaaagcgactccacatagaaagactctctgttctccagacaacacttgaaccaag 6936
|||||
QY 6661 agagcaaaaagcgactccacatagaaagactctctgttctccagacaacacttgaaccaag 6720
6937 tatgtgtgaacttgcaggaacaaagtgtatgtatgacacacttaaaagacactctcatc 6996
|||||
Db 6721 tatgtgtgaacttgcaggaacaaagtgtatgtatgacacacttaaaagacactctcatc 6780
6997 acaaaaacagacagtaatgtgagcgttgcaggttccacaactcttctcaagatagaagaag 7056
|||||
Db 6781 acaaaaacagacagtaatgtgagcgttgcaggttccacaactcttctcaagatagaagaag 6840
7057 tgaagaagactatgtatgaagaatcctgttcatatcaggggtgtgtgaagaatgaagaagaa 7116
|||||
QY 6841 tgaagaagactatgtatgaagaatcctgttcatatcaggggtgtgtgaagaatgaagaagaa 6900
7117 ctgaacttctcttgcacacatgtgaagtgtgtgtgagaaagagccagaaatgtatgtg 7176
|||||
Db 6901 ctgaacttctcttgcacacatgtgaagtgtgtgtgagaaagagccagaaatgtatgtg 6960
7177 gaaagaatgaactgtatgactgtactgtactatcaatgaacatgaacatgaatga 7236
|||||
QY 6961 gaaagaatgaactgtatgactgtactgtactatcaatgaacatgaacatgaatga 7020
6961 gaaagaatgaactgtatgactgtactgtactatcaatgaacatgaacatgaatga 7200
7237 aacacaatltccatatacaggggagtgcccttgtgactatgtctgtatgtgctccaag 7266
|||||
Db 7021 aacacaatltccatatacaggggagtgcccttgtgactatgtctgtatgtgctccaag 7200
7297 tgaagaacttgaatlttagtttttaccatatacagttgaagaactatatagaacccaa 7356
|||||
QY 7081 tgaagaacttgaatlttagtttttaccatatacagttgaagaactatatagaacccaa 7140
7357 tggacataggttctgaactcacac-ttttttttttttggctcctgtgatatctcaat 7415
|||||
Db 7141 tggacataggttctgaactcacac-ttttttttttttggctcctgtgatatctcaat 7200
7416 ggggttgcacaataatccatcaagaatcaatgtgcagcgatattgttcaaatcaaaa 7475
|||||
QY 7201 ggggttgcacaataatccatcaagaatcaatgtgcagcgatattgttcaaatcaaaa 7260
7476 ggtatgtcacatcctcattcaatgaagcatgtgcagcgagagatgttcccggtga 7535
|||||

QY	757	ggttcctatatcaaacctctctctcccaaaagtctactgttgacaagaatgctgagggctg	816
Db	541	ggttcctgataccaacctctctctcccaaaagtctactgttgacaagaatgctgagggctg	600
QY	817	atgtcatcttcacaagtgatttttgcgaagctacccggtatcaatlttgacaagctcttgca	876
Db	601	atgtcatcttcacaagtgatttttgcgaagctacccggtatcaatlttgacaagctcttgca	660
QY	877	atgtgataaatcaagaagaagatgatacttcaactgtgtgacaagaagattctcgagctttgtg	936
Db	661	atgtgataaatcaagaagaagatgatacttcaactgtgtgacaagaagattctcgagctttgtg	720
QY	937	gctctaccaaaaggaaactgtgctgcagcagagcgagctactctgttccacaatgacatcc	996
Db	721	gctctaccaaaaggaaactgtgctgcagcagagcgagctactctgttccacaatgacatcc	780
QY	997	tgaagccaatccctggaagaacaacttaactcaactctcccttcctcgagcaagaagctgtgctg	1056
Db	781	tgaagccaatccctggaagaacaacttaactcaactctcccttcctcgagcaagaagctgtgctg	840
QY	1057	aaagccacaanaaactgtgctgcatagtcttgygaactctgycgcgaagagctgttcaagcatga	1116
Db	841	aaagccacaanaaactgtgctgcatagtcttgygaactctgycgcgaagagctgttcaagcatga	900
QY	1117	gaagctgtgagtacatgycgacagagaggtgataatcttcttcaaccaagtgtacaagcctccagct	1176
Db	901	gaagctgtgagtacatgycgacagagaggtgataatcttcttcaaccaagtgtacaagcctccagct	960
QY	1177	cctccaccaaaatctacaagagctgtctctcgatattgtctgcygggcatalcccgagaggaagg	1236
Db	961	cctccaccaaaatctacaagagctgtctctcgatattgtctgcygggcatalcccgagaggaagg	1020
QY	1237	ggctcgagaatcaagtcctctctaactgtgatgagaagaacaactcaaaaagccctctcttgag	1296
Db	1021	ggctcgagaatcaagtcctctctaactgtgatgagaagaacaactcaaaaagccctctcttgag	1080
QY	1297	gcaatgycacatgagaaagaatgctgcgaaaccttctatgacaactctcaactccttactgtca	1356
Db	1081	gcaatgycacatgagaaagaatgctgcgaaaccttctatgacaactctcaactccttactgtca	1140
QY	1357	atgatttgaatgaagaatttggagtgatctagctccctcttcccgcatatctcggaaagctcttga	1416
Db	1141	atgatttgaatgaagaatttggagtgatctagctccctcttcccgcatatctcggaaagctcttga	1200
QY	1417	agccgcctgcctgttgggaaagaatccctgtatataccactgacactccacagccacaagcgaggttca	1476
Db	1201	agccgcctgcctgttgggaaagaatccctgtatataccactgacactccacagccacaagcgaggttca	1260
QY	1477	tggctgaggtgaaacagaacttccaggaactgtgcgtgttcttcaatgatacttgagaagcgatgt	1536
Db	1261	tggctgaggtgaaacagaacttccaggaactgtgcgtgttcttcaatgatacttgagaagcgatgt	1320
QY	1537	gggaaagaaactaagccccaagaatctcgcgaactcttcatgagaacaaggccaagaatgagaccttg	1596
Db	1321	gggaaagaaactaagccccaagaatctcgcgaactcttcatgagaacaaggccaagaatgagaccttg	1380
QY	1597	tccggaaatgcgtgtggacacgaaggaacaatgacacacttittgggaaacagcagcttggatgtgct	1656
Db	1381	tccggaaatgcgtgtggacacgaaggaacaatgacacacttittgggaaacagcagcttggatgtgct	1440
QY	1657	tgaagtgtgacagccccaagacactgctgacgttcttcttgccaagcaaccgaagagatgtctcaggt	1716
Db	1441	tgaagtgtgacagccccaagacactgctgacgttcttcttgccaagcaaccgaagagatgtctcaggt	1500
QY	1717	ccaaatgaatggtctctgttacaactcgtgagagaagcttcaacagagactaaaccaagcgatcc	1776
Db	1501	ccaaatgaatggtctctgttacaactcgtgagagaagcttcaacagagactaaaccaagcgatcc	1560
QY	1777	ggaacatatctcgtctcatgagatgagtgttcaactctgacaacagcttgaagaaccatataagaacag	1836
Db	1561	ggaacatatctcgtctcatgagatgagtgttcaactctgacaacagcttgaagaaccatataagaacag	1620
QY	1837	aagctcgtgctatacaacaagctcaatgagatgctgagctgtgagagaagattctgtgctgtata	1896

[illegible]

Db 2701 ctggtccacacagaaagaaatatacagaatctgcatgagaggaagaaacccacttga 2760
QY 2977 agctgggctgtccattcagaacctggttaaaagtctacagagatgagatgaagtgctg 3036
Db 2761 agctgggctgtccattcagaacctggttaaaagtctacagagatgagatgaagtgctg 2820
QY 3037 tcgaatgacctgagcaatgaaattttatagagggcagatcaacctctctctggccacaatg 3096
Db 2821 tcgaatgacctgagcaatgaaattttatagagggcagatcaacctctctctggccacaatg 2880
QY 3097 gggcgaggagaaagaaagaaacccatctgcaatccctgagccgggtgttcccccagacctgggca 3156
Db 2881 gggcgaggagaaagaaagaaacccatctgcaatccctgagccgggtgttcccccagacctgggca 2940
QY 3157 ccgctacacatccctgagaaagaaacatctgctctgagatgagagacccatccgggcaagaaacttg 3216
Db 2941 ccgctacacatccctgagaaagaaacatctgctctgagatgagagacccatccgggcaagaaacttg 3000
QY 3217 gggctgtccacagacatacgtgtgtgttgacatgctgacgtctgaaagaaacatactgtg 3276
Db 3001 gggctgtccacagacatacgtgtgtgttgacatgctgacgtctgaaagaaacatactgtg 3060
QY 3277 tctatgcccgtctgaaagagcctctctgagagcaagctgaaagcgagatgagagacatactg 3336
Db 3061 tctatgcccgtctgaaagagcctctctgagagcaagctgaaagcgagatgagagacatactg 3120
QY 3337 cccctgagatgtgtgtgtccatcaagcaagctgaaagcaaaacaaagccagctgtcaagtg 3396
Db 3121 cccctgagatgtgtgtgtccatcaagcaagctgaaagcaaaacaaagccagctgtcaagtg 3180
QY 3397 gaattgagagaaagctatctgtgctgctgctgctgtgctggggatctaaagtttcaatc 3456
Db 3181 gaattgagagaaagctatctgtgctgctgctgctgtgctggggatctaaagtttcaatc 3240
QY 3457 tggatgaaccccaagctggtgtgtgaccccttaccgccgaggggaaatgagggagctgtgc 3516
Db 3241 tggatgaaccccaagctggtgtgtgaccccttaccgccgaggggaaatgagggagctgtgc 3300
QY 3517 tgaataaccgaagaagccgacacatatactctctacacacacacatggaatgaagcgagacg 3576
Db 3301 tgaataaccgaagaagccgacacatatactctctacacacacacatggaatgaagcgagacg 3360
QY 3577 tccctggggagaaagattgtgcatcatctccatccctgaggaagctgtgctgtgtgagctctcc 3636
Db 3361 tccctggggagaaagattgtgcatcatctccatccctgaggaagctgtgctgtgtgagctctcc 3420
QY 3637 tgttcttgaaagaaacagctgaggaacaggtactactgagctctggttcaagaaagatgtg 3696
Db 3421 tgttcttgaaagaaacagctgaggaacaggtactactgagctctggttcaagaaagatgtg 3480
QY 3697 aatcctccctcaagttccctgcaagaacagtagtagcaactgtgtcatcaactgaaagaaagag 3756
Db 3481 aatcctccctcaagttccctgcaagaacagtagtagcaactgtgtcatcaactgaaagaaagag 3540
QY 3757 acaggtgttctcagagcaagttctgagctgagctgagcgagcgacatgagaaatgagacacg 3816
Db 3541 acaggtgttctcagagcaagttctgagctgagcgagcgagcgacatgagaaatgagacacg 3600
QY 3817 tgaaccaatgcatgtctctgcatctccaactcatcagaaagacatgtgtctgaagccggc 3876
Db 3601 tgaaccaatgcatgtctctgcatctccaactcatcagaaagacatgtgtctgaagccggc 3660
QY 3877 tgggtggaagacataagggcatgagctgagctgactatgtgtgcatatgaaagctgtgtaaggg 3936
Db 3661 tgggtggaagacataagggcatgagctgagctgactatgtgtgcatatgaaagctgtgtaaggg 3720
QY 3937 gaggctgtggaagacattctcatgagattgataccggctctcagaaacccgggcatcttca 3996
Db 3721 gaggctgtggaagacattctcatgagattgataccggctctcagaaacccgggcatcttca 3780
QY 3997 gttatggcatctcagagacagacctggaagaaatattcctcaagtggtgcggaagagatg 4056
Db 3781 gttatggcatctcagagacagacctggaagaaatattcctcaagtggtgcggaagagatg 3840

QY 4057 ggggtgagatgctgagacatccctcagatgtgtactcttgcagagcaagaaagcgagggctctg 4116
Db 3841 ggggtgagatgctgagacatccctcagatgtgtactcttgcagagcaagaaagcgagggctctg 3900
QY 4117 gggacaagcagagctgtctctgcccgttcaactgaaagtatgtctgtcatcacaatgatt 4176
Db 3901 gggacaagcagagctgtctctgcccgttcaactgaaagtatgtctgtcatcacaatgatt 3960
QY 4177 ctgacatagacccgaatctccagagagacagactgtctcagtgagatgagatgagcaaggt 4236
Db 3961 ctgacatagacccgaatctccagagagacagactgtctcagtgagatgagatgagcaaggt 4020
QY 4237 cctaccaggttgaagagcgtggaaacttacaacagcaacaggttggcccttcttggaaga 4296
Db 4021 cctaccaggttgaagagcgtggaaacttacaacagcaacaggttggcccttcttggaaga 4080
QY 4297 gactgtaattgccaagcagagctcggaagagatttttgcataagatgtctgcagctg 4356
Db 4081 gactgtaattgccaagcagagctcggaagagatttttgcataagatgtctgcagctg 4140
QY 4357 tgttgtctgcatgtcccttgtgttcaagctgcatcggtgcaccccttgggcaagtaacca 4416
Db 4141 tgttgtctgcatgtcccttgtgttcaagctgcatcggtgcaccccttgggcaagtaacca 4200
QY 4417 gctctgaacttcaagccctgagatgtatacaacgaaatatacatattgtcagcaatgtctc 4476
Db 4201 gctctgaacttcaagccctgagatgtatacaacgaaatatacatattgtcagcaatgtctc 4260
QY 4477 ctgagagacagggaaacccctggaactctttaaagcccttcaacaaagacccgtgtcgga 4536
Db 4261 ctgagagacagggaaacccctggaactctttaaagcccttcaacaaagacccgtgtcgga 4320
QY 4537 cccgctgtatggaagaaacccatcccaagacagcccttgcagagcgaggaagaaagt 4596
Db 4321 cccgctgtatggaagaaacccatcccaagacagcccttgcagagcgaggaagaaagt 4380
QY 4597 ggaacacatgcccagcttccccaagacatcatggaactcttccagaatggaacttgaca 4656
Db 4381 ggaacacatgcccagcttccccaagacatcatggaactcttccagaatggaacttgaca 4440
QY 4657 tgcagaaccccttcaactcagatgagctgtagcagcgacaacaaatcaagaagatgtgctg 4716
Db 4441 tgcagaaccccttcaactcagatgagctgtagcagcgacaacaaatcaagaagatgtgctg 4500
QY 4717 tgggtcccccagggagggggtgtgctctctccacaagaagaaacaaacactgcagata 4776
Db 4501 tgggtcccccagggagggggtgtgctctctccacaagaagaaacaaacactgcagata 4560
QY 4777 tccctcagacctgacagagaaagaaacatttcgattatctgtgtgaagacgtatgtgaca 4836
Db 4561 tccctcagacctgacagagaaagaaacatttcgattatctgtgtgaagacgtatgtgaca 4620
QY 4837 tcatagccaagaagcttaaagaacaaagatctgtgtgagatgagtttgaatgagatgagcgctt 4896
Db 4621 tcatagccaagaagcttaaagaacaaagatctgtgtgagatgagtttgaatgagatgagcgctt 4680
QY 4897 cccctgggtgtcattatattcaagcaacttcccccaggtcaagaagttaaagttaagtgcacata 4956
Db 4681 cccctgggtgtcattatattcaagcaacttcccccaggtcaagaagttaaagttaagtgcacata 4740
QY 4957 aacaatgaaagaaacacacttaagcttgccaagagacagctgtcagatcgatcttccaaca 5016
Db 4741 aacaatgaaagaaacacacttaagcttgccaagagacagctgtcagatcgatcttccaaca 4800
QY 5017 gcttgggaagatttatagacagagctgagacacaaagaaatattcaaggtgtgtgtaata 5076
Db 4801 gcttgggaagatttatagacagagctgagacacaaagaaatattcaaggtgtgtgtaata 4860
QY 5077 acaaggtctgcatgcaatagctcttctcagatgtcatcaacaatgcatcttccgg 5136
Db 4861 acaaggtctgcatgcaatagctcttctcagatgtcatcaacaatgcatcttccgg 4920

QY 5137 ccaactcgcacaaaggagagaaacccctagccattatggaattactgtcttccatcatccccc 5196
|||||
Db 4921 ccaacctgcacaaaggagagaaacccctagccattatggaattactgtcttccatcatccccc 4980
QY 5197 tgaattccacaaagcagcagctctcagaggtgtgtctgtatgacacacatcagtgatgtccc 5256
|||||
Db 4981 tgaattccacaaagcagcagctctcagaggtgtgtctgtatgacacacatcagtgatgtccc 5040
QY 5257 ttgtatcactgtgtctatcttctgcaatgtgtctgtccagcagccttctgtatcttccc 5316
|||||
Db 5041 ttgtatcactgtgtctatcttctgcaatgtgtctgtccagcagccttctgtatcttccc 5100
QY 5317 tgaatcagaagcggtgtcagcaagaacacacactgcagttcactcagtgagtgaaagcctg 5376
Db 5101 tgaatcagaagcggtgtcagcaagaacacacactgcagttcactcagtgagtgaaagcctg 5160
QY 5377 tcaatcactgtgtctatcttctgtgtgatagtgtcgaattacgtgtgtccctgtccacac 5436
|||||
Db 5161 tcaatcactgtgtctatcttctgtgtgatagtgtcgaattacgtgtgtccctgtccacacac 5220
QY 5437 tggatcattatcatctcatctgtcttccagcagaagtcctatgtgttccctccacacatctgc 5496
|||||
Db 5221 tggatcattatcatctcatctgtcttccagcagaagtcctatgtgttccctccacacatctgc 5280
QY 5497 ctgtgtcagcccttctactcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5556
|||||
Db 5281 ctgtgtcagcccttctactcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5340
QY 5557 cctccttctgttcaagaalcccacagacagcactatgtgtgtgtgtgtgtgtgtgtgtgtgt 5616
|||||
Db 5341 cctccttctgttcaagaalcccacagacagcactatgtgtgtgtgtgtgtgtgtgtgtgtgt 5400
QY 5617 tcaatgtcattatgtcagcagcggt 5676
|||||
Db 5401 tcaatgtcattatgtcagcagcggt 5460
QY 5677 tgaatataatcactatgataatccgtaagtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5736
|||||
Db 5461 tgaatataatcactatgataatccgtaagtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5520
QY 5737 gacagagctcactcagacatgt 5796
|||||
Db 5521 gacagagctcactcagacatgt 5580
QY 5797 gggagaatcgtctgt 5856
|||||
Db 5581 gggagaatcgtctgt 5640
QY 5857 tggcgt 5916
|||||
Db 5641 tggcgt 5700
QY 5917 tcaagccagacactgttaattgtcaagaatcttccctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5976
|||||
Db 5701 tcaagccagacactgttaattgtcaagaatcttccctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5760
QY 5977 ggcgggaaagacagagaattcctgt 6036
|||||
Db 5761 ggcgggaaagacagagaattcctgt 5820
QY 6037 agttgtacgaagatatataatgaagaagcgggaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6096
|||||
Db 5821 agttgtacgaagatatataatgaagaagcgggaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5880
QY 6097 tttccctcgt 6156
|||||
Db 5881 tttccctcgt 5940
QY 6157 tcaagatgttcaacagagatatccactgtttacacagagagatgtgtgtgtgtgtgtgtgtgtgtgt 6216
|||||
Db 5941 tcaagatgttcaacagagatatccactgtttacacagagagatgtgtgtgtgtgtgtgtgtgtgtgt 6000
QY 6217 gtatcttatacaaacatcactgaagtatcatcagaacatgtgtgtgtgtgtgtgtgtgtgtgtgt 6276
|||||

Db 6001 gtatcttatacaaacatcactgaagtatcatcagaacatgtgtgtgtgtgtgtgtgtgtgtgtgt 6060
QY 6277 ccatcacagagcgt 6336
Db 6061 ccatcacagagcgt 6120
QY 6337 tcccgagaagaaggt 6396
|||||
Db 6121 tcccgagaagaaggt 6180
QY 6397 agtatgtgaagaataatgt 6456
|||||
Db 6181 agtatgtgaagaataatgt 6240
QY 6457 ccatgt 6516
Db 6241 ccatgt 6300
QY 6517 atcccaagcccggt 6576
|||||
Db 6301 atcccaagcccggt 6360
QY 6577 cagtaagtgttacaatcactatgatagtgaagaatgtgaagccttctgtcactagatgtgcaa 6636
Db 6361 cagtaagtgttacaatcactatgatagtgaagaatgtgaagccttctgtcactagatgtgcaa 6420
QY 6637 tcatgtgtcaatgtgaaggt 6696
Db 6421 tcatgtgtcaatgtgaaggt 6480
QY 6697 gagaatgttatacaatagatgt 6756
Db 6481 gagaatgttatacaatagatgt 6540
QY 6757 aggaattcttctgt 6816
Db 6541 aggaattcttctgt 6600
QY 6817 tacaatccagcgtcactcacttcaattatctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6876
Db 6601 tacaatccagcgtcactcacttcaattatctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6660
QY 6877 agagcaaaaagcagactcactcactcactcactcactcactcactcactcactcactcactcact 6936
Db 6661 agagcaaaaagcagactcactcactcactcactcactcactcactcactcactcactcactcact 6720
QY 6937 tatttgtgaacttgcacaaagagacaaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6996
Db 6721 tatttgtgaacttgcacaaagagacaaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6780
QY 6997 acaaaaacacagacagtagtgcagctgt 7056
Db 6781 acaaaaacacagacagtagtgcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6840
QY 7057 tgaagaagaagctatgtatgaagaatcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7116
Db 6841 tgaagaagaagctatgtatgaagaatcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6900
QY 7117 ctgacttctccttgcacacatgt 7176
Db 6901 ctgacttctccttgcacacatgt 6960
QY 7177 gaagaagtaaacgt 7236
Db 6961 gaagaagtaaacgt 7020
QY 7237 aaacaaatccattacagagggcagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7296
Db 7021 aaacaaatccattacagagggcagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7080
QY 7297 tgaagaactgtgaattagtttttactatactctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7356
|||||

Dh 1 gtcctgtgtgagctctgcccgtccctccagagctcccgagccacacgctggggtg 60
Qy 277 ctggtcggaggaacatggtctgtgtgacctcagctgaagctgtgctgtgtgaaacatca 336
Db 61 ctggtcggaggaacatggtctgtgtgacctcagctgaagctgtgctgtgtgaaacatca 120
Qy 337 ctccaagaagaagaacaacatgtcagctgttactgtgaagtgtgcctgtcctattatct 396
Db 121 ctccaagaagaagaacaacatgtcagctgttactgtgaagtgtgcctgtcctattatct 180
Qy 397 tccgtatccgtatctgtcttcgtcgtgagctacccaacctatgaaacatgaatgcatt 456
Db 181 tccgtatccgtatctgtcttcgtcgtgagctacccaacctatgaaacatgaatgcatt 240
Qy 457 ttccaataaagccatgacctcctctgcaggaacacctcctgtgggttccagggtattatcgt 516
Db 241 ttccaataaagccatgacctcctctgcaggaacacctcctgtgggttccagggtattatcgt 300
Qy 517 atgcacaacaacccctgttccgttaccgacctcctgtgggaggtcccggaagtgtttgga 576
Db 301 atgcacaacaacccctgttccgttaccgacctcctgtgggaggtcccggaagtgtttgga 360
Qy 577 acttaacaatccatctgtgtcgcgcctgttccagatgctcggaggtcttcttataca 636
Db 361 acttaacaatccatctgtgtcgcgcctgttccagatgctcggaggtcttcttataca 420
Qy 637 gccagaagaacacagatgaaagacatgacatgcacaaagtcttcggaacatatacagacatca 696
Db 421 gccagaagaacacagatgaaagacatgacatgcacaaagtcttcggaacatatacagacatca 480
Qy 697 agaaatccagctcaaaccttgaagctcaagattccctgttgagacaaatgaacacctctctg 756
Db 481 agaaatccagctcaaaccttgaagctcaagattccctgttgagacaaatgaacacctctctg 540
Qy 757 gttctatataccaacccctcctcctccaaagtcttactgttgagacaaagtctgaggtctg 816
Db 541 gttctatataccaacccctcctcctccaaagtcttactgttgagacaaagtctgaggtctg 600
Qy 817 atgtcatctccaagaagtatttttgcaaggtaccagttacattgtgcaagatcgtgtca 876
Db 601 atgtcatctccaagaagtatttttgcaaggtaccagttacattgtgcaagatcgtgtca 660
Qy 877 atgatatcaaatcagaagaagatgattcaactgtgtgacccaagaagttctcgaacttgtg 936
Db 661 atgatatcaaatcagaagaagatgattcaactgtgtgacccaagaagttctcgaacttgtg 720
Qy 937 gcttaccaaaggagaactgtgtcagcagagcgagtactcgtttccaaatgaaacatcc 996
Db 721 gcttaccaaaggagaactgtgtcagcagagcgagtactcgtttccaaatgaaacatcc 780
Qy 997 tgaagccaatctctggaagaacatacctacatctccctcccgagcaagagctgtgctg 1056
Db 781 tgaagccaatctctggaagaacatacctacatctccctcccgagcaagagctgtgctg 840
Qy 1057 aagccaacaanaacatctgtgtcaatgcttctggaactgtgcccgaagctgttcaagctga 1116
Db 841 aagccaacaanaacatctgtgtcaatgcttctggaactgtgcccgaagctgttcaagctga 900
Qy 1117 gaaagctggaagtgaacatgcgaacaggaagtgtatgttcttgacaacatgtgaacagctcagct 1176
Db 901 gaaagctggaagtgaacatgcgaacaggaagtgtatgttcttgacaacatgtgaacagctcagct 960
Qy 1177 cctccaccaaatctacacagctgtgtctgtatgttctcgtggtcctcccgagggaggg 1236
Db 961 cctccaccaaatctacacagctgtgtctgtatgttctcgtggtcctcccgagggaggg 1020
Qy 1237 ggtctgaagatcaagctctctcaactggtatgaggaacaacatacaagggcctcttggag 1296
Db 1021 ggtctgaagatcaagctctctcaactggtatgaggaacaacatacaagggcctcttggag 1080
Qy 1297 gcaatggaactggaagaagatgtctaaacctctatgaacaactacaaactccttactga 1356
Db 1081 gcaatggaactggaagaagatgtctaaacctctatgaacaactacaaactccttactga 1140
Qy 1357 atgatttgatgaagaatatttgagctagctcccttcccgatattatctggaagctctga 1416
Db 1141 atgatttgatgaagaatatttgagctagctcccttcccgatattatctggaagctctga 1200
Qy 1417 agccgcgtcctgttgggaagaatcctgtatacacctgtgaacatccagcccaagaagctga 1476
Db 1201 agccgcgtcctgttgggaagaatcctgtgtatacacctgtgaacatccagcccaagaagctga 1260
Qy 1477 tggctggtgtgtaacaagaacctcccgaaactgtgtgttccatgatctggaagcatgt 1536
Db 1261 tggctggtgtgtaacaagaacctcccgaaactgtgtgttccatgatctggaagcatgt 1320
Qy 1537 gggaggaacctcaagcccaagatctggaacttatggaagaacggccaagaatgagacctg 1596
Db 1321 gggaggaacctcaagcccaagatctggaacttatggaagaacggccaagaatgagacctg 1380
Qy 1597 tccggtatgctgttggacaagcaggaacatgacaccttittgggaacagcatgtgagct 1656
Db 1381 tccggtatgctgttggacaagcaggaacatgacaccttittgggaacagcatgtgagct 1440
Qy 1657 taagattggaagcccaagacatgtgtgttttgccaagcaccagaagatgtccaagt 1716
Db 1441 taagattggaagcccaagacatgtgtgttttgccaagcaccagaagatgtccaagt 1500
Qy 1717 ccaagtaatgttctgtgtacacctggagaagaacttcaacagatatacagagcaatcc 1776
Db 1501 ccaagtaatgttctgtgtacacctggagaagaacttcaacagatatacagagcaatcc 1560
Qy 1777 ggaaccaatctcgtctcatgaggtgtgttcaaaccttgaaacatctgaacccatagcaacag 1836
Db 1561 ggaaccaatctcgtctcatgaggtgtgttcaaaccttgaaacatctgaacccatagcaacag 1620
Qy 1837 aagctgtgtctatcaacaagaatccatgagctgtgtgaaagaagaagtctcgggtctga 1896
Db 1621 aagctgtgtctatcaacaagaatccatgagctgtgtgaaagaagaagtctcgggtctga 1680
Qy 1897 ttgtgttccctgtgaattactccagagcagcatgtgagctgtgcccacatgtcaagtacaaga 1956
Db 1681 ttgtgttccctgtgaattactccagagcagcatgtgagctgtgcccacatgtcaagtacaaga 1740
Qy 1957 tccgaatggaacatgaaacatgtgaggaagaacaataaagaagatgggtactcggagacc 2016
Db 1741 tccgaatggaacatgaaacatgtgaggaagaacaataaagaagatgggtactcggagacc 1800
Qy 2017 ctgtgtccctcagatgaaaccccttggagacatgctgtaagctgtggggggtcgcctact 2076
Db 1801 ctgtgtccctcagatgaaaccccttggagacatgctgtaagctgtggggggtcgcctact 1860
Qy 2077 tgcagaatgtgtgtgagagcaggaacatcatcaggtgtgagcgggagccaggaagaagaacg 2136
Db 1861 tgcagaatgtgtgtgagagcaggaacatcatcaggtgtgagcgggagccaggaagaagaacg 1920
Qy 2137 --gtgtctatatgcaacagatgacctatccctgttactgttactgtgaacatcttctggggt 2194
Db 1921 gdtgtctatatgcaacagatgacctatccctgttactgttactgtgaacatcttctggggt 1980
Qy 2195 gatgagcgggtcgaatgtgccccttcatgagcgtgtgctgtgaattactcagtgctgtgat 2254
Db 1981 gatgagcgggtcgaatgtgccccttcatgagcgtgtgctgtgaattactcagtgctgtgat 2040
Qy 2255 catcaagggtcgtgtgatgagaagaagcagcgtgtgaagaagaacatgcggtacatggg 2314
Db 2041 catcaagggtcgtgtgatgagaagaagcagcgtgtgaagaagaacatgcggtacatggg 2100
Qy 2315 cctgtgacaacagcatactcgtgtttagcgtgttcaatgtagcctcatcctcttctgt 2374
Db 2101 cctgtgacaacagcatactcgtgtttagcgtgttcaatgtagcctcatcctcttctgt 2160
Qy 2375 gagcgtgacctgtgtatgtgtcatcctggaagttagaagaacctgtgccttaagtgacc 2434
Db 2161 gagcgtgacctgtgtatgtgtcatcctggaagttagaagaacctgtgccttaagtgacc 2220

```
OY 2435 cagcgtggtttgtcttcctcgtcgtgttctgtgtgtaacatccctcagctgtcct 2494
|||||
Db 2221 cagcgtggtttgtcttcctcctcgtcgtgttctgtgtgtaacatccctcagctgtcct 2280
OY 2495 gattagacacactctctccagagccaacctggaacagcctgttgagggaatcattact 2554
|||||
Db 2281 gattagacacactctctccagagccaacctggaacagcctgttgagggaatcattact 2340
OY 2555 cagcgtgtatcctgacctacgtccctgtgtgtgcaatgagcaactcgtgggttcaact 2614
|||||
Db 2341 cagcgtgtatcctgacctacgtccctgtgtgtgcaatgagcaactcgtgggttcaact 2400
OY 2615 caagatcttcgtctagcctcgtctcctcgtgtgcttgggttggcttgaattcttgc 2674
|||||
Db 2401 caagatcttcgtctagcctcgtctcctcgtgtgcttgggttggcttgaattcttgc 2460
OY 2675 ccttttggagagcagggagcttgagctgagctgagagcaaacctgttttgagagctgttga 2734
|||||
Db 2461 ccttttggagagcagggagcttgagctgagctgagagcaaacctgttttgagagctgttga 2520
OY 2735 ggaagatggtcttcaatctcaacttcgaatctccatgatagcgtgttgaaacttctcta 2794
|||||
Db 2521 ggaagatggtcttcaatctcaacttcgaatctccatgatagcgtgttgaaacttctcta 2580
OY 2795 tggagtgatgacctggtatcatgagcgtgtcttccagagccagtaacgaaatcccaagcc 2854
|||||
Db 2581 tggagtgatgacctggtatcatgagcgtgtcttccagagccagtaacgaaatcccaagcc 2640
OY 2855 ctgtatcttctccttgcaaccaagtcctactggttctggcgaagaaagtatgaaagagcca 2914
|||||
Db 2641 ctgtatcttctccttgcaaccaagtcctactggttctggcgaagaaagtatgaaagagcca 2700
OY 2915 ccttggttccaaacccaagaaagatgtcagaatcttgcatgagagggagaaacccaact 2974
|||||
Db 2701 ccttggttccaaacccaagaaagatgtcagaatcttgcatgagagggagaaacccaact 2760
OY 2975 gaaagctgggcgtgtcatcatcagaacccctgttaaaagtctacccagatgagatgaagtgcc 3034
|||||
Db 2761 gaaagctgggcgtgtcatcatcagaacccctgtgttaaaagtctacccagatgagatgaagtgcc 2820
OY 3035 tctgcatgagccttgcaactgaattttatgagggccaagatcaactcctctctggccacaa 3094
|||||
Db 2821 tctgcatgagccttgcaactgaattttatgagggccaagatcaactcctctctggccacaa 2880
OY 3095 tggagggggggaagacacacacatgcaatccttgaccgggtgttcccccgaaccccgag 3154
|||||
Db 2881 tggagggggggaagacacacacatgcaatccttgaccgggtgttcccccgaaccccgag 2940
OY 3155 caccgctacatccttggaagaagacattcgtctcgtgagatgagacacatcccgacagact 3214
|||||
Db 2941 caccgctacatccttggaagaagacattcgtctcgtgagatgagacacatcccgacagact 3000
OY 3215 gggggtctgtcccgacataaagctgtgtttgacatgtgactgtctgaagaacacatctg 3274
|||||
Db 3001 gggggtctgtcccgacataaagctgtgtttgacatgtgactgtctgaagaacacatctg 3060
OY 3275 gttctatgcccgtctgaaagggctctctgaaagacgctgaaagggcggaatggaagat 3334
|||||
Db 3061 gttctatgcccgtctgaaagggctctctgaaagacgctgaaagggcggaatggaagat 3120
OY 3335 ggcctctgagatgtgttctgccaatcaagcaagctgaaagcaaaacacagccagctgcag 3394
|||||
Db 3121 ggcctctgagatgtgttctgccaatcaagcaagctgaaagcaaaacacagccagctgcag 3180
OY 3395 tggaaatgcagaaagatctatctgtgaccttgacctgttgcgggggatactaaagtctcat 3454
|||||
Db 3181 tggaaatgcagaaagatctatctgtgaccttgacctgttgcgggggatactaaagtctcat 3240
OY 3455 tctgagatgaacccaacagctgtgttgagaccttaccacgaagggagatgtgagagctgc 3514
|||||
Db 3241 tctgagatgaacccaacagctgtgtgtgagaccttaccacgaagggagatgtgagagctgc 3300
OY 3515 gctgaaatatccgaacagccgcacatattctctctaacacacacatgataagcgga 3574
|||||

Db 3301 gctgaatatccgaacagccgcacatattctctctaacacacacatgataagcgga 3360
OY 3575 cgtccctgggagacagagattgccaatcatctcccatggaagctgtgtgtgtgtgtcctc 3634
|||||
Db 3361 cgtccctgggagacagagattgccaatcatctcccatggaagctgtgtgtgtgtgtcctc 3420
OY 3635 cctgttctgaaagacacagcctgggaacagctactacattgacctgtgtcgaagaagtgt 3694
|||||
Db 3421 cctgttctgaaagacacagcctgggaacagctactacattgacctgtgtcgaagaagtgt 3480
OY 3695 ggaatccctccctcagttcctcgaagaaacagtagtagcactgtgttcatatccgaagaaaga 3754
|||||
Db 3481 ggaatccctccctcagttcctcgaagaaacagtagtagcactgtgttcatatccgaagaaaga 3540
OY 3755 ggaacagtgttctcgaagacagttctgatagtctgacctgtggcagcagacatgaagatgacac 3814
|||||
Db 3541 ggaacagtgttctcgaagacagttctgatagtctgacctgtggcagcagacatgaagatgacac 3600
OY 3815 gctgaccaatgatagtctcgtctatctcccaactcatcaggaagcattgtctgagaccg 3874
|||||
Db 3601 gctgaccaatgatagtctcgtctatctcccaactcatcaggaagcattgtctgagaccg 3660
OY 3875 gctgtggaagacataagggcatalgagctgacatagtctgccaatgaaagtctgaaaga 3934
|||||
Db 3661 gctgtggaagacataagggcatalgagctgacatagtctgccaatgaaagtctgaaaga 3720
OY 3935 gggagcctctgttgaaactcttcaatgagatgtagagccgctcccaactctggacattc 3994
|||||
Db 3721 gggagcctctgttgaaactcttcaatgagatgtagagccgctcccaactctggacattc 3780
OY 3995 tagtatgatactcacaagacagcccttgaaagaaatcttccaaaggctggccgaagag 4054
|||||
Db 3781 tagtatgatactcacaagacagcccttgaaagaaatcttccaaaggctggccgaagag 3840
OY 4055 tggggtggaatgctgagacctcaatgatactgtccagcaagacgaaacagcgcgctc 4114
|||||
Db 3841 tggggtggaatgctgagacctcaatgatactgtccagcaagacgaaacagcgcgctc 3900
OY 4115 cggggaacaaagacagctgtcttccgcttcaactgaaagatgatactgtctgataccaatga 4174
|||||
Db 3901 cggggaacaaagacagctgtcttccgcttcaactgaaagatgatactgtctgataccaatga 3960
OY 4175 tt-ctgacatagaccacaatccagagagacagactgtgctcaagtggagatgagtgcaag 4233
|||||
Db 3961 ttgctgacatagaccacaatccagagagacagactgtgctcaagtggagatgagtgcaag 4020
OY 4234 gttcctacaaagtgaagagctggaactttacacagcaacagttgtgtgaccttctgtga 4293
|||||
Db 4021 gttcctacaaagtgaagagctggaactttacacagcaacagttgtgtgaccttctgtga 4080
OY 4294 aagaagctgtaattgacagagagctggaagagattttgtccagatgtctctgcag 4353
|||||
Db 4081 aagaagctgtaattgacagagagctggaagagattttgtccagatgtctctgcag 4140
OY 4354 cctgttctgtctgacatgtccctgtgttcaagcctgactgtgtccaccccttggcaagtaac 4413
|||||
Db 4141 cctgttctgtctgacatgtccctgtgttcaagcctgactgtgtgtccaccccttggcaagtaac 4200
OY 4414 ccaagcctggaacttaagccctggatgatacgaacgaatatacaattgttcaagcaatgatg 4473
|||||
Db 4201 ccaagcctggaacttaagccctggatgatacgaacgaatatacaattgttcaagcaatgatg 4260
OY 4474 ctcctgaaagacacgggaacccctggaactcttaaaagccctacaaagacccctgtctcg 4533
|||||
Db 4261 ctcctgaaagacacgggaacccctggaactcttaaaagccctacaaagacccctgtctcg 4320
OY 4534 ggaacccgtgtatgtgaagaaacccaatcccaagacagccctgcagcgagggaggaag 4593
|||||
Db 4321 ggaacccgtgtatgtgaagaaacccaatcccaagacagccctgcagcgagggaggaag 4380
OY 4594 agtgaacacatgccccagttccccaagacacatcagagacttccagatgtggaactgga 4653
|||||
```

D 4381 agtggacactgcgccagcttccccaacatcattgacactcttccgaatlyggaactgga 4440
Q 4554 caatgcgaacaccttcacacctgacatgtaacagcagcaaaataaagaatgctgc 4713
D 4441 caatgcgaacaccttcacacctgacatgtaacagcagcaaaataaagaatgctgc 4500
Q 4714 ctggtgttccccaggggagggggtgctcctcccaagaagaacaaacactgag 4773
D 4501 ctgtgtgtccccaggggagggggtgctcctcccaagaagaacaaacactgag 4560
Q 4774 atacccttcagagaccttacaggaagaaaccttcggaattctgtgtgaagactatgtgc 4833
D 4561 atacccttcagagaccttacaggaagaaaccttcggaattctgtgtgaagactatgtgc 4620
Q 4834 agatcatagccaaagcttaagaagaagaatctgtgtgaatgagttatgagtcgagct 4893
D 4621 agatcatagccaaagcttaagaagaagaatctgtgtgaatgagttatgagtcgagct 4680
Q 4894 ttccccgtgtgtcagtaataactcaagacctcctccgagtcgaagatlaattgagtcga 4953
D 4681 ttccccgtgtgtcagtaataactcaagacctcctccgagtcgaagatlaattgagtcga 4740
Q 4954 tcaacaacatggaagaacacactaaagcttgccaggaacattctgcagatcgattctca 5013
D 4741 tcaacaacatggaagaacacactaaagcttgccaggaacattctgcagatcgattctca 4800
Q 5014 acagcttgggaagaattatgacagagacttgacacccaagaataatgtaagaatgctgca 5073
D 4801 acagcttgggaagaattatgacagagacttgacacccaagaataatgtaagaatgctgca 4860
Q 5074 ataaacaaaggctgacatgacatcaagctcttcctgaatgtaacatcaatgacatctcc 5133
D 4861 ataaacaaaggctgacatgacatcaagctcttcctgaatgtaacatcaatgacatctcc 4920
Q 5134 gggccaaacccgcaaaaaggagagaaaccttagacattatggaattactgcttcaatcacc 5193
D 4921 gggccaaacccgcaaaaaggagagaaaccttagacattatggaattactgcttcaatcacc 4980
Q 5194 cccctgaaatctcaacaaagcagacgtctcagaaggctgctcgtatgacacacatcgagtg 5253
D 4981 cccctgaaatctcaacaaagcagacgtctcagaaggctgctcgtatgacacacatcgagtg 5040
Q 5254 tccctgtgtccatctgtgtatcttttgcaatgtctccttcgtccagcagcttctgtcgtat 5313
D 5041 tccctgtgtccatctgtgtatcttttgcaatgtctccttcgtccagcagcttctgtcgtat 5100
Q 5314 tccctgataccagagcggttcagcaaaagcaaacactgacattcagtgagtgagag 5373
D 5101 tccctgataccagagcggttcagcaaaagcaaacactgacattcagtgagtgagag 5160
Q 5374 ctgtcatctactgtgtcttaatttctgtctggatagtgtgaattacgttgcctgcga 5433
D 5161 ctgtcatctactgtgtcttaatttctgtctggatagtgtgaattacgttgcctgcga 5220
Q 5434 caatggtcatatcatcttatctgtcttcagagagaatgctctatgtctctccacaatc 5493
D 5221 caatggtcatatcatcttatctgtcttcagagagaatgctctatgtctctccacaatc 5280
Q 5494 tgcctgtgtagcccttctactcttctgtatgtgtgtaacatcaacactcattatgc 5553
D 5281 tgcctgtgtagcccttctactcttctgtatgtgtgtaacatcaacactcattatgc 5340
Q 5554 cagcctccttctgttcaagaatcccaagacagcctatgtgtgtcaccagcgtagaac 5613
D 5341 cagcctccttctgttcaagaatcccaagacagcctatgtgtgtcaccagcgtagaac 5400
Q 5614 tctcataggcatatagtcagagtggtgcaaccttggtctgtagagctgttccacgaataa 5673
D 5401 tctcataggcatatagtcagagtggtgcaaccttggtctgtagagctgttccacgaataa 5460
Q 5674 agctgataataatcaatgatatctgaagtcggttctctgtagcttccacaatttctgc 5733
D 5461 agctgataataatcaatgatatctgaagtcggttctctgtagcttccacaatttctgc 5520

Q 5734 tggagaaaggcttcacatcagatggtgaaacaaacagcaatgctatgctccctggaagt 5793
D 5521 tggagaaaggcttcacatcagatggtgaaacaaacagcaatgctatgctccctggaagt 5580
Q 5794 ttgggagaatctgcttctgttccacattacttggagcttggttgagcgaacctctgc 5853
D 5581 ttgggagaatctgcttctgttccacattacttggagcttggttgagcgaacctctgc 5640
Q 5854 ccatggccgtggaaggggtgtctctccattacagcttctgttccagatgattct 5913
D 5641 ccatggccgtggaaggggtgtctctccattacagcttctgttccagatgattct 5700
Q 5914 tcatcagggccagacctgttaaatgcaaaagctatctcctctgaatgataatgaaatg 5973
D 5701 tcatcagggccagacctgttaaatgcaaaagctatctcctctgaatgataatgaaatg 5760
Q 5974 tgaagcggaagaagacagagaatcttgatggttgagggccagaatgacaactgaataca 6033
D 5761 tgaagcggaagaagacagagaatcttgatggttgagggccagaatgacaactgaataca 5820
Q 6034 aggaattgcggaagatatagaagaagcggaagcgtgctgttgcagagattgctg 6093
D 5821 aggaattgcggaagatatagaagaagcggaagcgtgctgttgcagagattgctg 5880
Q 6094 gcatcctcctgtgtgagcttgggctcctgggaggttaatggggcttggaataatcaaa 6153
D 5881 gcatcctcctgtgtgagcttgggctcctgggaggttaatggggcttggaataatcaaa 5940
Q 6154 cttcaagaatgtaacaggaatcaccactgttaccagaagagatgcttcccttaacaaa 6213
D 5941 cttcaagaatgtaacaggaatcaccactgttaccagaagagatgcttcccttaacaaa 6000
Q 6214 ata-gtatcttatacaaatccatcgaatgatacgaacatgagcttactgcccacttt 6272
D 6001 ataagttatctatacaaatccatcgaatgatacgaacatgagcttactgcccacttt 6060
Q 6273 gatgcatcacaagaagctgttgacttggagagaacacggtgagcttcttgccttttga 6332
D 6061 gatgcatcacaagaagctgttgacttggagagaacacggtgagcttcttgccttttga 6120
Q 6333 ggaatcccaagaaagaagtttggcaaggttggtgagtgggcgatctggaaactgagctc 6392
D 6121 ggaatcccaagaaagaagtttggcaaggttggtgagtgggcgatctggaaactgagctc 6180
Q 6393 gtaaggtatggaagaataatgctgtgtaactatggtgaggaacaaacgaagctctct 6452
D 6181 gtaaggtatggaagaataatgctgtgtaactatggtgaggaacaaacgaagctctct 6240
Q 6453 acaagcattgcttgaatcgcgagcctcctgtgtgttctgtgaatgaaccacacagc 6512
D 6241 acaagcattgcttgaatcgcgagcctcctgtgtgttctgtgaatgaaccacacagc 6300
Q 6513 atggtatcccaaaagcccggttcttctgtggaattgtggtcccaaatgtgttgaagaagg 6572
D 6301 atggtatcccaaaagcccggttcttctgtggaattgtggtcccaaatgtgttgaagaagg 6360
Q 6573 agatcagtagtcttactatcctcactagtaatggaagaatggaagcttcttcaacagatg 6632
D 6361 agatcagtagtcttactatcctcactagtaatggaagaatggaagcttcttcaacagatg 6420
Q 6633 gcaatcatgctcaatggaagttcaagtgcttggcagtgctcagcaatcctaaanaatag 6692
D 6421 gcaatcatgctcaatggaagttcaagtgcttggcagtgctcagcaatcctaaanaatag 6480
Q 6693 ttggagagtggttatacaaatggtgtacgaatagcaggttccaaaccccgagctgaagct 6752
D 6481 ttggagagtggttatacaaatggtgtacgaatagcaggttccaaaccccgagctgaagct 6540
Q 6753 gtccaagattctcttggactgcaatcctccctggaggttcttcaaaagaagaacccggaac 6812
D 6541 gtccaagattctcttggactgcaatcctccctggaggttcttcaaaagaagaacccggaac 6600

QY 6813 atgtacataaccagcttcacatcttcattatcttctctgcccagatatcaacatctc 6872
 |||||||
 Db 6601 atgtacataaccagcttcacatcttcattatcttctctgcccagatatcaacatctc 6660
 QY 6873 tcccagagaacaaacgactccacatagagaactactcgtttcccaacaacacttgac 6932
 |||||||
 Db 6661 tcccagagaacaaacgactccacatagagaactactcgtttcccaacaacacttgac 6720
 QY 6933 caagtaattgtgaacttgcagagcaacaaagtgaatgaaccacttaaaagactctca 6992
 |||||||
 Db 6721 caagtaattgtgaacttgcagagcaacaaagtgaatgaaccacttaaaagactctca 6780
 QY 6993 ttacacaaaacacagacagtaagtgaactgtgaacttccactcttctaagatag 7052
 |||||||
 Db 6781 ttacacaaaacacagacagtaagtgaactgtgaacttccactcttctaagatag 6840
 QY 7053 aaagtgaagaagatbtaatgaagaatccgttcacatacaggggtgctgaagtaaga 7112
 |||||||
 Db 6841 aaagtgaagaagatbtaatgaagaatccgttcacatacaggggtgctgaagtaaga 6900
 QY 7113 ggaactagaacttctcttgcaccacatgtgaagtgtgtggaagaagagccagaattgat 7172
 |||||||
 Db 6901 ggaactagaacttctcttgcaccacatgtgaagtgtgtggaagaagagccagaattgat 6960
 QY 7173 gtggagaagaagtaaaactgtgatactgtactactactatcaatgcaatgcaatgca 7232
 |||||||
 Db 6961 gtggagaagaagtaaaactgtgatactgtactactactatcaatgcaatgcaatgca 7020
 QY 7233 atgaacaacaaatccattacacaggggagtgcttctgtacatgtctgtatgctct 7292
 |||||||
 Db 7021 atgaacaacaaatccattacacaggggagtgcttctgtacatgtctgtatgctct 7080
 QY 7293 caagtgaagaactgtgaattagtcttctccatacactatggaactatataatgaac 7352
 |||||||
 Db 7081 caagtgaagaactgtgaattagtcttctccatacactatggaactatataatgaac 7140
 QY 7353 ccaatgacataatgtgtgaactacac-ttttttttttttttttctctgtatct 7411
 |||||||
 Db 7141 ccaatgacataatgtgtgaactacac-ttttttttttttttttctctgtatct 7200
 QY 7412 cactgggtgtgcaacaataatcaatgaatgaatgaatgaatgaatgaatgaatgaatga 7471
 |||||||
 Db 7201 cactgggtgtgcaacaataatcaatgaatgaatgaatgaatgaatgaatgaatgaatga 7260
 QY 7472 aaaaagtaatgacatccatccatccatccatccatccatccatccatccatccatccatcc 7531
 |||||||
 Db 7261 aaaaagtaatgacatccatccatccatccatccatccatccatccatccatccatccatcc 7320
 QY 7532 gtgacacatccatctgtgcaatgaatgtgcaagatgaatgaatgaatgaatgaatgaatga 7591
 |||||||
 Db 7321 gtgacacatccatctgtgcaatgaatgtgcaagatgaatgaatgaatgaatgaatgaatga 7380
 QY 7592 agtttgaagacacatgtgtgtcactcacttctgtgaagctgtctgtcagaagct 7651
 |||||||
 Db 7381 agtttgaagacacatgtgtgtcactcacttctgtgaagctgtctgtcagaagct 7440
 QY 7652 ataaacttgaataatgaatgtgacagaatgtgacagcggtgacataatcctgtctgtat 7711
 |||||||
 Db 7441 ataaacttgaataatgaatgtgacagaatgtgacagcggtgacataatcctgtctgtat 7500
 QY 7712 tccctctgaataagctgttctgtgcaatgaatgaatgaatgaatgaatgaatgaatgaatga 7771
 |||||||
 Db 7501 tccctctgaataagctgttctgtgcaatgaatgaatgaatgaatgaatgaatgaatgaatga 7560
 QY 7772 caacgggaactgttccatgttatatgttctcactgtgcagcagatgggtctacaggg 7831
 |||||||
 Db 7561 caacgggaactgttccatgttatatgttctcactgtgcagcagatgggtctacaggg 7620
 QY 7832 tcatccttaagagacttataataataataataataataataataataataataataataataagc 7891
 |||||||
 Db 7621 tcatccttaagagacttataataataataataataataataataataataataataataataagc 7880
 QY 7892 caactgtctgggtgcaagctgtgcaagcagcgatggatgaagagatgtctgct 7951

Db 7681 caactgtctgggtgcaagctgtgcaagcagcgatggatgaagagatgtctgct 7739
 |||||||
 QY 7952 caacctaagggaagcgtgtgccatctgtccctgactgtctgtcctaactgttaccatgcat 8011
 |||||||
 Db 7740 caacctaagggaagcgtgtgccatctgtccctgactgtctgtcctaactgttaccatgcat 7799
 QY 8012 ctcaagatgttatctgacacaaagtatattctgtgcttctgtgaatgaatgaatgaatga 8071
 |||||||
 Db 7800 ctcaagatgttatctgacacaaagtatattctgtgcttctgtgaatgaatgaatgaatga 7859
 QY 8072 tgaag 8076
 |||||||
 Db 7860 tgaag 7864

RESULT 12
 AAC69385
 ID AAC69385 standard; cDNA; 7864 BP.
 XX
 AC AAC69385;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human ABC1 cholesterol transporter TD-1 mutant cDNA (T4503C).
 XX
 KW Human ABC1 cholesterol transporter; chromosome 9q31;
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
 KW Tangier disease; TD; familial HDL deficiency; FHL; polymorphism;
 KW cardiovascular disease; coronary artery disease; coronary restenosis;
 KW cerebrovascular disease; peripheral vascular disease;
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
 KW prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO20005318-A2.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-IB00532.
 XX
 PR 15-MAR-1999; 99US-0124702.
 XX 08-JUN-1999; 99US-0138048.
 XX 17-JUN-1999; 99US-0139600.
 PR 01-SEP-1999; 99US-0151977.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (XENO-) XENON BIORESEARCH INC.
 XX
 PI Hayden MR, Wilson AR, Plimstone SN;
 XX
 DR WPI: 2000-587528/55.
 DR P-PSDB: AAB38104.
 XX
 PT New ABC1 polypeptide is useful for treating diseases associated with
 PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
 PT disease and cancer -
 XX
 PS Examples; Page -: 229pp; English.
 CC The invention relates to the human ABC1 cholesterol transporter protein
 CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
 CC a member of the ATP-binding cassette (ABC transporter) superfamily of
 CC proteins, and plays a crucial role in cholesterol transport, particularly
 CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
 CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
 CC located on chromosome 9q31, and mutations in this gene are associated
 CC with two genetic HDL (high density lipoprotein) deficiency disorders,
 CC Tangier disease (TD) and familial HDL deficiency (FHL). These diseases
 CC are distinguishable in that TD is an autosomal recessive disorder, while
 CC FHL is inherited as an autosomal dominant trait. Low levels of HDL ('good

QY	1897	ttggttcaactgagatattactccagcgacgaactgagctgccccatcaltgltcaagtacaaga	1956
Db	1681	ttgtgttcaactgagatattactccagcgacgaactgagctgccccatcaltgltcaagtacaaga	1740
QY	1957	tcggaatggaacttgacaatgltgagagagacaataaatacaagatggttactgtggacc	2016
Db	1741	tcggaatggaacttgacaatgltgagagagacaataaatacaagatggttactgtggacc	1800
QY	2017	ctgtgtccctcgagctgagacccctttgagagacatgctggttaactctgtggggggttctgcctact	2076
Db	1801	ctgtgtccctcgagctgagacccctttgagagacatgctggttaactctgtggggggttctgcctact	1860
QY	2077	tgcaggaatgtgtgtgagcagagcaatacacaaggtgtcgtacggcgacacgcgaaagaanaactg	2136
Db	1861	tgcaggaatgtgtgtgagcagagcaatacacaaggtgtcgtacggcgacacgcgaaagaanaactg	1920
QY	2137	--gtgtctataatgacaagaatagtccttatccctgttactggttagaacattttctgtcggtg	2194
Db	1921	gdgtgtctataatgacaagaatagtccttatccctgttactggttagaacattttctgtcggtg	1980
QY	2195	gataagccggttcaaatgtccccctctcatalgacgctgctggtatttatactcaagtgtgcat	2254
Db	1981	gataagccggttcaaatgtccccctctcatalgacgctgctggtatttatactcaagtgtgcat	2040
QY	2255	catcaaaaggcatctgttatgagaagagagcaagcgctgaagaagacaatctgcgagatctggg	2314
Db	2041	catcaaaaggcatctgttatgagaagagagcaagcgctgaagaagacaatctgcgagatctggg	2100
QY	2315	cctgtgacaacaagcatctactctgtgttagctgtgttattagatagccttcacttcctctctgt	2374
Db	2101	cctgtgacaacaagcatctactctgtgtgttagctgtgttattagatagccttcacttcctctctgt	2160
QY	2375	gagcgctgagcctgtgactgt	2434
Db	2161	gagcgctgagcctgtgactgt	2220
QY	2435	cagcgctgt	2494
Db	2221	cagcgctgt	2280
QY	2495	gatttagcaactctctctccagagcaaacctgtgacagcgccgtgtgtgggcatcactactct	2554
Db	2281	gatttagcaactctctctccagagcaaacctgtgacagcgccgtgtgtgggcatcactactct	2340
QY	2555	caagctgtgacactgtccctactcgtccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2614
Db	2341	caagctgtgacactgtccctactcgtccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2400
QY	2615	caagaactctgcgtagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt	2674
Db	2401	caagaactctgcgtagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt	2460
QY	2675	ccttttttgaagagcagggcatctgtgaggtgtgcagttgagacaacctgttttgaagatccctgtgga	2734
Db	2461	ccttttttgaagagcagggcatctgtgaggtgtgcagttgagacaacctgttttgaagatccctgtgga	2520
QY	2735	ggaagaatggtcttcaaatctccacacactctgaltcaltcaltgaltgtgtgtttgaacacttccctta	2794
Db	2521	ggaagaatggtcttcaaatctccacacactctgaltcaltcaltgaltgtgtgtttgaacacttccctta	2580
QY	2795	tgggtgtgtagcctgtgtacatctgtagagctgtccttccacagcgacgtacggaatctccacagcc	2854
Db	2581	tgggtgtgtagcctgtgtacatctgtagagctgtccttccacagcgacgtacggaatctccacagcc	2640
QY	2855	cttggatatttcccttgacacaagctcctactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2914
Db	2641	cttggatatttcccttgacacaagctcctactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2700
QY	2915	ccctgtgttccaaaccgaagagagatgtgtgcagaatctgtcaatgtgagagaggaacccacccact	2974
Db	2701	ccctgtgttccaaaccgaagagagatgtgtgcagaatctgtcaatgtgagagaggaacccacccact	2760

QY	2975	gaacfcvvgcgtvtlccatlccagaaacctvgltaaagtctcacccgagatvggtatgaaagctvggc	3034
Db	2761	gaacfcvvgcgtvtlccatlccagaaacctvgltaaagtctcacccgagatvggtatgaaagctvggc	2620
QY	3035	tgctgagcgcctvgcacaatgaaattttatgaaagccagatcacactctctccvggccacaa	3094
Db	2821	tgctgagcgcctvgcacaatgaaattttatgaaagccagatcacactctctccvggccacaa	2880
QY	3095	tgagagcgggaaagagacgacccacatgtlcaactctgaaacccggtgtgttccccccgacctcg	3154
Db	2881	tgagagcgggaaagagacgacccacatgtlcaactctgaaacccggtgtgttccccccgacctcg	2940
QY	3155	caccgcctacatcctctvggaaagaacatctgcctctgagatgagacccatcccgcgaaacct	3214
Db	2941	caccgcctacatcctctvggaaagaacatctgcctctgagatgagacccatcccgcgaaacct	3000
QY	3215	gggggtctgctccccaagataacgtgctcgttttgacatgacgtacgtgctcgaaagacacatctg	3274
Db	3001	gggggtctgctccccaagataacgtgctcgttttgacatgacgtacgtgctcgaaagacacatctg	3060
QY	3275	gtlclatgcccgccttgaaagagcgtcctctgaaagacagltgaaagccgagatvgagacagat	3334
Db	3061	gtlclatgcccgccttgaaagagcgtcctctgaaagacagltgaaagccgagatvgagacagat	3120
QY	3335	ggccctvgagatvtgtgttgcctacaaagcaagctcgaaagcaaaacaaagccagctgttcaag	3394
Db	3121	ggccctvgagatvtgtgttgcctacaaagcaagctcgaaagcaaaacaaagccagctgttcaag	3180
QY	3395	tggaatgcaagaaagatcatctgtgacgttgcccttgccggggatcctaaagtgtgcat	3454
Db	3181	tggaatgcaagaaagatcatctgtgacgttgcccttgccggggatcctaaagtgtgcat	3240
QY	3455	lctgagatgaaacccacagctgtgtgtgagaccttaccctccgcaagggaataatgagagctgtct	3514
Db	3241	lctgagatgaaacccacagctgtgtgtgagaccttaccctccgcaagggaataatgagagctgtct	3300
QY	3515	gctgaataacccgacaaggtccgcacacatattctctctacacacacacagatgaaagccgga	3574
Db	3301	gctgaataacccgacaaggtccgcacacatattctctctacacacacacagatgaaagccgga	3360
QY	3575	cgctccctggggaacagaggtttccacatctcccatgagagccgtgtgtgtgtgagctctcc	3634
Db	3361	cgctccctggggaacagaggtttccacatctcccatgagagccgtgtgtgtgtgagctctcc	3420
QY	3635	ccgtgttcttgaaagaaacagctctgagaaacaggtctactaccctgagacttgtlccaaagaagatgt	3694
Db	3421	ccgtgttcttgaaagaaacagctctgagaaacaggtctactaccctgagacttgtlccaaagaagatgt	3480
QY	3695	ggaaatccctccctcagcttctctgcagaaacagtagtagcaactgtgtcatctactcgaaaaagga	3754
Db	3481	ggaaatccctccctcagcttctctgcagaaacagtagtagcaactgtgtcatctactcgaaaaagga	3540
QY	3755	ggacagatgtttctcgaagcagttctctgtgtgtgtgcccgtggagagacacatgaaagtgtgacac	3814
Db	3541	ggacagatgtttctcgaagcagttctctgtgtgtgtgcccgtggagagacacatgaaagtgtgacac	3600
QY	3815	gcttgacacatcgatgtctctgtactactcaacccatccacaggaagcatgtgtctgaaagcccg	3874
Db	3601	gcttgacacatcgatgtctctgtactactcaacccatccacaggaagcatgtgtctgaaagcccg	3660
QY	3875	gctgtgtgaagacatagggacatgagctgtgacctatgtgtctgcacatgaaagctgtctaaagga	3934
Db	3661	gctgtgtgaagacatagggacatgagctgtgacctatgtgtctgcacatgaaagctgtctaaagga	3720
QY	3935	gggagacctttgtgaaactctttatgagatltgagtgcggctctctaaagacttgggacttc	3994
Db	3721	gggagacctttgtgaaactctttatgagatltgagtgcggctctctaaagacttgggacttc	3780
QY	3995	tggatgatgcatlccaaagacagacccctggaagaataatctccaaaggtgtgcccgaagagag	4054
Db	3781	tggatgatgcatlccaaagacagacccctggaagaataatctccaaaggtgtgcccgaagagag	3840
QY	4055	tgagggtgagatcctgagaaactcagatgtgtactctgtgcagacgaacgaacaaagctgggctt	4114

Db 3841 tggggtgagatgctgagaccagatggtacctgtgcagagaagacgaagaagcgggcctt 3900
QY 4115 cggggaacagcagagctgtcttcgcgcgttcaactgaagatgagtcgctgcatccaatga 4174
Db 3901 cggggaacagcagagctgtcttcgcgcgttcaactgaagatgagtcgctgcatccaatga 3960
QY 4175 tt-ctgaatagacccaagaatccagaagacagactgtccagttggatgagtgcaag 4233
Db 3961 ttctgacatagacccaagaatccagaagacagactgtccagttggatgagtgcaag 4020
QY 4234 ggtccacacaggtgaaagcctggaaccttacacagaacagtttgggccccttggta 4293
Db 4021 ggtccacacaggtgaaagcctggaaccttacacagaacagtttgggccccttggta 4080
QY 4294 agagactgtaattgtccagacagagtcggaagagatctttgtccagatgtcttgccag 4353
Db 4081 agagactgtaattgtccagacagagtcggaagagatctttgtccagatgtcttgccag 4140
QY 4354 ctgtgtttgtctgcatgcccctgtgttcaagcctgtatctgtccacccttggcaagtaac 4413
Db 4141 ctgtgtttgtctgcatgcccctgtgttcaagcctgtatctgtccacccttggcaagtaac 4200
QY 4414 ccagcctggaacttcagccctgagttacacagacagfacacatctgtcagcaatgagtc 4473
Db 4201 ccagcctggaacttcagccctgagttacacagacagfacacatctgtcagcaatgagtc 4260
QY 4474 ctctctgagacaaaggaaacccctggaaacctttaacgcctccacaaagacccctgtccg 4533
Db 4261 ctctctgagacaaaggaaacccctggaaacctttaacgcctccacaaagacccctgtccg 4320
QY 4534 ggaacccgtgtatgtgaaagaaacccaatccagacagccctgtgcagagagggagag 4593
Db 4321 ggaacccgtgtatgtgaaagaaacccaatccagacagccctgtgcagagagggagag 4380
QY 4594 agtggacacactgcccagttccccagacacatcatggaacctctccagaaatgggaactgga 4653
Db 4381 agtggacacactgcccagttccccagacacatcatggaacctctccagaaatgggaactgga 4440
QY 4654 caatgacagaaccccttcaactgcagtcgcaagtgtacagcgacgaacaaatcaagaagatgtcc 4713
Db 4441 caatgacagaaccccttcaactgcagtcgcaagtgtacagcgacgaacaaatcaagaagatgtcc 4500
QY 4714 ctgtgttccccccagggaggggtgtccctccacaaagaacaaacaaacactgtcag 4773
Db 4501 ctgtgttccccccagggaggggtgtccctccacaaagaacaaacaaacactgtcag 4560
QY 4774 atatacttaagacactgacagagaagaacatttcggtatatactgtgtgaagaagtatgtgc 4833
Db 4561 atatacttaagacactgacagagaagaacatttcggtatatactgtgtgaagaagtatgtgc 4620
QY 4834 agatcatagccaagaacttaagaacaagatctgggtgaatgagtttaagtctggcggtc 4893
Db 4621 agatcatagccaagaacttaagaacaagatctgggtgaatgagtttaagtctggcggtc 4680
QY 4894 ttctccctgggtgtcagtaactcaagacacttccctccgagtcgaagaagttaatgtgcca 4953
Db 4681 ttctccctgggtgtcagtaactcaagacacttccctccgagtcgaagaagttaatgtgcca 4740
QY 4954 tcaaaacaatgaaagacacacttaagaactgtggcaagacagttctcgaagtcgattcttca 5013
Db 4741 tcaaaacaatgaaagacacacttaagaactgtggcaagacagttctcgaagtcgattcttca 4800
QY 5014 acagcttgggaagatcttaagacagagctggaacccaagaataatgtcgaagtgtgttca 5073
Db 4801 acagcttgggaagatcttaagacagagctggaacccaagaataatgtcgaagtgtgttca 4860
QY 5074 ataaacaagggtgtgcatgcaatcagctcttccctgaatgtcaatcaaatgcatcttcc 5133
Db 4861 ataaacaagggtgtgcatgcaatcagctcttccctgaatgtcaatcaaatgcatcttcc 4920
QY 5134 gggccaactgtcaaaaggagagaaacccctagcattatggaattactgtcttcaatc 5193
Db 4921 gggccaactgtcaaaaggagagaaacccctagcattatggaattactgtcttcaatc 4980
QY 5194 ccttgaatctcaacaagacagagcttcaagagtgagtcgtgatgacacatcagttgagtc 5253
Db 4981 ccttgaatctcaacaagacagagcttcaagagtgagtcgtgatgacacatcagttgagtc 5040
QY 5254 tccctgtgcatcctgtgtcatccttggcaatgtccctccctccagcagcttgtgcat 5313
Db 5041 tccctgtgcatcctgtgtcatccttggcaatgtccctccctccagcagcttgtgcat 5100
QY 5314 tccctgaatcagagcggtgtcagcaagaacaaacacccctgattcatagtggaagtgaagc 5373
Db 5101 tccctgaatcagagcggtgtcagcaagaacaaacacccctgattcatagtggaagtgaagc 5160
QY 5374 ctgtcatcactgtgctcctcaatttgtctgagatgtgcaatgcaatgacgtgtccctgcca 5433
Db 5161 ctgtcatcactgtgctcctcaatttgtctgagatgtgcaatgcaatgacgtgtccctgcca 5220
QY 5434 caactgtatataatcttcaatctgtctccagacgaagaagtctatagttctcccaacatc 5493
Db 5221 caactgtatataatcttcaatctgtctccagacgaagaagtctatagttctcccaacatc 5280
QY 5494 tgcctgtgctagcccttcaacttctgtgtatggtgtgtcaatcaacccctcatgtacc 5553
Db 5281 tgcctgtgctagcccttcaacttctgtgtatggtgtgtcaatcaacccctcatgtacc 5340
QY 5554 cagctccttgtgttcaagaatccccaagacagcctatgtgtgtctaacagcgttgaaac 5613
Db 5341 cagctccttgtgttcaagaatccccaagacagcctatgtgtgtctaacagcgttgaaac 5400
QY 5614 tcttcattgtgcatlaatgtgcagcggtggccaccccttgtgcgagagctgttcaacgacata 5673
Db 5401 tcttcattgtgcatlaatgtgcagcggtggccaccccttgtgcgagagctgttcaacgacata 5460
QY 5674 agctggaataataatgaatatactctgaagtcggtgtcttcatgaccttccacatlttggc 5733
Db 5461 agctggaataataatgaatatactctgaagtcggtgtcttcatgaccttccacatlttggc 5520
QY 5734 tgggacaggggctatcagacatgtgtgaaaaacaggaatggcgctgagtcgacctggaaggt 5793
Db 5521 tgggacaggggctatcagacatgtgtgaaaaacaggaatggcgctgagtcgacctggaaggt 5580
QY 5794 ttggggagaatcgcttgtgtcaacatatacttgggaactgtgtgtggaacgaaccccttgc 5853
Db 5581 ttggggagaatcgcttgtgtcaacatatacttgggaactgtgtgtgtggaacgaaccccttgc 5640
QY 5854 ccatggccgtggaaagggtgtgttcttcccatatactgttctgacatcaagaattct 5913
Db 5641 ccatggccgtggaaagggtgtgttcttcccatatactgttctgacatcaagaattct 5700
QY 5914 tcatcagggcccaagacactgaatcaagaactatctctcgaatgaatgaatgaatg 5973
Db 5701 tcatcagggcccaagacactgaatcaagaactatctctcgaatgaatgaatgaatg 5760
QY 5974 tgaagcggggaagaacagaatctctgtatgtgtggaagccgaatgtacatcttgaatca 6033
Db 5761 tgaagcggggaagaacagaatctctgtatgtgtggaagccgaatgtacatcttgaatca 5820
QY 6034 agaggttgaacgaatataatagaaggaagcggaagcctgtgttgaagaatttggcgtg 6093
Db 5821 agaggttgaacgaatataatagaaggaagcggaagcctgtgttgaagaatttggcgtg 5880
QY 6094 gcatctcctctgtgagtgcttgggtctcctgagagttaaatggggctggaataatca 6153
Db 5881 gcatctcctctgtgagtgcttgggtctcctgagagttaaatggggctggaataatca 5940
QY 6154 ctttcaagatgttaacagagataccactgttacccagaagagatgtcttcttaacaaa 6213
Db 5941 ctttcaagatgttaacagagataccactgttacccagaagagatgtcttcttaacaaa 6000
QY 6214 ata-gtatattatcaaacatccatgaagtatacagaaatgggtctacgtcctcagttt 6272
Db 6001 atagtatcttatacaaacatccatgaagtatacagaaatgggtctacgtcctcagttt 6060

[illegible]

QY	7353	ccatgtgacatagtggtttggaactcaac-ttttttttttttttcttcctgtatct	7411
Db	7141	ccatgtgacataagggtttgaactcaaccttttttttttttttcttcctgtatct	7200
QY	7412	catgtggtttgcacaataatcatcaagtaacatgcgcagatattatgtacaaalc	7471
Db	7201	catgtggtttgcacaataatcatcaagtaacatgcgcagatattatgtacaaalc	7260
QY	7472	aaaagtaatgcacatccctcatcctaagcattgtccatgcccagaagatgtttccg	7531
Db	7261	aaaagtaatgcacatccctcatcctaagcattgtccatgcccagaagatgtttccg	7320
QY	7532	gtgcacatccatctgtcgcgaatgagtggtccagattatagtccaagtttttcagaa	7591
Db	7321	gtgcacatccatctgtcgcgaatgagtggtccagattatagtccaagtttttcagaa	7380
QY	7592	agtttgaagcaccaatggtgtgtcattgcacacttttgaaagctgtctgcacagct	7651
Db	7381	agtttgaagcaccaatggtgtgtcattgcacacttttgaaagctgtctgcacagct	7440
QY	7652	atcaacttgaataatagtttgacaagatgtgtgcacgtcgtgtcaatcccttgat	7711
Db	7441	atcaacttgaataatagtttgacaagatgtgtgcacgtcgtgtcaatcccttgat	7500
QY	7712	tcctctcgataagctgtctctgtgtgcagtaacatgacacaaaatgltggtctctag	7771
Db	7501	tcctctcgataagctgtctctgtgtgcagtaacatgacacaaaatgltggtctctag	7560
QY	7772	caagggaacttggtttccattgttatatttctctatgtcttcgcagccatggtctacagg	7831
Db	7561	caagggaacttggtttccattgttatatttctctatgtcttcgcagccatggtctacagg	7620
QY	7832	tcactcttatagagctcttcaataactattgatctcctgtaagagccaagaatccaacag	7891
Db	7621	tcactcttatagagctcttcaataactattgatctcctgtaagagccaagaatccaacag	7680
QY	7892	caaatctgtctgggctgtcaagctgtctgaagccaggccatggatataagaaattgtgcgt	7951
Db	7681	caaatctgtctgggctgtcaagctgtctgaagccaggccatggatataagaaattgtgcgt	7739
QY	7952	caaaccttagggaaagccgtgtgccattgtccctgactcttcgcacaactgttacaactgc	8011
Db	7740	caaaccttagggaaagccgtgtgccattgtccctgactcttcgcacaactgttacaactgc	7799
QY	8012	ctcaagatgtttatctgcacacaagtatattattctgtgcttttgaactaatcagaataa	8071
Db	7800	ctcaagatgtttatctgcacacaagtatattattctgtgcttttgaactaatcagaataa	7859
QY	8072	tgaaa 8076	
Db	7860	tgaaa 7864	
RESULT 13			
ID	AAAC69386		
XX	AAAC69386	standard; cDNA: 7864 BP.	
AC			
XX			
DT	29-JAN-2001	(first entry)	
XX			
DE	Human ABC1 cholesterol transporter TD-2 mutant cDNA (A1864C).		
XX			
KM	Human ABC1 cholesterol transporter; chromosome 9q31;		
KM	ATP-binding cassette; HDL deficiency disorder; high density lipoprotein,		
KM	Tangier disease; TD; familial HDL deficiency; FHD; polymorphism;		
KM	cardiovascular disease; coronary artery disease; coronary restenosis;		
KM	cerebrovascular disease; peripheral vascular disease;		
KM	Alzheimer's disease; Niemann-Pick disease; Huntington's disease;		
KM	X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;		
KM	prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.		
OS	Homo sapiens.		

XX XX W0200055318-A2.
XX XX 21-SEP-2000.
XX XX 15-MAR-2000; 2000MO-IB00532.
XX XX 15-MAR-1999; 9905-0124702.
XX XX 08-JUN-1999; 9905-0138048.
XX XX 17-JUN-1999; 9905-0139600.
XX XX 01-SEP-1999; 9905-0151977.
XX XX (UYBR-) UNIV. BRITISH COLUMBIA.
XX XX (XEN-) XENON BIORESEARCH INC.
XX XX Hayden MR, Wilson AR, Pimstone SN;
XX XX WPI; 2000-587528/55.
XX XX P-PDB; AAB38105.
XX XX
XX XX New ABC1 polypeptide is useful for treating diseases associated with
XX XX ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
XX XX disease and cancer -
XX XX
XX XX Examples: Page -: 229pp; English.
XX XX
XX XX The invention relates to the human ABC1 cholesterol transporter protein
XX XX (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
XX XX a member of the ATP-binding cassette (ABC transporter) superfamily of
XX XX proteins, and plays a crucial role in cholesterol transport, particularly
XX XX intracellular cholesterol trafficking in monocytes and fibroblasts, being
XX XX involved in cholesterol efflux from the cell. The gene encoding ABC1 is
XX XX located on chromosome 9q31, and mutations in this gene are associated
XX XX with two genetic HDL (high density lipoprotein) deficiency disorders,
XX XX Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
XX XX are distinguishable in that TD is an autosomal recessive disorder, while
XX XX FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
XX XX cholesterol") in the blood correlate with a high risk of cardiovascular
XX XX disease, particularly coronary artery disease, but also cerebrovascular
XX XX disease, coronary restenosis, and peripheral vascular disease.
XX XX Conversely, a high level of HDL has protective effects against
XX XX cardiovascular disease. The invention provides genetic constructs and
XX XX transgenic cells and non-human animals comprising human ABC1 nucleic
XX XX acids, and methods of gene therapy for the treatment or prevention of
XX XX cardiovascular disease comprising the administration of an expression
XX XX vector encoding ABC1 or an active fragment thereof. The invention also
XX XX encompasses compounds which mimic ABC1 activity, compounds which
XX XX stimulate ABC1 expression and methods of screening for such compounds.
XX XX It further relates to methods for determining whether a patient has an
XX XX increased risk for cardiovascular disease due to polymorphisms in the
XX XX ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
XX XX or prevent cardiovascular disease, especially coronary artery disease,
XX XX cerebrovascular disease, coronary restenosis or peripheral vascular
XX XX disease. They may also be used in the treatment of diseases associated
XX XX with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
XX XX disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
XX XX The invention specifically excludes proteins with the exact amino acid
XX XX sequences of Genbank Accession No: CAA10005.1 and X75926, and the nucleic
XX XX acid with the exact sequence as Genbank Accession No: AJ012376.1. The
XX XX present sequence represents a cDNA encoding a mutant human ABC1 cholesterol
XX XX transporter associated with an altered cholesterol level and therefore an
XX XX altered risk of cardiovascular disease.
XX XX Note: The present sequence is not shown in the specification, but is
XX XX derived from the native human ABC1 cDNA shown on pages 157-160.
XX XX
XX XX Sequence 7864 BP: 2013 A; 1860 C; 2012 G; 1978 T; 1 other;

Query Match 74.6%; Score 7790.2; DB 21; Length 7864;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7851; Conservative 0; Mismatches 8; Indels 6; Gaps 5;

QY 217 gtcctgtgtgagctctgcccgtctccacaggtcccgagcacacagctggcgctg 276

Db 1 gtcctgtgtgagctctgcccgtctccacaggtcccgagcacacagctggcgctg 60
QY 277 ctggtctgaggaacatggtctgttggcctcaagctgaggtgtgtgtggaacactca 336
Db 61 ctggtctgaggaacatggtctgttggcctcaagctgaggtgtgtgtggaacactca 120
QY 337 ctccaagaagaagaacaacatgcaagctgttaccgagtgagtgccctcattatctc 396
Db 121 ctccaagaagaagaacaacatgcaagctgttaccgagtgagtgccctcattatctc 180
QY 397 tccgtatccctgctgttgcgtgagctaccaccctatgaacaacatgacatc 456
Db 181 tccgtatccctgctgttgcgtgagctaccaccctatgaacaacatgacatc 240
QY 457 ttccaataaagcagatgcccctcaggaacacttctgttgcagggatattctgta 516
Db 241 ttccaataaagcagatgcccctcaggaacacttctgttgcagggatattctgta 300
QY 517 atgccaacaacccctgttccgttaccgactccttgaggaggtcccgaggtgtgaa 576
Db 301 atgccaacaacccctgttccgttaccgactccttgaggaggtcccgaggtgtgaa 360
QY 577 acttaacaacatcattgtgtgtcgcctgttctcaagatgctcggaggtctcttata 636
Db 361 acttaacaacatcattgtgtgtcgcctgttctcaagatgctcggaggtctcttata 420
QY 637 gccagaagaacacacagatgagaagacatgcgcaagttctgagacacttaacagatca 696
Db 421 gccagaagaacacacagatgagaagacatgcgcaagttctgagacacttaacagatca 480
QY 697 agaattcagctcaacttgaagtttaagatttccgtgtggaacatgaaactctctg 756
Db 481 agaattcagctcaacttgaagtttaagatttccgtgtggaacatgaaactctctg 540
QY 757 ggtcctatatacaacactcctctcccaagatctatgtggaacatgctagggctg 816
Db 541 ggtcctatatacaacactcctctcccaagatctatgtggaacatgctagggctg 600
QY 817 atgtcatctccacaagatattttgcaaggtctacacgtatcatltgacaagctgtgca 876
Db 601 atgtcatctccacaagatattttgcaaggtctacacgtatcatltgacaagctgtgca 660
QY 877 atgataataatgagaagatgataacttggtgacccaagaagtttcgaactttgtg 936
Db 661 atgataataatgagaagatgataacttggtgacccaagaagtttcgaactttgtg 720
QY 937 gccaccacaaggaagaactgtgcaagcagagcagacttctccaacatgacatcc 996
Db 721 gccaccacaaggaagaactgtgcaagcagagcagacttctccaacatgacatcc 780
QY 997 tgaagccaatctgtgagacacataactctacatctccctcccgagcaagagctgtg 1056
Db 781 tgaagccaatctgtgagacacataactctacatctccctcccgagcaagagctgtg 840
QY 1057 aagcacaacaacatgtgtcatagcttctggaactcggccaggaggtcttgaagata 1116
Db 841 aagcacaacaacatgtgtcatagcttctggaactcggccaggaggtcttgaagata 900
QY 1117 gaagctgagatgacatgcaagcagaggtgatttctgtaacaatgcaacagctcagat 1176
Db 901 gaagctgagatgacatgcaagcagaggtgatttctgtaacaatgcaacagctcagat 960
QY 1177 cctccacccaacatctacacagctgtgtctctgtattgtctcgaggcatcccgaggagg 1236
Db 961 cctccacccaacatctacacagctgtgtctctgtattgtctcgaggcatcccgaggagg 1020
QY 1237 ggtcgaagatcaagctctcaactgtgtatgaggaacaacatacaagccctcttgag 1296
Db 1021 ggtcgaagatcaagctctcaactgtgtatgaggaacaacatacaagccctcttgag 1080
QY 1297 gcaatgacatgaggaagatgtctgaaacctctatgacaacttaacaactctactgca 1356

Db	1081	gcaatgacactgtaggaagaatgctgaaaccttatagaaacttcaaaccttactgca	1140
Qy	1357	atgattatgaataaatttgagatcagtcctcttctcccgatatatctgaaagctctga	1416
Db	1141	atgattatgaataaatttgagatcagtcctcttctcccgatatatctgaaagctctga	1200
Qy	1417	agccgcctgcctgttggagaagatccctgtataaccctgaaactccagcccaagagaagtc	1476
Db	1201	agccgcctgcctgttggagaagatccctgtataaccctgaaactccagcccaagagaagtc	1260
Qy	1477	tgagctgagtgaaacaagaccttccagaaactgctgttccatgattctgaaagcagtc	1536
Db	1261	tgagctgagtgaaacaagaccttccagaaactgctgttccatgattctgaaagcagtc	1320
Qy	1537	ggagagaaactcagccccaagatctgaccttcaatgagaaacagcccaagaaatgacctg	1596
Db	1321	ggagagaaactcagccccaagatctgaccttcaatgagaaacagcccaagaaatgacctg	1380
Qy	1597	tcggagatgcctgttgagcaagagaaatgaaactttttggaaacagagattgagtcct	1656
Db	1381	tcggagatgcctgttgagcaagagaaatgaaactttttggaaacagagattgagtcct	1440
Qy	1657	taagattgaaacagcccaagacatctgagcttttttgccaagcaccacagagagattccagt	1716
Db	1441	taagattgaaacagcccaagacatctgagcttttttgccaagcaccacagagagattccagt	1500
Qy	1717	ccagtaatgcttctgtgtacacctgagagagaagcttccaagagataccaagacatcc	1776
Db	1501	ccagtaatgcttctgtgtacacctgagagagaagcttccaagagataccaagacatcc	1560
Qy	1777	ggaccaatctcgcttcaatgagtggtgtcaacctgaacaagctaaagccaatgaacaag	1836
Db	1561	ggaccaatctcgcttcaatgagtggtgtcaacctgaacaagctaaagccaatgaacaag	1620
Qy	1837	aagctctgcttcaatcaacaagaatccatgagagctctgagatgagagaagaattctgggctgtga	1896
Db	1621	aagctctgcttcaatcaacaagaatccatgagagctctgagatgagagaagaattctgggctgtga	1680
Qy	1897	ttgtgttccatctgaaatatacccaagagagattgaaactgcccatacttcaagaatcaaga	1956
Db	1681	ttgtgttccatctgaaatatacccaagagagattgaaactgcccatacttcaagaatcaaga	1740
Qy	1957	tcggaatgagcatctgacaatctgtagagagaagacaataaatacaagataggtactgggacc	2016
Db	1741	tcggaatgagcatctgacaatctgtagagagaagacaataaatacaagataggtactgggacc	1800
Qy	2017	ctgtgtcttcagcctgagacccctttgagagaatctcggttaagctctcgagggggctctgcctact	2076
Db	1801	ctgtgtcttcagcctgagacccctttgagagaatctcggttaagctctcgagggggctctgcctact	1860
Qy	2077	tgagagagatgtgtgtgagagcaatcaatcaaggtctgtagcgggacccagagaagaanaatg	2136
Db	1861	tgagagagatgtgtgtgagagcaatcaatcaaggtctgtagcgggacccagagaagaanaatg	1920
Qy	2137	- - -ggtctataatgaaagaatgagctccctatccctgttaacgttgaatgacatcttctcggggt	2194
Db	1921	gdtgtctataatgaaagaatgagctccctatccctgttaacgttgaatgacatcttctcggggt	1960
Qy	2195	gattagcccggttcaatgccccttctcaatgtagcgtctgagcttgatcttcaatgattgagctgagat	2254
Db	1981	gattagcccggttcaatgccccttctcaatgtagcgtctgagcttgatcttcaatgattgagctgagat	2040
Qy	2255	catcaagggcatctgtatataagaagaaggaagcagcctgaaagaagaccatgagatcataggg	2314
Db	2041	catcaagggcatctgtatataagaagaaggaagcagcctgaaagaagaccatgagatcataggg	2100
Qy	2315	ccctggaacaacgcaactcctgcttttagctgtgttcatatgaacccatcttccctctgt	2374
Db	2101	ccctggaacaacgcaactcctgcttttagctgtgttcatatgaacccatcttccctctgt	2160
Qy	2375	gagcgcctgctctagtgatcatcctgaaagttagaanaactgtgcccatacagtgatcc	2434
Db	2161	gagcgcctgctctctagtgatcatcctgaaagttagaanaactgtgcccatacagtgatcc	2220

QY	2435	cagcgtggtgtttgtctctctgtccgttggtttgttcgtgtgttgaaatactccgcagtgcttcc	2494
Db	2221	cagcgttggtgtttgtctctctctgtccgttggtttgttcgtgtgttgaaatactccgcagtgcttcc	2280
QY	2495	gattagcaactctctccagagccaacctggcagaagcctgtggggacatactaact	2554
Db	2281	gattagcaactctctccagagccaacctggcagaagcctgtggggacatactaact	2340
QY	2555	caagctgtaacctgtccctaagtcctgtgtgttgcaatggcagatacgttggcttcaact	2614
Db	2341	caagctgtaacctgtccctaagtcctgtgtgttgcaatggcagatacgttggcttcaact	2400
QY	2615	caagatcttcgtctagcctgtgtctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2674
Db	2401	caagatcttcgtctagcctgtgtctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2460
QY	2675	ccttttgaagagacagagcacttggagtgagtgagtgagcaaacctgttcttgagagcttcgtgga	2734
Db	2461	ccttttgaagagagagagcacttggagtgagtgagtgagcaaacctgttcttgagagcttcgtgga	2520
QY	2735	ggaagatgagcttcaatctccaacacctgcatactccatgatgctgtttgacaccttcccta	2794
Db	2521	ggaagatgagcttcaatctccaacacctgcatactccatgatgctgtttgacaccttcccta	2580
QY	2795	tgggtgtgttgagccgtgagacatttgagctgtgcttccagagccagatccagaaatcccaagcc	2854
Db	2581	tgggtgtgtgtgagccgtgagacatttgagctgtgcttccagagccagatccagaaatcccaagcc	2640
QY	2855	ctggtatcttccctgtgcaacccaagtccactactgtgtgttgagaggaatgtatgagaagagcca	2914
Db	2641	ctggtatcttccctgtgcaacccaagtccactactgtgtgttgagaggaatgtatgagaagagcca	2700
QY	2915	ccctgtgtcccaacagaagaggaatgtgaaatactgtcatgtggagggggagacccaacctt	2974
Db	2701	ccctgtgtcccaacagaagaggaatgtgaaatactgtcatgtggagggggagacccaacctt	2760
QY	2975	gaagctgtggcgtgtgtccatttcagaacctgtgtaaaggtctacccagatctggagatgaaggtg	3034
Db	2761	gaagctgtggcgtgtgtccatttcagaacctgtgtaaaggtctacccagatctggagatgaaggtg	2820
QY	3035	tgtctgattgctgtgcaactgaatttttatgtggggccagataccaactcttccctgtggggcca	3094
Db	2821	tgtctgattgctgtgcaactgaatttttatgtggggggccagataccaactcttccctgtggggcca	2880
QY	3095	tggagccgggagagagccacccaatgttaactccctggaacgggtgtgttcccccgaacctcg	3154
Db	2881	tggagccgggagagagccacccaatgttaactccctggaacgggtgtgttcccccgaacctcg	2940
QY	3155	caacgctacatctcctgggaaagaacattcgctcttgatgtgagcaaccatcccgacgaacct	3214
Db	2941	caacgctacatctcctgggaaagaacattcgctcttgatgtgagcaaccatcccgacgaacct	3000
QY	3215	gggggtgtgttccccaagcaatacgt	3274
Db	3001	gggggtgtgttccccaagcaatacgt	3060
QY	3275	gttctatgcccgtcttgaaagggctctcttgagaagcaggtgaagggcggagatgagagagat	3334
Db	3061	gttctatgcccgtcttgaaagggctctcttgagaagcaggtgaagggcggagatgagagagat	3120
QY	3335	ggccctgtgattgt	3394
Db	3121	ggccctgtgattgt	3180
QY	3395	tggaaatgacagaaagacatactgtgagcctgtgagccttctgttcgggggagatctcaaggtgtcat	3454
Db	3181	tggaaatgacagaaagacatactgtgagcctgtgagccttctgttcgggggagatctcaaggtgtcat	3240
QY	3455	tcttgatgaaaccaacagctgtgtgtgagaccttactccgcagagggagataatgtggagctgtc	3514
Db	3241	tcttgatgaaaccaacagctgtgtgtgagaccttactccgcagagggagataatgtggagctgtc	3300

QY	3515	gcugaataacccgacaaggccgacccattatctctcttaacacacacatgatagtgaagccgga	3574
Db	3301	gcttgaataacacgacaagaagccgcacccattatctctctcttaacacacacatgatagtgaagccgga	3366
QY	3575	gcctctggggagacaggaattgccaatctccatctcgaaactgtgtgtgtgtggctcc	363
Db	3361	gcctctggggagacaggaattgccaatctccatctcgaaactgtgtgtgtgtggctcc	3422
QY	3635	cctgttcttgaaagacaagctgggaacagctactacatgaccttvgctcaagaagaatgt	3694
Db	3421	ccctgttcttgaaagacaagctgggaacagctactacatgaccttvgctcaagaagaatgt	3480
QY	3695	ggaatccccctccagcttccctccgaagaacaaatgaagactgttctactgttaaaaaaga	3755
Db	3481	ggaatccccctccagcttccctccgaagaacaaatgaagactgttctactgttaaaaaaga	3540
QY	3755	ggacagatgttctccagagcaagttctgaatgtgtgcttggcgagagacacatgagatgagac	3814
Db	3541	ggacagatgttctccagagcaagttctgaatgtgtgcttggcgagagacacatgagatgagac	3600
QY	3815	gctgacccatcgatgtctctctgtactctccaaacctccatccaggaagcattgtctcgaagccg	3874
Db	3601	gctgacccatcgatgtctctctgtactctccaaacctccatccaggaagcattgtctcgaagccg	3660
QY	3875	gcttgaatgaagaacataagggcctgaagctgacactatgtgtctccatataagagctgctcaaga	3934
Db	3661	gcttgaatgaagaacataagggcctgaagctgacactatgtgtctccatataagagctgctcaaga	3722
QY	3935	ggagagccttvtggaactcttcaatgatattgatacagcgctctccagaccvtgggacttc	3994
Db	3721	ggagagccttvtggaactcttcaatgatattgatacagcgctctccagaccvtgggacttc	3780
QY	3995	taqtaatgacatcccaagagacagaccctgggaagaatatctccataagvtggccgaagaag	4054
Db	3781	taqtaatgacatcccaagagacagaccctgggaagaatatctccataagvtggccgaagaag	3840
QY	4055	tggggatggaatgcctgagacactcaagatgtacacctgacagacaagaacgaagccgggctt	4114
Db	3841	tggggatggaatgcctgagacactcaagatgtacacctgacagacaagaacgaagccgggctt	3900
QY	4115	cggggacaagaagagcgctctctctggcccgcttccatctgaatgaatgtatgctgcgtacccaatga	4174
Db	3901	cggggacaagaagagcgctctctctggcccgcttccatctgaatgaatgtatgctgcgtacccaatga	3960
QY	4175	tt-ctgaacatagaccccaagatcccaagagagacaagacttgcctcagttgagatgtgacaag	4233
Db	3961	ttgctgacatagaccccaagatcccaagagagacaagacttgcctcagttgagatgtgacaag	4020
QY	4234	ggtctacacaggtgaagggctcgtggaanaattacacaagacaagtttgtggccctttgtgga	4293
Db	4021	ggtctacacaggtgaagggctcgtggaanaattacacaagacaagtttgtggccctttgtgga	4080
QY	4294	agaagactctaaattgccaagacaggtctcgaagaagaatttttgcctcagattgtcttgcag	4353
Db	4081	agaagactctaaattgccaagacaggtctcgaagaagaatttttgcctcagattgtcttgcag	4140
QY	4354	ctgtgttctgtctgcatctgcccctgtgtgttcaagctgatactgtgcaacccttggcaagtaac	4413
Db	4141	ctgtgttctgtctgcatctgcccctgtgtgttcaagctgatactgtgcaacccttggcaagtaac	4200
QY	4414	ccaagcttggaacttcaagccctgtgatacacaagaacagataacattgttgcagaacaatga	4473
Db	4201	ccaagcttggaacttcaagccctgtgatacacaagaacagataacattgttgcagaacaatga	4260
QY	4474	ctccttgaggaacggggaaccctvggaactctttaaagcgcctccaaacgaagcccttggcttg	4533
Db	4261	ctccttgaggaacggggaaccctvggaactctttaaagcgcctccaaacgaagcccttggcttg	4320
QY	4534	ggagccgcctgataatgaaagggaacccaatcccaagacacggccctgcgaagcaggaaggagag	4593
Db	4321	ggagccgcctgataatgaaagggaacccaatcccaagacacggccctgcgaagcaggaaggagag	4380
QY	4594	agttgacacactgccccagttccccacacatcatggaactcttccagaatgtggaactgtga	4653

[illegible]

Db 5461 agctgaataatcaatgatatacttcgaatcggtgttcttgatcttcccaattttgc 5520
QY 5734 tggagacagaggtcattcagacatggtgtaaaaaacagagcaatgctga tgccttggaaaagt 5793
Db 5521 tggagacagaggtcattcagacatggtgtaaaaaacagagcaatgctga tgccttggaaaagt 5580
QY 5794 ttggagagaatcgcttctgttccacattatcttggacttgtgtggagcaaacctcttg 5853
Db 5581 ttggagagaatcgcttctgttccacattatcttggacttgtgtggagcaaacctcttg 5640
QY 5854 ccatggccggtggagaggtgtgttcttcccaattactgttctgacccaagtaacagttcc 5913
Db 5641 ccatggccggtggagaggtgtgttcttcccaattactgttctgacccaagtaacagttcc 5700
QY 5914 tcatcaagcccaagacctgttaaatgtcaaaagctatctcctctgaatgtatgaagatgtg 5973
Db 5701 tcatcaagcccaagacctgttaaatgtcaaaagctatctcctctgaatgtatgaagatgtg 5760
QY 5974 tggagcgaggaaagacagagatcttctgtgtgtggagccgaatgacattcttagaatac 6033
Db 5761 tggagcgaggaaagacagagatcttctgtgtgtggagccgaatgacattcttagaatac 5820
QY 6034 agaggttgacgaagataatagaaagagcgagagcctgtctgtgacagagatttgcgtg 6093
Db 5821 agaggttgacgaagataatagaaagagcgagagcctgtctgtgtgacagagatttgcgtg 5880
QY 6094 gcatctcctgtgtgagtgcttgggctcctctggaggttaattggggctggaataatcata 6153
Db 5881 gcatctcctgtgtgagtgcttgggctcctctggaggttaattggggctggaataatcata 5940
QY 6154 ctctcaagagttaacagagagatcacctgttccagagagatgtcttcccttaacaaa 6213
Db 5941 ctctcaagagttaacagagagatcacctgttccagagagatgtcttcccttaacaaa 6000
QY 6214 ata-gtatctatcaaacatccatgaaagtacatcaagaaatggtgtactgtccctcagtt 6272
Db 6001 ataggtatcttatcaaacatccatgaaagtacatcaagaaatggtgtactgtccctcagtt 6060
QY 6273 gatgcatcaacagagctgttgcactggagagaaacagtggaattcttggcctttbaga 6332
Db 6061 gatgcatcaacagagctgttgcactggagagaaacagtggaattcttggcctttbaga 6120
QY 6333 ggaatcccaagaaagaaatgtgcaaggttggtagtggcgatctcgaaacttgagcct 6392
Db 6121 ggaatcccaagaaagaaatgtgcaaggttggtagtggcgatctcgaaacttgagcct 6180
QY 6393 gtgaagtagagaaaaataatgctgtgtaactatagtggaagcaacaaacgaaactctct 6452
Db 6181 gtgaagtagagaaaaataatgctgtgtaactatagtggaagcaacaaacgaaactctct 6240
QY 6453 acaagcatggtcttgatcgcggcgccctcctgtgtgtttcttggatgaaacccaacagc 6512
Db 6241 acaagcatggtcttgatcgcggcgccctcctgtgtgtgtttcttggatgaaacccaacagc 6300
QY 6513 atggaatcccaagcccgcggttctgttgaatgttgcctaaatgtgttcaaaagaaaggg 6572
Db 6301 atggaatcccaagcccgcggttctgttgaatgttgcctaaatgtgttcaaaagaaaggg 6360
QY 6573 agatcaagtagtgaatcatcatagatagtgaaagaaatgtgaagctcttgcataagatg 6632
Db 6361 agatcaagtagtgaatcatcatagatagtgaaagaaatgtgaagctcttgcataagatg 6420
QY 6633 gcaatcatggtcaatgtgaaggttcaagttgaccttggcaggtgcaggaatcttaaaaaatagg 6692
Db 6421 gcaatcatggtcaatgtgaaggttcaagttgaccttggcaggtgcaggaatcttaaaaaatagg 6480
QY 6693 ttggagatggttatacatatagttgaagaaatagcaaggtccaaacccgagacttaagcct 6752
Db 6481 ttggagatggttatacatatagttgaagaaatagcaaggtccaaacccgagacttaagcct 6540
QY 6753 gtccagagattcttcttgagctgtcatcttcgtgaaggtgttcttaaaagaaacacccggac 6812
Db 6541 gtccagagattcttcttgagctgtcatcttcgtgaaggtgttcttaaaagaaacacccggac 6600
QY 6813 atgtcaaatataccagctcccatcttcatatcttctcgtgccagagataatagacatcct 6872
Db 6601 atgtcaaatataccagctcccatcttcatatcttctcgtgccagagataatagacatcct 6660
QY 6873 tcccaagcaaaaagcgactccacataagaactactctgttcttccaaacacttgac 6932
Db 6661 tcccaagcaaaaagcgactccacataagaactactctgttcttccaaacacttgac 6720
QY 6933 caagtaattgtgaacttttgccaaggaaccaagtgatgtaaccacttaaaagactctca 6992
Db 6721 caagtaattgtgaacttttgccaaggaaccaagtgatgtaaccacttaaaagactctca 6780
QY 6993 ttacacaaaacccaacagtagtgaagttgagtttccaaacttcttccaaagatgag 7052
Db 6781 ttacacaaaacccaacagtagtgaagttgagtttccaaacttcttccaaagatgag 6840
QY 7053 aaagtgaagaagaactatgaaagaaatccgttccatagcgggtgtgctgaagtaaga 7112
Db 6841 aaagtgaagaagaactatgaaagaaatccgttccatagcgggtgtgctgaagtaaga 6900
QY 7113 ggaactagaacttcccttgaccacatgtgaagtggtgtggaagaaagccagaaatgat 7172
Db 6901 ggaactagaacttcccttgaccacatgtgaagtggtgtggaagaaagccagaaatgat 6960
QY 7173 gtggagagaagtaaaacttgatacttactgataactatccatgaacatgcaattcaatgca 7232
Db 6961 gtggagagaagtaaaacttgatacttactgataactatccatgaacatgcaattcaatgca 7020
QY 7233 atgaaacaaaatccatcacagggcagtgaccttgtagcctatgctgtatgacct 7292
Db 7021 atgaaacaaaatccatcacagggcagtgaccttgtagcctatgctgtatgacct 7080
QY 7293 caagtgaagaacttgaaatttatttaccatatacctatgfgaaactatagagac 7352
Db 7081 caagtgaagaacttgaaatttatttaccatatacctatgfgaaactatagagac 7140
QY 7353 ccaatgacataggtgtggaactcacac-ttttttttttttctgttctgtatctt 7411
Db 7141 ccaatgacataggtgtggaactcacac-ttttttttttttctgttctgtatctt 7200
QY 7412 catlgtgtgtgcaacaataatccatcaagtaacatgagccagagattatgataaac 7471
Db 7201 catlgtgtgtgcaacaataatccatcaagtaacatgagccagagattatgataaac 7260
QY 7472 aaaagtaatgacatcccatccatccactaagccaatgccaaggaagactgttcccg 7531
Db 7261 aaaagtaatgacatcccatccatccactaagccaatgccaaggaagactgttcccg 7320
QY 7532 gtgacacatccatctgtcgaatagtgctgcagaaatlaatgagccaagttttcaaga 7591
Db 7321 gtgacacatccatctgtcgaatagtgctgcagaaatlaatgagccaagttttcaaga 7380
QY 7592 agttgaaagccaatgtgtgtaacatcttctgaagcgtcgtccagagct 7651
Db 7381 agttgaaagccaatgtgtgtaacatcttctgaagcgtcgtccagagct 7440
QY 7652 atcaaatgtgaatataagttgacagaatgttgcaatgctgtgcaacatcccgcttgat 7711
Db 7441 atcaaatgtgaatataagttgacagaatgttgcaatgctgtgcaacatcccgcttgat 7500
QY 7712 tccctgtgaatagctgttctgtgtgcaatgcaatgcaaaaatgttggtgttctcag 7771
Db 7501 tccctgtgaatagctgttctgtgtgcaatgcaatgcaaaaatgttggtgttctcag 7560
QY 7772 cacgggaactgttccatgttataatgttccatgttccatgttccagcaatgtgtccagag 7831
Db 7561 cacgggaactgttccatgttataatgttccatgttccatgttccagcaatgtgtccagag 7620
QY 7832 tcaatccttaagaactcttaataatataatcttagatccctgtgaagaaaggaagaaatcaaac 7891
Db 7621 tcaatccttaagaactcttaataatataatcttagatccctgtgaagaaaggaagaaatcaaac 7680


```
Db 541 ggtctcgtatcaaacctctctccccaagctcgtgagcaagctcgtgagctg 600
Qy 817 atgtatctctcacaaaggtatcttctgcaaggctacacagcttcatctgacagctctgca 876
Db 601 atgtatctctcacaaaggtatcttctgcaaggctacacagcttcatctgacagctctgca 660
Qy 877 atgtatcaaatcagaagaagatgatctcaactgtgtgacccaagaagcttctgagctgtg 936
Db 661 atgtatcaaatcagaagaagatgatctcaactgtgtgacccaagaagcttctgagctgtg 720
Qy 937 gctctcccaagaagaagaatctgctgacagagagcgagtaactctgttcccaactgagacacc 996
Db 721 gctctcccaagaagaagaatctgctgacagagagcgagtaactctgttcccaactgagacacc 780
Qy 997 tgaagccaactcctgagacaactaactatcatctccctcccgagcaaggagctgctg 1056
Db 781 tgaagccaactcctgagacaactaactatcatctccctcccgagcaaggagctgctg 840
Qy 1057 aagccaacaaaacatctgtctgcatagctctgtgagctctgcccagagctctgcatgta 1116
Db 841 aagccaacaaaacatctgtctgcatagctctgtgagctctgcccagagctctgcatgta 900
Qy 1117 gaagctgtagtgatgacatgacagagagtgatgttctctgacaatgtgaacagctcagct 1176
Db 901 gaagctgtagtgatgacatgacagagagtgatgttctctgacaatgtgaacagctcagct 960
Qy 1177 cctccacccaactctacacagctgtgtctgtatgtctgtcgagacatcccgagagaggg 1236
Db 961 cctccacccaactctacacagctgtgtctgtatgtctgtcgagacatcccgagagaggg 1020
Qy 1237 ggcctgaagatcaagctctcaactgtgtatgagagacaacatcaacaaagcctcttggag 1296
Db 1021 ggcctgaagatcaagctctcaactgtgtatgagagacaacatcaacaaagcctcttggag 1080
Qy 1297 ggaatggcactgaggaagaatgtctgaaacctctatgacaactctcaactctctactgca 1356
Db 1081 ggaatggcactgaggaagaatgtctgaaacctctatgacaactctcaactctctactgca 1140
Qy 1357 atgatttgaatgaagaatttgaagctagctcctctctccgcattatctgaaagctctga 1416
Db 1141 atgatttgaatgaagaatttgaagctagctcctctctccgcattatctgaaagctctga 1200
Qy 1417 agccgctgtctgttgggaagaatccctgtataacacctgacacatccacccaagagcggtca 1476
Db 1201 agccgctgtctgttgggaagaatccctgtataacacctgacacatccacccaagagcggtca 1260
Qy 1477 tggctgaagtgagaagaagacctccaggaactgtgctgttcatgatctggaagcgatgt 1536
Db 1261 tggctgaagtgagaagaagacctccaggaactgtgctgttcatgatctggaagcgatgt 1320
Qy 1537 gggagaagaatcagcccagaagatctgacaccttcatgagaagacagccaagaatctgacctg 1596
Db 1321 gggagaagaatcagcccagaagatctgacaccttcatgagaagacagccaagaatctgacctg 1380
Qy 1597 tccggaatgtctgttggacagcagggagacaatgacaccttctgggaaacagcagttgtagtct 1656
Db 1381 tccggaatgtctgttggacagcagggagacaatgacaccttctgggaaacagcagttgtagtct 1440
Qy 1657 taatattggacagcccagaagcatgtgctgttcttggcagaagcaccagaagagtgcccaat 1716
Db 1441 taatattggacagcccagaagcatgtgctgttcttggcagaagcaccagaagagtgcccaat 1500
Qy 1717 ccagtaaatgttctgttgaacacctggaagaagcttctcaacgagataacccaagcaatcc 1776
Db 1501 ccagtaaatgttctgttgaacacctggaagaagcttctcaacgagataacccaagcaatcc 1560
Qy 1777 ggaacatactcgtctcagagagtggtgttaacctggaacagcttagaaccataagcaacag 1836
Db 1561 ggaacatactcgtctcagagagtggtgttaacctggaacagcttagaaccataagcaacag 1620
Qy 1837 aaatcgtgcatcaacaagaatcctagagagctgtgatatagaggaagctctggtctgta 1896
Db 1621 aaatcgtgcatcaacaagaatcctagagagctgtgatatagaggaagctctggtctgta 1680
Qy 1897 ttgttgttaactggaataactctccagcgagaatctgagctgcccacatctgtcaagtacaaga 1956
Db 1681 ttgttgttaactggaataactctccagcgagaatctgagctgcccacatctgtcaagtacaaga 1740
Qy 1957 tccgaatgagcattgagaagaatgtgagagaggaacaataaatacaagagatggttacttgacc 2016
Db 1741 tccgaatgagcattgagaagaatgtgagagaggaacaataaatacaagagatggttacttgacc 1800
Qy 2017 ctgtctccctcagctgacacctctgagagacatgctgttaactgtgagggggtcttcgctact 2076
Db 1801 ctgtctccctcagctgacacctctgagagacatgctgttaactgtgagggggtcttcgctact 1860
Qy 2077 tgcagagatgtgtgtgagagcaggaatcatcaagagtgctgtacggtgcaaccgagaagaaactg 2136
Db 1861 tgcagagatgtgtgtgagagcaggaatcatcaagagtgctgtacggtgcaaccgagaagaaactg 1920
Qy 2137 --gtgtctatataagacaagaatgccccttccctgttactgttactgtgacatcttctgcggt 2194
Db 1921 gdtgtctatataagacaagaatgccccttccctgttactgttactgtgacatcttctgcggt 1980
Qy 2195 gatgagccggttcaatgtccctcttcaatgagcgtggtcctgtgattactcagtggtgcat 2254
Db 1981 gatgagccggttcaatgtccctcttcaatgagcgtggtcctgtgattactcagtggtgcat 2040
Qy 2255 catcaagagcactgtgtatagaagaagagcagcgctgtaaagagacatctgagatcatggg 2314
Db 2041 catcaagagcactgtgtatagaagaagagcagcgctgtaaagagacatctgagatcatggg 2100
Qy 2315 ccttgacaacagcactctctgctgtttagctgttactatagtagctcatctctctctgt 2374
Db 2101 ccttgacaacagcactctctgctgtttagctgttactatagtagctcatctctctctgt 2160
Qy 2375 gacgctgtgctgtctagtgatcactcctgaagltgaagaacctgtgctccctacagtgatcc 2434
Db 2161 gacgctgtgctgtctagtgatcactcctgaagltgaagaacctgtgctccctacagtgatcc 2220
Qy 2435 cagctgtgtgttctgtctctgtctgtctgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2494
Db 2221 cagctgtgtgttctgtctctgtctgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2280
Qy 2495 gattagcaacactcttcccaagagccaacccgagagcagcgtgtgagggatcatctact 2554
Db 2281 gattagcaacactcttcccaagagccaacccgagagcagcgtgtgagggatcatctact 2340
Qy 2555 cagcgtgtacactgtccctacagctcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2614
Db 2341 cagcgtgtacactgtccctacagctcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2400
Qy 2615 caagatctcgtcagcctgtcctgtcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2674
Db 2401 caagatctcgtcagcctgtcctgtcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2460
Qy 2675 ccttlttgagagcagggagcatctgaggtgtgaggtgtggaacaacctgtgtgagagctgtgga 2734
Db 2461 ccttlttgagagcagggagcatctgaggtgtgaggtgtggaacaacctgtgtgagagctgtgga 2520
Qy 2735 ggaagatgtgtctcaatctcaacacctctgcatctcatatgagtgttggacacctctctca 2794
Db 2521 ggaagatgtgtctcaatctcaacacctctgcatctcatatgagtgttggacacctctctca 2580
Qy 2795 tggggtgtatgactgtgtatctatgaggtgtcttctccagggcagtaaggaattcccaagcc 2854
Db 2581 tggggtgtatgactgtgtatctatgaggtgtcttctccagggcagtaaggaattcccaagcc 2640
Qy 2855 ctgtgtatttctctgtacacaaagctcactgtgttggcagaggaaggtatagagaagacca 2914
Db 2641 ctgtgtatttctctgtacacaaagctcactgtgttggcagaggaaggtatagagaagacca 2700
Qy 2915 ccctgtgttccaacgaagaagaatgtcaagaaatctgtcatgtgagaggaaccacccaact 2974
Db 2701 ccctgtgttccaacgaagaagaatgtcaagaaatctgtcatgtgagaggaaccacccaact 2760
```

QY	2975	gaagctggcggtgtccatctcagaaccggtgtaaagtctacccgagatggatgtgaagtgccg	3034
Db	2761	gaagctggcggtgtccatctcagaaccggtgtaaagtctacccgagatggatgtgaagtgccg	2820
QY	3035	tgtcgtatggcctggcactggaattttttttgtggggccagatccactctctctgtggccaca	3094
Db	2821	tgtcgtatggcctggcactggaattttttttgtggggccagatccactctctctgtggccaca	2880
QY	3095	tggagcggggagaagacgaaccacatgttcaatctctgaaccgggtgttttcccccgaacctggg	3154
Db	2881	tggagcggggagaagacgaaccacatgttcaatctctgaaccgggtgttttcccccgaacctggg	2940
QY	3155	caaccgcctacatctctgggaaagaacatctggctcttgagatggagcacatctccgacgaacct	3214
Db	2941	caaccgcctacatctctgggaaagaacatctggctcttgagatggagcacatctccgacgaacct	3000
QY	3215	ggggggtctgtccccaagataaacgtgtgcgttttgaacatgctgaactgtctgaaagaacatctg	3274
Db	3001	ggggggtctgtccccaagataaacgtgtgcgttttgaacatgctgaactgtctgaaagaacatctg	3060
QY	3275	gtctcatgcccgtctgaaagggtctctcttgagaagcagtgaaagcgggagatvgagacagat	3334
Db	3061	gtctcatgcccgtctgaaagggtctctcttgagaagcagtgaaagcgggagatvgagacagat	3120
QY	3335	ggcccttgatgtgtgttcttgccatcaagccaagctgaaagaacaagaaccgcgctgtcag	3394
Db	3121	ggcccttgatgtgtgttcttgccatcaagccaagctgaaagaacaagaaccgcgctgtcag	3180
QY	3395	tggaaatgcagagaaaagctacatctgtgacctgtgcggttctcggggagctcaagatgtgtcat	3454
Db	3181	tggaaatgcagagaaaagctacatctgtgacctgtgtgcggttctcggggagctcaagatgtgtcat	3240
QY	3455	tctgatatgaaccaccaacgctgtgtgtgagccctctcccccgaagggaatatgtgagctgct	3514
Db	3241	tctgatatgaaccaccaacgctgtgtgtgagccctctcccccgaagggaatatgtgagctgct	3300
QY	3515	gctgaataaccgaacagggccgacccatctctctctacacacacatgtagtgaagcggga	3574
Db	3301	gctgaataaccgaacagggccgacccatctctctctacacacacatgtagtgaagcggga	3360
QY	3575	cgctctggggagacaggtgttgcatactctccacctgggaagctgtcctgtgtggctctctc	3634
Db	3361	cgctctggggagacaggtgttgcatactctccacctgggaagctgtcctgtgtggctctctc	3420
QY	3635	ccgtgttctcgaagaaccagctgtggaaaccaggtactacccctgaacctgtgtcgaagaagatgt	3694
Db	3421	ccgtgttctcgaagaaccagctgtggaaaccaggtactacccctgaacctgtgtcgaagaagatgt	3480
QY	3695	ggaatccctccctcaggttccctgcagaaacaggtgtagcacgtgtgtatacctcgaaaagga	3754
Db	3481	ggaatccctccctcaggttccctgcagaaacaggtgtagcacgtgtgtatacctcgaaaagga	3540
QY	3755	ggacagtggttctcgaagcaggttctctgaatctctggccctgggcgaacgacatagaagtgacac	3814
Db	3541	ggacagtggttctcgaagcaggttctctgaatctctggccctgggcgaacgacatagaagtgacac	3600
QY	3815	gctgaacatcgatgtctctgtctatctcccaacctcatcaggaagcatgtgtctgaagcccg	3874
Db	3601	gctgaacatcgatgtctctgtctatctcccaacctcatcaggaagcatgtgtctgaagcccg	3660
QY	3875	gctgtgtgaagaacataagggaatgagctgtgacatagtgtgcctgcacatatggaagtgtctaagga	3934
Db	3661	gctgtgtgaagaacataagggaatgagctgtgacatagtgtgcctgcacatatggaagtgtctaagga	3720
QY	3935	ggagaccttctgtggaacctcttcatatgagatgtgataccggctctcaagaccctgggcatctc	3994
Db	3721	ggagaccttctgtggaacctcttcatatgagatgtgataccggctctcaagaccctgggcatctc	3780
QY	3995	tagtattagcatctcagagagacgaacctgtgaagaagaatatctctcaagatgtgcgaagagag	4054
Db	3781	tagtattagcatctcagagagacgaacctgtgaagaagaatatctctcaagatgtgcgaagagag	3840

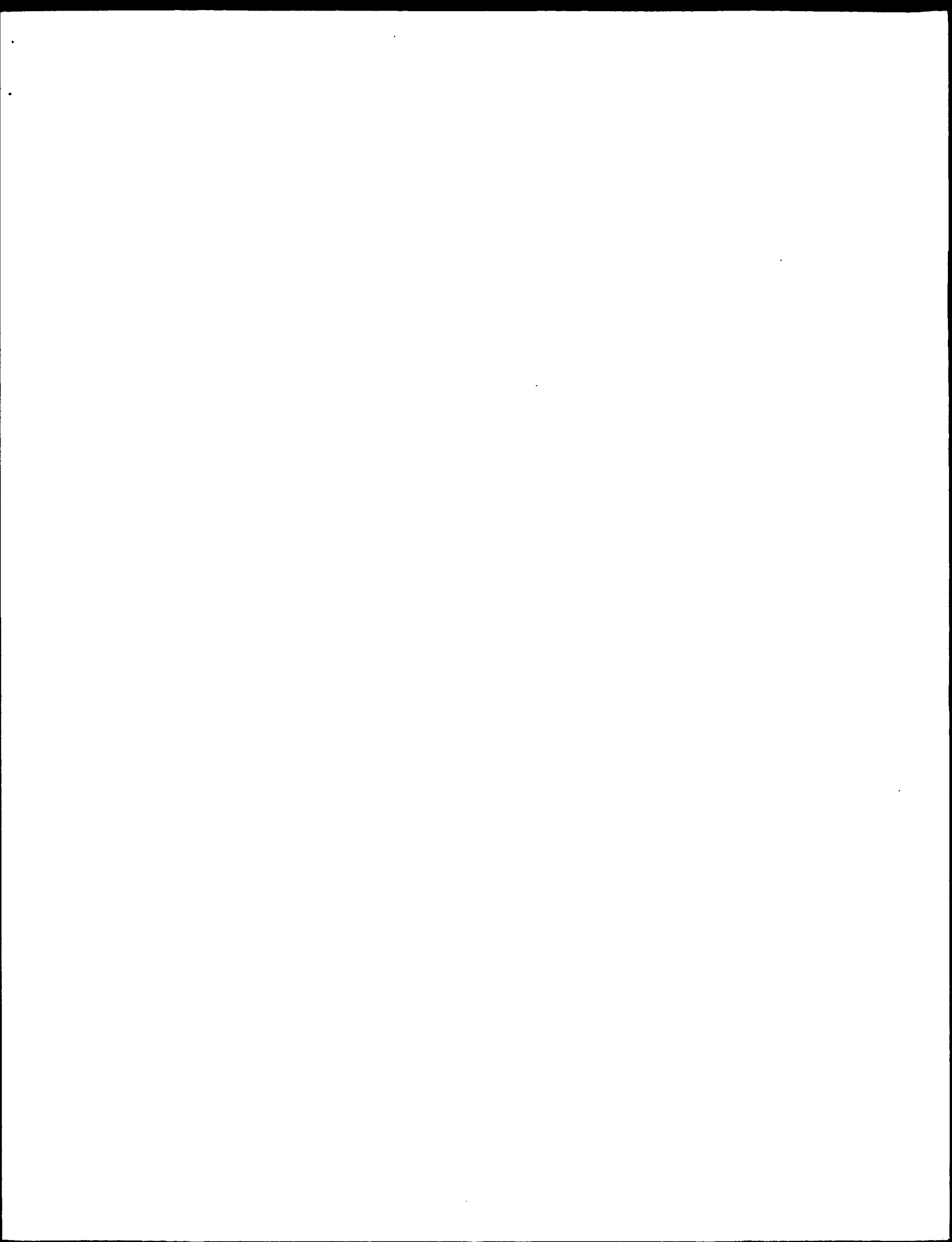
QY	4055	tgaggctgagatgctctgagacctaagaatggtlactcttgccagcgaaagcgaataaaggcgggctt	4114
Db	3841	tggggtgagatgctctgagacctaagaatggtlactcttgccagcgaaagcgaataaaggcgggctt	3900
QY	4115	cggggacaagaagagctgtctctgcgccccgttccatctgaaagatgagctgcgtcgaaccgaatga	4174
Db	3901	cggggacaagaagagctgtctctgcgccccgttccatctgaaagatgagctgcgtcgaaccgaatga	3966
QY	4175	tc - ctgacacatgagcccaagaatccagagagagacagactgtctcagttggtatgtagtgcgaag	4233
Db	3961	ttcgctgacacatgagcccaagaatccagagagagacagactgtctcagttggtatgtagtgcgaag	4020
QY	4234	ggctccacaagctgaaagagctgcgaaacttaacagacaaagtttgggcccctttgtga	4293
Db	4021	ggctccacaaggtgaaagagctgcgaaacttaacagacaaagtttgggcccctttgtga	4080
QY	4294	agagacgtcctaattgcagacgcgaagctgcgaagaagatattttgctcagatgtctgtccag	4353
Db	4081	agagacgtcctaattgcagacgcgaagctgcgaagaagatattttgctcagatgtctgtccag	4140
QY	4354	ctgtgtttgtctgtagatggcccttgctgttaagccttgatctgtgcacacctttggcaagtacc	4413
Db	4141	ctgtgtttgtctgtagatggcccttgctgttaagccttgatctgtgtcacacctttggcaagtacc	4200
QY	4414	ccagcctvggaacttcgaagcccttgcgaatgtagacgaacgaatatacatattgtcgaacaaatgag	4473
Db	4201	ccagcctvggaacttcgaagcccttgcgaatgtagacgaacgaatatacatattgtcgaacaaatgag	4260
QY	4474	ctccctgagagacacgggagaccccttggaactctttaaagcccttcacaaagacccctgtcttcg	4533
Db	4261	ctccctgagagacacgggagaccccttggaactctttaaagcccttcacaaagacccctgtcttcg	4320
QY	4534	ggagcccgctgtgtagaagagaaacccaatcccaacacacgccttcgcagagcaggggagagag	4593
Db	4321	ggagcccgctgtgtagaagagaaacccaatcccaacacacgccttcgcagagcaggggagagag	4380
QY	4594	agtggaaccactgcccccaagttcccccagacataatgaaactcttcagagatgggaactgga	4653
Db	4381	agtggaaccactgcccccaagttcccccagacataatgaaactcttcagagatgggaactgga	4440
QY	4654	caatlgcagaaccccttcacacgtgcatactgcagatgtagcgcgcgcgcgcgcgcgcgcgcgcgc	4713
Db	4441	caatlgcagaaccccttcacacgtgcatactgcagatgtagcgcgcgcgcgcgcgcgcgcgcgcgc	4500
QY	4714	ctgtgtgtccccccaggggcagggggggtcgtcctctccacaaagaaacaaacaaactcgcag	4773
Db	4501	ctgtgtgtccccccaggggcagggggggtcgtcctctccacaaagaaacaaacaaactcgcag	4560
QY	4774	atatccttcagagaccttcacgcggaagaaacatttcgcgattatctgtgtgaagaagtatgagc	4833
Db	4561	atatccttcagagaccttcacgcggaagaaacatttcgcgattatctgtgtgaagaagtatgagc	4620
QY	4834	agatcatagcccaaaagctttaaagaacaaagatctgggtgaatgagtttagttagtggcggt	4893
Db	4621	agatcatagcccaaaagctttaaagaacaaagatctgggtgaatgagtttagttagtggcggt	4680
QY	4894	tttcccttggtgtgtaagtaaatcctcaagacactcctccgcggtcaaaagaattatgatgcca	4953
Db	4681	tttcccttggtgtgtaagtaaatcctcaagacactcctccgcggtcaaaagaattatgatgcca	4740
QY	4954	tcaaaacaatltgaagaaacaccttaaaagctggtccgaagagacagttcttcgaatcgattttcca	5013
Db	4741	tcaaaacaatltgaagaaacaccttaaaagctggtccgaagagacagttcttcgaatcgattttcca	4800
QY	5014	acagctctgggaagaattttaagacagagctggaacccagaaataatgttcaaggtgtgtttca	5073
Db	4801	acagctctgggaagaattttaagacagagctggaacccagaaataatgttcaaggtgtgtttca	4860
QY	5074	ataacaagggtctgcacatgcaataagctcttcttccttaagttaagttcaaaatgcattcttc	5133
Db	4861	ataacaagggtctgcacatgcaataagctcttcttccttccttaagttaagttcaaaatgcattcttc	4920
QY	5134	gggcgaacctgcaaaaggggagagaaacccctlagcattatgaaattactgtcttccatcatc	5193

Db 4921 gggccaactgcaaaaggagagaaacctagccattatgaaattactgttcacatc 4980
QY 5194 cccgtgaatccaaagcagcagctctcagaggctgtctgtatgacacacatcagtgtg 5253
Db 4981 cccgtgaatccaaagcagcagctctcagaggctgtctgtatgacacacatcagtgtg 5040
QY 5254 tccctgtgcaatctgtgtacatcttggcaatgtccctgtcccaagccttgtcgtat 5313
Db 5041 tccctgtgcaatctgtgtacatcttggcaatgtccctgtcccaagccttgtcgtat 5100
QY 5314 tccctgtgcaatctgtgtacatcttggcaatgtccctgtcccaagccttgtcgtat 5373
Db 5101 tccctgtgcaatctgtgtacatcttggcaatgtccctgtcccaagccttgtcgtat 5160
QY 5374 ctgtcaactactgtgtctcctaatttgtctggatagtgtcaatcagltgtccctgca 5433
Db 5161 ctgtcaactactgtgtctcctaatttgtctggatagtgtcaatcagltgtccctgca 5220
QY 5434 cactgtgcatatcatctctcatctgtctccagcaagaagctcctgtctccacaac 5493
Db 5221 cactgtgcatatcatctctcatctgtctccagcaagaagctcctgtctccacaac 5280
QY 5494 tgcctgtgtagccctcctactcttctgtatgtgtgtcaatccacccctcctgtaac 5553
Db 5281 tgcctgtgtagccctcctactcttctgtatgtgtgtcaatccacccctcctgtaac 5340
QY 5554 cagcctccttgtgtcaagaatcccaagcagcctaagtgtgtgtcaccagcgtgaac 5613
Db 5341 cagcctccttgtgtcaagaatcccaagcagcctaagtgtgtgtcaccagcgtgaac 5400
QY 5614 tctctgtgcatatgtgcaagctgtgccaactgtgtgtgtgagctgttccacagaaata 5673
Db 5401 tctctgtgcatatgtgcaagctgtgccaactgtgtgtgtgagctgttccacagaaata 5460
QY 5674 agctggaataataatcgaatcgaatcctgaatcctgtctgtctgtacccacatttgc 5733
Db 5461 agctggaataataatcgaatcgaatcctgaatcctgtctgtctgtacccacatttgc 5520
QY 5734 tgggacgagggctcatcgcatactgtgaaacacaggaatgtgcctgtgaaagt 5793
Db 5521 tgggacgagggctcatcgcatactgtgaaacacaggaatgtgcctgtgaaagt 5580
QY 5794 tttgggagaaatcgtctgtgtccatcttctgtggaactgtgtggagcaaaccttgc 5853
Db 5581 tttgggagaaatcgtctgtgtccatcttctgtggaactgtgtggagcaaaccttgc 5640
QY 5854 ccatggtcgtggaagggtgtgtcttctcctcatctactgtctgtacccagtaacatct 5913
Db 5641 ccatggtcgtggaagggtgtgtcttctcctcatctactgtctgtacccagtaacatct 5700
QY 5914 tcatcagggccagacctgttaaatcgaagaactatccctctgaatgataagatgagatg 5973
Db 5701 tcatcagggccagacctgttaaatcgaagaactatccctctgaatgataagatgagatg 5760
QY 5974 tggggtcgggaaacagagaaatcttgatgtgtgaggaagcaagaaatgacattgaataa 6033
Db 5761 tggggtcgggaaacagagaaatcttgatgtgtgaggaagcaagaaatgacattgaataa 5820
QY 6034 aggaattggaagaatataatagaagaagcaggaagcctgtctgtacaggaattgtgtg 6093
Db 5821 aggaattggaagaatataatagaagaagcaggaagcctgtctgtacaggaattgtgtg 5880
QY 6094 gcaatcctcgtgtgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6153
Db 5881 gcaatcctcgtgtgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5940
QY 6154 ctctcaagatgtaaacaggaagatacactgtgtacagagagatgttcccttaacaaaa 6213
Db 5941 ctctcaagatgtaaacaggaagatacactgtgtacagagagatgttcccttaacaaaa 6000
QY 6214 ata-gtaattatcaaacatcgaagtaacatcagaacatgtggtactgtccctgatt 6272
Db 6001 ata-gtaattatcaaacatcgaagtaacatcagaacatgtggtactgtccctgatt 6060
QY 6273 gatgcatcacagagctgtgtactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6332
Db 6061 gatgcatcacagagctgtgtactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6120
QY 6333 ggaatcccaagaaagatgtgtgcaagttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6392
Db 6121 ggaatcccaagaaagatgtgtgcaagttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6180
QY 6393 gtgaagtatggaagaaatatgtctgtgtatcatagtgtgaagcaacaaacgaagctct 6452
Db 6181 gtgaagtatggaagaaatatgtctgtgtatcatagtgtgaagcaacaaacgaagctct 6240
QY 6453 acagcaatgcttggatctgt 6512
Db 6241 acagcaatgcttggatctgt 6300
QY 6513 atggaatcccaagcccggtctctgtgtgaattgtgccttaagtgtgtcaaggaagg 6572
Db 6301 atggaatcccaagcccggtctctgtgtgaattgtgccttaagtgtgtcaaggaagg 6360
QY 6573 agatcagtagtgtgtacatcctcatagtaaggaaatgtgaagctcttgcataagatg 6632
Db 6361 agatcagtagtgtgtacatcctcatagtaaggaaatgtgaagctcttgcataagatg 6420
QY 6633 gcaatcagtagtgtgtacatcctcatagtaaggaaatgtgaagctcttgcataagatg 6692
Db 6421 gcaatcagtagtgtgtacatcctcatagtaaggaaatgtgaagctcttgcataagatg 6480
QY 6693 tttgggagatgtgtatcatatagttgtgaagtaaggaagtcacacccggaactaaact 6752
Db 6481 tttgggagatgtgtatcatatagttgtgaagtaaggaagtcacacccggaactaaact 6540
QY 6753 gtccaggaattctgtgaactgtgaatcttccctgtgaagtgcttcaaaagaaacacccgga 6812
Db 6541 gtccaggaattctgtgaactgtgaatcttccctgtgaagtgcttcaaaagaaacacccgga 6600
QY 6813 atgtcaataatcagacatccatcttcatctctcctgtgccaagatataatgaatctc 6872
Db 6601 atgtcaataatcagacatccatcttcatctctcctgtgccaagatataatgaatctc 6660
QY 6873 tcccaagcaaaaacgagctccacataagaagatactctgttctcagaaacacctgtac 6932
Db 6661 tcccaagcaaaaacgagctccacataagaagatactctgttctcagaaacacctgtac 6720
QY 6933 caagiatattgtgaacttgcgaaggaacaaagtgtatgtatgacacattaaagactctca 6992
Db 6721 caagiatattgtgaacttgcgaaggaacaaagtgtatgtatgacacattaaagactctca 6780
QY 6993 ttacacaaaacacgaacgttagtgaagctgtgaagttccatcttctcatagatgag 7052
Db 6781 ttacacaaaacacgaacgttagtgaagctgtgaagttccatcttctcatagatgag 6840
QY 7053 aaagtgaagaagctatgtatgaagaaatccgttcatcagcgggtgtgtcgtgaagtaaga 7112
Db 6841 aaagtgaagaagctatgtatgaagaaatccgttcatcagcgggtgtgtcgtgaagtaaga 6900
QY 7113 ggaactagaacttctcctgtgacacatgtgaagtggtgtgtgtgtgtgtgtgtgtgtgtgt 7172
Db 6901 ggaactagaacttctcctgtgacacatgtgaagtggtgtgtgtgtgtgtgtgtgtgtgtgt 6960
QY 7173 gtgggaagaagaatgaactgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgt 7232
Db 6961 gtgggaagaagaatgaactgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgt 7020
QY 7233 atgaaacaaaatltccatcacaggggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7292
Db 7021 atgaaacaaaatltccatcacaggggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7080
QY 7293 caagtgaagaagctgaatttagtttttaactataactatgtgaacatttatggaac 7352
Db 7081 caagtgaagaagctgaatttagtttttaactataactatgtgaacatttatggaac 7140

QY 217 gtccctgtgtgagctctgacgctgcttcccaagggtccccagaccacaacgctggagctg 276
|||||
Db 1 gtccctgtgtgagctctgacgctgcttcccaagggtccccagaccacaacgctggagctg 60
QY 277 ctggtctgaggaacatggtctgttgcctcctcaagctgaggtctgtctgttggaaacctca 336
|||||
Db 61 ctggtctgaggaacatggtctgttgcctcctcaagctgaggtctgtctgttggaaacctca 120
QY 337 ctctcagaagaacacaacatgctcagctgttactggaagtgtgcgtggtcctattatct 396
|||||
Db 121 ctctcagaagaacacaacatgctcagctgttactggaagtgtgcgtggtcctattatct 180
QY 397 tccctgacctgacctgtgtctgcgtgagctaccaccctcatgaacacatgagatgacct 456
|||||
Db 181 tccctgacctgacctgtgtctgcgtgagctaccaccctcatgaacacatgagatgacct 240
QY 457 ttccaaataaagacatgacctctgcaggaacacctctgtggtttcagggtatattctgta 516
|||||
Db 241 ttccaaataaagacatgacctctgcaggaacacctctgtggtttcagggtatattctgta 300
QY 517 atgccaacaacccctgttccctgtaccgacctctgaggaggtcccgaggtgttggaa 576
|||||
Db 301 atgccaacaacccctgttccctgtaccgacctctgaggaggtcccgaggtgttggaa 360
QY 577 accttaacaatcatctgtgtgcgtctgttccagatgctcgaggtcctttatca 636
|||||
Db 361 accttaacaatcatctgtgtgtgcgtctgttccagatgctcgaggtcctttatca 420
QY 637 gccagaagaacacacagcatgaaagagacatgacgcaaaattctggaacattacagcagatca 696
|||||
Db 421 gccagaagaacacacagcatgaaagagacatgacgcaaaattctggaacattacagcagatca 480
QY 697 agaaatcccgcttaaaacttgaagcttcaagattctctgtgtgacaattgaaaccttctcg 756
|||||
Db 481 agaaatcccgcttaaaacttgaagcttcaagattctctgtgtgacaattgaaaccttctcg 540
QY 757 ggttcctatatacacaacctctctcccaagagtctactgtgacaagaagtctgaggctg 816
|||||
Db 541 ggttcctatatacacaacctctctcccaagagtctactgtgacaagaagtctgaggctg 600
QY 817 atgtcatcttcccaaggtatttttgcagaaggtcccaagttaactttgacaagtctgtga 876
|||||
Db 601 atgtcatcttcccaaggtatttttgcagaaggtcccaagttaactttgacaagtctgtga 660
QY 877 atgcatcaaaatcagaagagatgattcaactgtgtgacccaagaagtctcgagcttctg 936
|||||
Db 661 atgcatcaaaatcagaagagatgattcaactgtgtgacccaagaagtctcgagcttctg 720
QY 937 gctbaccacaaggaaactgtgtgcagcagagcgagtaactcgttccaaatgagatcc 996
|||||
Db 721 gctbaccacaaggaaactgtgtgcagcagagcgagtaactcgttccaaatgagatcc 780
QY 997 tgaagccaatcctgagagaacactaactctacatctccctcccgagcaagagatcgctg 1056
|||||
Db 781 tgaagccaatcctgagagaacactaactctacatctccctcccgagcaagagatcgctg 840
QY 1057 aagccacaanaaactgtctcatagctcttggaactctgcccagaggtcttcaagatga 1116
|||||
Db 841 aagccacaanaaactgtctcatagctcttggaactctgcccagaggtcttcaagatga 900
QY 1117 gaagctgagtgagatgagacagagagtgatgttcttgcacaaatgtgaaacagctccagct 1176
|||||
Db 901 gaagctgagtgagatgagacagagagtgatgttcttgcacaaatgtgaaacagctccagct 960
QY 1177 cctccaccacaatctaccagagctgtgtctgtatgtgtctgcgggactcccgagggaggg 1236
|||||
Db 961 cctccaccacaatctaccagagctgtgtctgtatgtgtctgcgggactcccgagggaggg 1020
QY 1237 ggtctgaagatcaagttctctcaactggtatgaggaacaacaactcaaaagcccttctggag 1296
|||||
Db 1021 ggtctgaagatcaagttctctcaactggtatgaggaacaacaactcaaaagcccttctggag 1080
QY 1297 gcaatggaactgaggaagatgctgaaaccttctatgacaacctcaactccttactgca 1356

|||||
Db 1081 gcaatggaactgaggaagatgctgaaaccttctatgacaacctcaactccttactgca 1140
QY 1337 atgattgtatgaagaatttgaagctagctctcttcccgatattatctgaaagcttga 1416
|||||
Db 1141 atgattgtatgaagaatttgaagctagctctcttcccgatattatctgaaagcttga 1200
QY 1417 agccgtctgtgttggaagatccctgtatatacactggaaccccgacaagcgagtgca 1476
|||||
Db 1201 agccgtctgtgttggaagatccctgtgtatatacactggaaccccgacaagcgagtgca 1260
QY 1477 tgcgtgaagtgtaacaagaccttccaggaactgtgtgttccatgactctggaagcagt 1536
|||||
Db 1261 tgcgtgaagtgtaacaagaccttccaggaactgtgtgttccatgactctggaagcagt 1320
QY 1537 gggaggaactcaagccccaagatctggaacttcatggaagaacagccaagaaatgagcttg 1596
|||||
Db 1321 gggaggaactcaagccccaagatctggaacttcatggaagaacagccaagaaatgagcttg 1380
QY 1597 tccgagatgctgttgagacagcgaggaacatgacacacttcttggaacagagttgagct 1656
|||||
Db 1381 tccgagatgctgttgagacagcgaggaacatgacacacttcttggaacagagttgagct 1440
QY 1657 tagatttgacaagccccaagacatggtgtgcttcttgccaagcacccagagatgtcaagt 1716
|||||
Db 1441 tagatttgacaagccccaagacatggtgtgcttcttgccaagcacccagagatgtcaagt 1500
QY 1717 ccagtaaatggtctgtgtatcacaccttggaagaagactttaaagagatcaacaggaatcc 1776
|||||
Db 1501 ccagtaaatggtctgtgtatcacaccttggaagaagactttaaagagatcaacaggaatcc 1560
QY 1777 ggaacatctcgtcttcaatgagatgtgtcaacctgaacaaactgaacccaatgaacag 1836
|||||
Db 1561 ggaacatctcgtcttcaatgagatgtgtcaacctgaacaaactgaacccaatgaacag 1620
QY 1837 aagttctgctcaatcaacaagttccatgagctgtgtgataaggaagatctcgtgctgta 1886
|||||
Db 1621 aagttctgctcaatcaacaagttccatgagctgtgtgataaggaagatctcgtgctgta 1680
QY 1897 ttgtgttcaactggaattactccagacagcatgagatgtcccatcatgttcaagtacaaga 1956
|||||
Db 1681 ttgtgttcaactggaattactccagacagcatgagatgtcccatcatgttcaagtacaaga 1740
QY 1957 tccgaatgagacatgacaagtgtgagaggaacaataaatacaagatgagtaactggagcc 2016
|||||
Db 1741 tccgaatgagacatgacaagtgtgagaggaacaataaatacaagatgagtaactggagcc 1800
QY 2017 ctgtgtccctcgaatcaaccccttggagacatgagctgtacgtctggggggcttgcctact 2076
|||||
Db 1801 ctgtgtccctcgaatcaaccccttggagacatgagctgtacgtctggggggcttgcctact 1860
QY 2077 tgcagatgtgtgtgagcagcgaatcaatcaaggtgtctgaagcagccagagaanaaactg 2136
|||||
Db 1861 tgcagatgtgtgtgagcagcgaatcaatcaaggtgtctgaagcagccagagaanaaactg 1920
QY 2137 --gtgtctatatagacaagatgacctatccctgttaagttgatacatcttctgagggt 2194
|||||
Db 1921 gdtgtctatatagacaagatgacctatccctgttaagttgatacatcttctgagggt 1980
QY 2195 gatgagccgttaatgcccccttctatgagctgtgcccgtgattactaagtgagctgtat 2254
|||||
Db 1981 gatgagccgttaatgcccccttctatgagctgtgcccgtgattactaagtgagctgtat 2040
QY 2255 catcaagagcatctgtatgagaagaagcagcgtgtaaaaggaacatgagcatatggg 2314
|||||
Db 2041 catcaagagcatctgtatgagaagaagcagcgtgtaaaaggaacatgagcatatggg 2100
QY 2315 cctggaacaacgacatactctgtgttaagctgtgtcaattagtagcctatctctctgt 2374
|||||
Db 2101 cctggaacaacgacatactctgtgttaagctgtgtcaattagtagcctatctctctgt 2157
QY 2375 gaggctgtgctgtgagttgtatctgaagtttaagaaacccgtgtccctacagttgaccc 2434
|||||

Qy	7892	caaacctgctgggctgcgaacgtctcgaagccaagcgatbgagattaaagatttgcgt	7951
Db	7678	caaacctgctgggctgcgaac-ctgcgaagccagcgatbgagattaaagatttgcgt	7736
Qy	7952	caaacctagaagaaacgtgaccattgttcctgacgtctgtcctacaatggtacactgat	8011
Db	7737	caaacctagaagaaacgcctggccattgttcctgaacgtctgcctacaatggtacactgat	7796
Qy	8012	ctcaagatggttatctacacaaatglatattctcgtccttttgaatcatctagaana	8071
Db	7797	ctcaagatggttatctacacaaatglatattctcgtccttttgaatcatctagaana	7856
Qy	8072	tgaaa 8076 	
Db	7857	tgaaa 7861	



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2002, 10:15:42 ; Search time 277.92 seconds
(without alignments)
9228.933 Million cell updates/sec

Title: US-09-595-526b-1
Perfect score: 10442
Sequence: 1 ggcgcggaccgcagagccg.....aaaaaaaaaaaaaaaaaa 10442

Scoring table: IDENTITY_NIC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents - NA: *
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PTCUS.COMB.seq: *
6: /cgn2_6/ptodata/2/ina/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	430.8	4.1	5894	3	US-08-665-259-24
2	430.8	4.1	5894	3	US-08-762-500-24
3	430.8	4.1	6525	3	US-08-762-500-74
4	96.2	0.9	240	1	US-08-628-417-6
5	93.8	0.9	2447	2	US-09-014-969-14
6	91.4	0.9	1117	4	US-09-247-373B-33
7	86.6	0.8	1474	4	US-08-821-994-64
8	86	0.8	260	2	US-08-520-678A-29
9	85.2	0.8	1582	4	US-08-897-126-29
10	85.2	0.8	1582	3	US-08-545-196B-12
11	85.2	0.8	1582	3	US-08-545-196B-12
12	85	0.8	3410	4	US-09-020-956-110
13	85	0.8	3410	4	US-09-030-607-110
14	85	0.8	3410	4	US-09-439-313-110
15	84.4	0.8	144	1	US-08-702-344-26
16	84.4	0.8	2671	6	5168051-9
17	84	0.8	1129	4	US-09-227-357-40
18	83.6	0.8	1066	1	US-08-157-101A-4
19	83.6	0.8	1641	1	US-08-300-903A-8
20	83.4	0.8	1736	3	US-09-182-816-22
21	83.4	0.8	1736	3	US-09-182-816-24
22	83.4	0.8	1736	3	US-09-471-528-22
23	83.4	0.8	1736	3	US-09-471-528-22
24	83.4	0.8	1736	4	US-09-634-530-22
25	83.4	0.8	1736	4	US-09-634-530-24
26	83.2	0.8	140	1	US-08-628-417-5
27	83	0.8	1441	4	US-08-821-994-63

28	83	0.8	1817	1	US-08-473-981A-5	Sequence 5, Appli
29	83	0.8	1817	2	US-08-474-087-5	Sequence 5, Appli
30	82.6	0.8	2280	3	US-08-813-150-1	Sequence 1, Appli
31	82.4	0.8	1602	1	US-08-530-950-3	Sequence 3, Appli
32	82.4	0.8	1602	3	US-08-888-429A-3	Sequence 3, Appli
33	82.4	0.8	1602	4	US-09-149-879-3	Sequence 3, Appli
34	82.2	0.8	1813	4	US-09-071-224-3	Sequence 3, Appli
35	82.2	0.8	2852	3	US-09-027-137-2	Sequence 3, Appli
36	82	0.8	1454	4	US-09-372-422A-19	Sequence 19, Appli
37	82	0.8	1882	4	US-09-370-253-1	Sequence 1, Appli
38	82	0.8	6671	1	US-08-280-443-1	Sequence 1, Appli
39	82	0.8	6671	1	US-08-457-459-1	Sequence 1, Appli
40	82	0.8	6671	1	US-08-555-678-1	Sequence 1, Appli
41	82	0.8	6671	5	PCR-US95-02275-1	Sequence 1, Appli
42	81.4	0.8	1279	3	US-09-248-335-25	Sequence 25, Appli
43	81.4	0.8	1493	1	US-08-340-820-24	Sequence 24, Appli
44	81.4	0.8	1493	1	US-08-593-535-24	Sequence 24, Appli
45	81.4	0.8	2184	4	US-08-955-918C-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-665-259-24
; Sequence 24, Application US/08665259
; Patent No. 6028173
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klingler, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,259
; FILING DATE: 17-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IG5-9.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; MOLECULE TYPE: CDNA
; NAME/KEY: CDS
; LOCATION: 2..5053
; US-08-665-259-24

QY 3685 agaa 3688
Db 2232 AGGA 2235

RESULT 3
US-08-762-500-74
Sequence 74, Application US/08762500
Patent No. 6030806
GENERAL INFORMATION:
APPLICANT: Landes, Gregory M.
APPLICANT: Burns, Timothy C.
APPLICANT: Connors, Timothy D.
APPLICANT: Dackowski, William R.
APPLICANT: Van Raay, Terence J.
APPLICANT: Klinger, Katherine W.
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: One Mountain Road
CITY: Framingham
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,500
FILING DATE: 03-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,259
FILING DATE: 17-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10469
FILING DATE: 17-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: IGS-9.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 872-8400
TELEFAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 6525 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 573..5684
US-08-762-500-74

Query Match 4.1%; Score 430.8; DB 3; Length 6525;
Best Local Similarity 56.1%; Pred. No. 5,5e-89;
Matches 944; Conservative 0; Mismatches 692; Indels 48; Gaps 5;

QY 2050 gtaagctcgggggggcttcgctactgacagatggtgtggaagcaagcaatcaatcaaggg 2109
Db 1186 ggaacatcggaaggaagcttctgagcctgacacatgctgtggaacggggcattcagaggt 1245

QY 2110 tctcagcggcagcag 2154
Db 1246 accatcgcatgagcggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1305

QY 2155 tgcctatccctgttaagtgatgaacatcttcgagggtgataagccgtcaatgcgcc 2214
Db 1306 tcccgatcccgccggttcatgacgaccccttctgtagccatccagatccagcagcagc 1365

QY 2215 tcttcatgacgtggtccggtatctacgtacgtggtgatacatcaagagcagtgatg 2274
Db 1366 tgcctgctgctgctgacgttcaacgttcaacccgcttaccattgcccgtctgctgacag 1425

QY 2275 agaagagagcagcgtgaaagacatcgagatcaatgagcgttgagacacagacatctc 2334
Db 1426 acaagaaagagcgtgaaagagatgacatgacatgagagagcgtcagacagcgtcagc 1485

QY 2335 gtttaagctgttcatctgtagtccatctctctgtgtagcgtgagcgtgtagtgg 2394
Db 1486 gtagtgcctggttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1545

QY 2395 tcatctgaagta-----ggaacctgtccctacagtgatccagcg 2439
Db 1546 tgccttctgctgctgacgtgaaagcgaatgagccgtgcttcccgacagcagcagcagc 1605

QY 2440 tgggttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 2499
Db 1606 tgcctgctgagccttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1665

QY 2500 gacaccttcttccagagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2559
Db 1666 gacaccttcttccagagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1725

QY 2560 tgaactgacctagcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 2619
Db 1726 cctaatatccctgcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1785

QY 2620 tcttctgtagcctgtcttcttcttcttcttcttcttcttcttcttcttcttcttctt 2679
Db 1786 tctgcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1845

QY 2680 ttgaagagcagagcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 2739
Db 1846 ttgaagagcagagcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1905

QY 2740 atggttcaatcaccac 2799
Db 1906 acgacttctgcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1965

QY 2800 tgaagacgttgatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 2859
Db 1966 tgaagacgttgatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2025

QY 2860 atttctcttgac 2910
Db 2026 atttctcttgac 2085

QY 2911 gccacacctgttccac 2970
Db 2086 aagaaagac 2145

QY 2971 acttgaagcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3028
Db 2146 accctggtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2205

QY 3029 ----gttgcgttgcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 3084
Db 2206 acagagggggggcgtgagagac 2265

QY 3085 tgggac 3144
Db 2266 tgggac 2325

QY 3145 cgaacctgggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3204
Db 2326 ccacacatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2385


```

? INFORMATION FOR SEQ ID NO: 29:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 260 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
US-08-897-126-29

Query Match 0.8%; Score 86; DB 4; Length 260;
Best Local Similarity 75.4%; Pred. No. 1.4e-10;
Matches 107; Conservative 0; Mismatches 35; Indels 0; Gaps 0.

Qy 10299 agatttaaatcgtatcttctatgttgaataataatgagtcacaaataagcttgaca 10358
Db 249 AGGCGTAAAGTGGAGCCACCTAAGAAGCAAAATTGAGAGTCGAGAAAGAAAGGAAA 190
Qy 10359 gtctctgttaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 10418
Db 189 AAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 130

Qy 10419 aaaaaaaaaaaaaaaaaaaaaa 10440
Db 129 AAAAAAAAAACCAAAAAACGAA 108

RESULT 10
US-08-545-196B-10
: Sequence 10, Application US/08545196B
: Patent No. 6080577
: GENERAL INFORMATION:
: APPLICANT: MELKI, JUDITH
: APPLICANT: MUMNICH, ARNOLD
: TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
: NUMBER OF SEQUENCES: 65
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
: STREET: PO BOX 747
: CITY: FALLS CHURCH
: STATE: VA
: COUNTRY: USA
: ZIP: 22040-0747
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/545,196B
: FILING DATE: 19-OCT-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: FARACI, C. J.
: REGISTRATION NUMBER: 32,350
: REFERENCE/DOCKET NUMBER: 2121-110P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 205-8000
: TELEFAX: (703) 205-8050
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1582 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
US-08-545-196B-10

Query Match 0.8%; Score 85.2; DB 3; Length 1582;
Best Local Similarity 79.6%; Pred. No. 5.7e-10;
Matches 113; Conservative 0; Mismatches 28; Indels 1; Gaps 1.

```

Qy	10302	attnaaatgcatcttctctgtctga-ctaaatgagcacaataagcttgcact	10360
Db	1424	ATTGACTGTTTTTCTATCTTATATGTTAAAGTATATATATTAATTTAAT	1483
Qy	10361	tctgttataaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaa	10420
Db	1484	TTTTTTTAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	1543
Qy	10421	aaaaaaaaaaaaaaaaaaaaa	10442
Db	1544	AAAAAAAAAAAAAAAAAAAAA	1565

RESULT 11
 US-08-545-196B-12
 : Sequence 12, Application US/08545196B
 : Patent No. 6080577
 :
 : GENERAL INFORMATION:
 : APPLICANT: MELKI, JUDITH
 : APPLICANT: MUMNICH, ARNOLD
 : TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
 : TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
 : NUMBER OF SEQUENCES: 65
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
 : STREET: PO BOX 747
 : CITY: FALLS CHURCH
 : STATE: VA
 :
 : COUNTRY: USA
 : ZIP: 22040-0747
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/545,196B
 : FILING DATE: 19-OCT-1995
 : CLASSIFICATION: A35
 : ATTORNEY/AGENT INFORMATION:
 : NAME: PARACI, C. J.
 : REGISTRATION NUMBER: 32,350
 : REFERENCE/DOCKET NUMBER: 2121-110P
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (703) 205-8000
 : TELEFAX: (703) 205-8050
 : INFORMATION FOR SEQ. ID NO: 12:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1582 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 :
 : MOLECULE TYPE: cDNA
 :
 : US-08-545-196B-12

	Query Match	0.8%;	Score 85.2;	DB 3;	Length 1582;
	Best Local Similarity	79.6%;	Pred. No. 5.7e-10;		
	Matches 113;	Conservative	0;	Mismatches 28;	Indels 1;
				Gaps	1
QY	10302	atlaaaatgacatacttcctcatgtgtga-atataatgagtcacacaaataaagctgagcagt	10360		
Db	1424	ATGTACTGTTTTTTCATCTTCATAGCTTTAAAGTATATATATAATATTATTT	1483		
QY	10361	tctgttaaaaaa	10420		
Db	1484	TTTTTTTAAAAA	1543		
QY	10421	aaaaaaaaaaaaa	10442		
Db	1544	AAAAAAAAAAAAA	1565		

RESULT 12
 US-09-020-956-110
 ; Sequence 110 Application US/09020956
 ; Patent No. 6261562
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillin, Davin C.
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
 ; NUMBER OF SEQUENCES: 178
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED AND BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ;

[illegible]

RESULT 13
 US-09-030-607-110
 Sequence 110, Application US/09030607
 Patent No. 6262245
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
 NUMBER OF SEQUENCES: 224
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: WA
 COUNTRY: USA

[illegible]

0.88; Score 85; DB 4; Length 3410;

```

RESULT 15
US-08-702-344-26
: Sequence 26, Application US/08702344
: Patent No. 572315
: GENERAL INFORMATION:
: APPLICANT: Jacobs, Kenneth
: APPLICANT: McCoy, John
: APPLICANT: Lavalie, Edward
: APPLICANT: Racie, Lisa
: APPLICANT: Werberg, David
: APPLICANT: Treacy, Maurice
: APPLICANT: Spaulding, Vikki
: TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
: TITLE OF INVENTION: ENCODING THEM
: NUMBER OF SEQUENCES: 37
: COMMENT:

```

Query	Match	Best Local	Similarity	74.6%	Score 84.4	DB 1	Length 144
Matches	103	Conservative	0	Mismatches 35	Indels 0	Gaps 0	
QY 10305	aaatgcatattctctatgtgtgaataataatgagtcacaaataagctgtgacagtcttg	10364					
Db 1	AAAAAAAAAANNNTNTTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	60					
QY 10365	ttcaa	10424					
Db 61	AA	120					
QY 10425	aaaaaaaaaaaaaaaaaaaaa	10442					

Mon Sep 16 10:19:47 2002

us-09-595-526b-1.rni

Page 10

Db 121 AAAAAAAAAAAAAAAAAA 138

Search completed: September 14, 2002, 07:01:42
Job time: 74760 sec

Result	Score	Match	Length	DB	ID	Description
No.						
1	714	6.8	3065	11	AK019548	AK019548 Mus muscu
2	697.4	6.6	809	10	B1754756	B1754756 603025477
3	656.8	6.3	705	10	B6484804	B6484804 602502599
4	639.8	6.1	854	10	B1854140	B1854140 6033814440
5	633.2	6.1	640	10	B6436050	B6436050 602508836
6	606.8	5.8	878	10	B1827919	B1827919 UNL - P-FN
c	598	5.7	670	9	AL048434	AL048434 DKFZ5861
7	596.2	5.7	906	9	AU135588	AU135588 AU135588
8	576	5.5	739	10	BF216316	BF216316 601884344
9	574.2	5.5	913	10	BF216316	BF216316 602447068
10	574.2	5.5	913	10	BF216316	BF216316 602447068
11	567.8	5.4	631	9	AL048638	AL048638 DKFZP5644
12	563.8	5.4	784	10	B6879645	B6879645 601491738
13	549.6	5.3	608	9	BE177973	BE177973 RCI - HMO59
c	549.4	5.3	771	10	BE574931	BE574931 6020131601
14	545.8	5.2	648	10	B6567118	B6567118 602589265
15	545.8	5.2	648	10	B6567118	B6567118 602589265
16	543.6	5.2	856	10	BF160011	BF160011 601768197
17	543	5.2	837	10	B6567595	B6567595 602586356

18	538.8	5.2	702	10	B1658600	603284333
19	536.8	5.1	652	9	B4668374	B4668374
20	534.8	5.1	678	10	B6971402	B6971402
21	532.4	5.1	724	10	B6920223	602822304
22	531	5.1	870	10	B6711104	B6711104
23	526.6	5.0	720	10	B1248317	602966918
24	523.2	5.0	528	9	AM051752	AM051752
25	517.2	5.0	523	10	BF116114	71777402.x
26	516.2	4.9	709	9	AL048433	AL048433
27	511.4	4.9	548	10	BF433708	BF433708
28	494.4	4.7	601	9	AA521292	a47e905.s
29	487.8	4.7	492	10	BF439764	BF439764
30	484	4.6	491	9	AA814091	AA814091
31	473	4.5	486	9	A1707785	A1707785
32	473	4.5	562	10	B6665489	154542
33	459.4	4.4	515	10	BF094554	BF094554
34	455	4.4	492	9	A1807534	A1807534
35	449.4	4.3	451	9	AA434152	AA434152
36	449	4.3	487	10	N94914	N94914
37	447.6	4.3	554	10	BF076322	BF076322
38	444.8	4.3	646	9	AM019972	AM019972
39	443	4.2	557	9	AM006879	AM006879
40	433.2	4.1	518	10	BF042703	BF042703
41	431.8	4.1	435	9	A1693068	A1693068
42	428.8	4.1	463	10	BE715104	BE715104
43	428	4.1	940	10	B6880894	601490437
44	425.8	4.1	527	9	A1628099	A1628099
45	425.4	4.1	427	10	BM153363	BM153363

ALIGNMENTS

RESULT	1
LOCUS	AK019548
DEFINITION	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:921533G24:ATP-binding cassette, sub-family A (ABC1), member 1, full insert sequence.
ACCESSION	AK019548
VERSION	AK019548.1 GI:12859824
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (Strain:C57BL/6J) adult male testis cDNA to mRNA, clone_1b:RIKEN full-length enriched mouse cDNA library clone:4921533G24.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (sites)
TITLE	Carninci, P. and Hayashizaki, Y.
JOURNAL	High-efficiency full-length cDNA cloning
MEDLINE	Meth. Enzymol. 303, 19-44 (1999)
PUBMED	99279253
PUBMED	10349636
AUTHORS	2 (sites)
TITLE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
MEDLINE	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	20469374
PUBMED	11042159
AUTHORS	3 (sites)
TITLE	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, K., Kira, A. and Hayashizaki, Y.
JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillarary sequencer
MEDLINE	Genome Res. 10 (11), 1157-1171 (2000)

	MEDLINE	20530913
	PUBMED	11076861
	REFERENCE	4 (sites)
	AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE		Functional annotation of a full-length mouse cDNA collection
JOURNAL		Nature 409, 685-690 (2001)
REFERENCE		5 (bases 1 to 3065)
AUTHORS		Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., But,C., Carinelli,F., Fukuda,S., Fukushima,Y., Furuno,M., Hanaoka,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiroaka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,I., Kojima,Y., Konno,H., Kouda,M., Koyama,S., Kurihara,C., Matsuyama,T., Miyazaki,Y., Nishii,K., Nomura,K., Nunazaki,R., Ono,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Salto,R., Sakai,C., Sakai,K., Sano,H., Sasai,D., Schirini,L., Shibata,K., Shibata,Y., Shingawa,A., Shiraki,T., Soebae,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission	
JOURNAL	Submitted (Jl-AUG-2000)	yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	Please visit our web site (http://genome.gsc.riken.go.jp/) for further details	
	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGACAGAAGATCCAGACGCCTTTTTCCTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAAGAGAGACTTCGCAATTAAATTAATATCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size compressed longer than 7 kb was selected before cloning. Vector: a modified pBlueScript KS(+) after bulk excision from lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.	
FEATURES	Location:Qualifiers	
source	/organism="Mus musculus"	
	/strain="C57BL/6J"	
	/db_xref="MGD:GI:1912764"	
	/db_xref="taxon:10090"	
	/clone="4921353G24"	
	/sex="male"	
	/tissue_type="testis"	
	/clone_lib="RIKEN full-length enriched mouse cDNA library"	
	/dev_stage="adult"	
gene	1..3065	
	/gene="Abca1"	
misc_feature	1..3065	
	/gene="Abca1"	
	/note="ATP-binding cassette, sub-family A (ABC1), member 1"	
BASE COUNT	930 a 581 c 567 g 987 t	data source:MCD, source_key:MGI:99607, evidence:ISS"
ORIGIN		
	Query Match	6.8%; Score 714; DB 11; Length 3065;
	Best Local Similarity	63.4%; Pred. No. 7,66-68;
	Matches 2058; Conservative	0; Mismatches 954; Indels 234; Gaps 54;
xy	7168 ttgatgttggaagaagttaactggaactctactgatactatcattcaatgcgaatgcacattca 7227	

Dh	2	TTTTCTGTGGAGAAACAAATGGATACCTGATCTGACACTATTCAATGCATGCACCTTCA	61
Oy	7228	atgcaatgnaaaacaanaatlccatctacaggggcagctgttcttgagctatgtctgtatg	7287
Dh	62	ATGCACAGACGAACCAATTCATTCATACAGGGGAGTGCCTTTGAGCCATTGCTTGTAAG	121
Oy	7288	gctctcaagtgaaa--gacttgatattagttttttacc--tatacctatgttgaaactctat	7344
Dh	122	GCTCTCTAGTGAATAATACCTTGAAAGTTAGTTCAATTACCTTATACAGATGTGAACCTGG	181
Oy	7345	tatgaaacccaatgagacatatggttgtaactcaactttttttttttttttttttttttt	7404
Dh	182	TGTGGAAACCAAGCAGACTCTGGGTTTGGG-----TTCAATACTTTTTTTGTTCCGT	232
Oy	7405	gtattctcatttgggtgttgcaacataatctatcaatgaatcatcatctgtgcagcgatttga	7466
Dh	233	GTATTCTCAGTAGGATTGGCAACAACAGTCATATATAATGCTATGGCCACTGTGTAATCAA	292
Oy	7465	caaatcaaaagtgaaatgacatctcc--tcaatcaactaagcaatgacatgcagccagagga	7522
Dh	293	GTCMAAGGCACACACATCTCTGTCATTAAGCATTAAGCATTAAGCATGCGAACCAACAAACG	352
Oy	7524	gttcccggtgacacatccatctgtctggcaatgagtgctgcagaagtattatgtgcaagt	7583
Dh	353	GTTTCCCGGTGCACATCCATCTCTGGCATAGTGTGGCAAGTTCACAGTTCAGTCCCAAGTT	412
Oy	7584	ttccagaaagtgttaagcacacatggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	7643
Dh	413	GCTCAGAAAGCTGTGAACCACTGA--GTGTGTCAACAAACCTTTGTGTGAACCGCCCTACT	471
Oy	7644	cagaagtctacaacattgaaatcagttgtac--agaatgtgccatgctgtgtcaatcc	7702
Dh	472	GTCGGT--TGACATCATTTAAATATCAGGTGCAAAAAAGGTGGCACATGTGACTTAATCCC	530
Oy	7703	tgtcttgattccctctgataagctgtgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	7762
Dh	531	CATTTCCTCTCTCTTTGATGAGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	586
Oy	7763	gtctctagcagcaggaactgtgttccatgttataatgttccatgtcttgagccatgtg	7822
Dh	587	ATTCCTGTAACCCAGGTACTTGGTTCCTTTGACGTTTGGCCATGGCCCTGTGATGGC	646
Oy	7823	tctcacaggttcatctctatagagctctttaaataac--tagatctctgttgaagagcgaag	7881
Dh	647	TTGGCATAG--CATCTTCTGAGACTTTTTCAAATACATTAGATTCCTCTTAACACACAAAG	705
Oy	7882	aatcaacagccaaactgtctgggtctgaagctgtctgaagccagggcatgaggaattaaag	7941
Dh	706	-ATTAGACGCCAAACTGCTGGGGCTGCMAACGGCTCAGTTCAAGGTTGTGCAATGAATAT	764
Oy	7942	atgtgtcgttccaacactaggaagcctgtgcccattgtctcactgtctcgtactaaca--	7998
Dh	765	CCAGTCGATTTTACACGT--GGCAGGTCTGGGTGGTTGTGTGCACTGTCCTCTAACAA	823
Oy	7999	----tgtaacactgcatctcaaga----tgttatctgcaacaaaggtt--tattctgtgc	8050
Dh	824	GATGGGTACACTACACCTTTGAGATCCTTCAATTTATACAGAAATCTAGTCTTTCTTAC	883
Oy	8051	tttttgaaattcaatcagaanaatgnaaagaatggagtgttattttttgcaaaaatgtttgtac	8110
Dh	884	TGTTGTAATTAACCTAGAAAATGAAGGGGTGGCATTTTCATTTTGACAAAATAATGTTCGA	942
Oy	8111	tttttaatgttatitggaaatttaagtcctctatcagtgactctgaacccctagaatggcc	8170
Dh	943	TTGTGTACTATTATTGGAAATTTTAATTTTATTCATGCTTTCGAAAGCTTGAACTGTAC	1002
Oy	8171	tctttgagaagccctgtgatagaggagtgtgacacgtgcagcccccactatttttcttct	8230
Dh	1003	ACGTGTGATGTCACTACATAGAGGAATGGCCCGGACTGCTTCATGCTTTATTTTCT	1062
Oy	8231	t-----atgtaaagtgtgataatcatcatgactgtatgtgtcctagaagaagcaatgtatgtgc	8284

Db 1063 TGGTAATTTTGAAGATAGATGTCTGACTAGCGAGTGACCAAGAAAACATGTGGTAGTC 1122
Qy 8285 aggaatcgaatgacatataatttgagttcttcacagatcaattagagatacttcaatctca 8344
Db 1123 AACACTCAGGCGCA-----TATTTTAAGATCTGTAGAGCACTATTCATTTCA 1170
Qy 8345 cttcaatcaaatatttttttgagtgatgctgtagtgaagaagatagtgagtgagta 8404
Db 1171 GGTTCAGATGAGATGATTTTGAACATCATATATGTAAATGCTTGGA----- 1222
Qy 8405 taagatagagagatataagctcagacactcctcgtgcatttcaagctcagctcag 8464
Db 1223 -----GAGATGAGGGGAGGAGTACAGATTTCTGTGCAT-TTATTCAGCTGATG 1272
Qy 8465 gttcaaatataggttgcttggttgtaggagccacgtgaacatattgagcagcc 8524
Db 1273 ATGTACAGATGAGGT-----TATTTGTAAATCCACTGAAAGATATGGCCACAC 1326
Qy 8525 ttttttttttttttaataatgcaaatgcaagaagcaagaagatagtaggtaagtaagt 8584
Db 1327 CTTCGCTACTTG-----ATAGCATCATACAGAACGCCAAGAGACACT----- 1371
Qy 8585 ttaaacatgaatcttcaacagggaaaacagctagctgaacacttgctgaacacaca 8644
Db 1372 ---AGTAAACCCCTCTTCCAGGAGAGCATGTGAATCTCTCGATACATCG 1428
Qy 8645 acttggtttatgg-----cattagtaacctcaaatatgcttgtagatattgg 8697
Db 1429 ATGCGCTGACCTTGGGATCCTCACCATATGGGCAAAACATGGCTTGGACGATGAGA 1488
Qy 8698 ataccacatataa---ctgacagctcaaatcttcaatcttcaatcactagcaga 8754
Db 1489 GACACCCACTTAAACCTCTGAGATCTGATGTTCACTCTTCCGATTAACCAATG 1548
Qy 8755 aaaaataaaaaaacaaatacttccatataagagca-ttttcagagtttccaaacag 8813
Db 1549 ATGGAACCAATCAACAACTCGCCAGCTGAAATATTTTTCAGACTTTCTAACCCCA 1608
Qy 8814 tcttattttct-----agtcagtaaacatttgtaaaatactgttccactaacta 8867
Db 1609 GCTTATTTGTTTCATCTGACAGCAACGTGAAAAAATATGTTTACACAGTCTCA 1668
Qy 8868 cgtttaaactgcttgagaaaaaataatagagaaactatgttggggg--aaagttc 8925
Db 1669 ATGTATCGCTTTCACAAACAAACAAATATAGTAACTTCTTATTTGGCAAGTTC 1728
Qy 8926 aagtgatcttcaatataacttaactctcacttccacttttccaaatltgaataaac 8985
Db 1729 AAGTAGCTTTGCTATC-----CTTATTTACTTCTTCTAAAAAT----- 1770
Qy 8986 gctaaagtgtagaacttcaagtttcaaatatcttctataatttttaattacaga 9045
Db 1771 --TGGAGATTAAGATTTTCAGATCTATTTCA-----TTATGTTTATATA 1814
Qy 9046 atatatatacccaactgctgtaaaaaaataatgattgtttagaagttlaaagctat 9105
Db 1815 ATGTATATGTAATTCATTTGCTTGAAGGAAATGACAAAGTTT---GATACATAATGTCAC 1871
Qy 9106 attgatttaataataagaatgaaggaatcttccaaactagtgataggaactcgt 9165
Db 1872 ATAGGTTTCTAAATGA--TAAAGAAAGTGTTGTTCCAGTAGTTATTTGGCATACATTCAT 1930
Qy 9166 gaaattttagatcttcaaaaaatacagaattatagaaatattctctcaatlaaat 9225
Db 1931 TTTAGATA-----TCAAGATACCGAATCAAGAGCATGTGCTT-----TAT 1973
Qy 9226 ttttcaaaatcaagttatggtttcctcaatttcaataaactgtaattcacttcaatc 9285
Db 1974 TTTTCAAAAACAACTTCGTTGCGCTTCTCTAGTCATATACACATGACAGC----- 2027
Qy 9286 atagtaaatctatgagcaactcctactcgttccctcgtatcttaaggcatatttaa 9345
Db 2028 -----CCTTGAATAATCTCTGTTTAACTACTGATTTTGAAGC-----CAC 2073

Qy 9346 aaaaataaagcactgtagactatlttgaagaacacagcaatttaacagattgaa 9405
Db 2074 AAACACACAAAGATGAGCCACCATTTTGAAGAACAAATCAATGAGTGTGATTTAA 2133
Qy 9406 aggaacctcttgaagctaaacacataagttatatacttcaatcaactgtagta 9465
Db 2134 A--ATCTTTCTGAGCTTAAGACAAATCTGTACTAT-----ATGTTACTTTTAC 2183
Qy 9466 cctttaaataagtaatttttcaatttccctgltglaaacctaatgtgtagaattc 9525
Db 2184 ACTATCTGAAGAGCAATCTTCAAC--TTTCTGTTTAAAGTAAATTTTGAAGAGTTA 2241
Qy 9526 taccactataactcaatacagaacaaatttcgtatataccctgtaggaatgactag 9585
Db 2242 AAATCAATCTATCT--TCAATTAAGAAATTTCTTACATTTCCCTATGAGATGTGATG 2299
Qy 9586 tgaatcagaataatctcaataatagtgltcaaaaattctcgttcttgcacttggagc 9645
Db 2300 TGAG-TGAGAAATTTCCAA-----GTGCAAACACTTCTGTGTT---ACTTAAATA 2347
Qy 9646 acctcaaaaaactataaacaactgtaataatagagaatacagaagaataaagccc 9705
Db 2348 AAATAGTGAAGAACTTACTACTGTAATATGAGAAAGCAAAAGAA--AGTGAAGTCC 2404
Qy 9706 tctatataaatgcccagaacatctatgtttaaataaacaacacccacactagc 9765
Db 2405 TCTCGTAGATATACATGATATTTCA---TTATGAAGAACAAACCTCAAACTACTG 2461
Qy 9766 tattcattatctgtaactgaagaacatgcttltgagacttaa--atgtgacacatc 9824
Db 2462 TATTTGGTGTCTGACCGAGCATATGCCCTCATGCTAAATATGTATCATATCATAT 2521
Qy 9825 cattcactgtagtaactgaactgactaagccattgctgtgttcttcttctgtgntgn 9884
Db 2522 TGCTCTGTATATGATGACATGACTTAAAGGATTT--TTTGTGCTTCTCTATGTTGT 2580
Qy 9885 atataatgtaaaaatatttccaaagagcaatgctgactgaataactagacc--cttga 9943
Db 2581 ATATATCAGTAAAT--TGTTCCAAAGACCATGTGTATGTAAATGGGAAACCATTTGA 2639
Qy 9944 tatgaacattaaatttggaccccttgglatatctactag--aataatgtaatactgna 10002
Db 2640 TACTGAATTTACTATTTGTTACTTTCATTTACTTATTTGCTGTAAATAGTAAAGCCACAGT 2699
Qy 10003 aatattgcttaatttccaaatggtgcatccccccttaaanagtctatccataag 10062
Db 2700 AATACTGTTGATTCAAAACTGTTGCATCCCTTTTGTAGAACATTTATATTTCCATTA 2759
Qy 10063 gattagcttgctatcccttctataaccctaagaatgaagctgttltggtccttgtt 10122
Db 2760 GGATTCGGTATGTTCTTTTCCCTCCTGCTCCTAGATGAACCTGGTTTGTGCTTTTCT 2819
Qy 10123 catcattggccctcattcccaagcattacgctgtcgtlaagggatcatatttgcact 10182
Db 2820 TATCATTTGGCCCTCATTCACAGCACTTATGCTGTCTGTAT--GAGCTATTTTGGACT 2878
Qy 10183 ggaatattcgggaattgcaaaactagaacaaagtltcaacagatttcaagttaatc 10242
Db 2879 GGAATATCTGAGTTTGCAAAACATGACAAAAGTTTGAAGAGCATTTGAAGTTAAATC 2938
Qy 10243 atttcaataaagaaaga--aaaaaatttctatgcaataacttatalgaag 10300
Db 2939 GTTTTCATTAACAAAAAATAAACTGAAAAAATTTGATGTGAATATCTTATATGACG 2998
Qy 10301 tattaatgcatatttctatgltgtaataatagtgacaaataaagctgtgagct 10360
Db 2999 TGT-----TTTTTAAAGCTTGTCTATGTATGATGCTCAAAATTAAGCTGACAGT 3054
Qy 10361 tctgtt 10366
Db 3055 CCTGCT 3060

```

RESULT 2
B1754756 809 bp mRNA linear EST 25-SEP-2001
LOCUS 603025477F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5195995 5',
DEFINITION mRNA sequence.
ACCESSION B1754756
VERSION B1754756.1 GI:15746334
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 809)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11490 row: 1 column: 20
High quality sequence stop: 768.
Location/Qualifiers
1..809
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5195995"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library site is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH-MGC Library."
BASE COUNT 151 a 199 c 220 g 239 t
ORIGIN
Query Match 6.6%; Score 692.4; DB 10; Length 809;
Best Local Similarity 99.6%; Pred. No. 2.8e-65;
Matches 715; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
QY 2118 ggaacgagaagaactgctctatgagaagaatgacctatccctgttagcttgaat 2177
DB 1 GGCACCGAAGAAACTGCTCTATATGCAACAGATCCCTATCCCTGTTACGTTGAT 60
QY 2178 gacatctctcggggtgtagcgcggtcaatgagccctctcaatgagcgtggcctgatt 2237
DB 61 GACATCTTCTGGCGGTGATGAGCCGGTCAATGCCCTCTTCATGACGCTGGAT 120
QY 2238 tactcgtgctgtagtcatcaaggacatcgtagtagaagaagacgcgtgaaagag 2297
DB 121 TACTCAGTGGCTGTGATCAACAGGCAATCGTTATGAGACAGAGCAGCGCTGAAAGAG 180
QY 2298 accatcgatcatgagcctgagcaacacatcactctgtttagcgtggttactagtagc 2357
DB 181 ACCATCGGATCATGGGCTTGAGCAACAGCATACCTGTTTAACTGGTTCTTTAGTAC 240
QY 2358 ctcaatctctctctgtgtagcgcgtgctgtagtgcattcattcgaagtagaagacctg 2417
DB 241 CTCATTCCCTCTCTCTGTGTGAGCGCGCTGCTAGTGCATCTGTAAGTAGAAACCTG 300
QY 2418 ctgacctagagtagatccacgagtggtgtgtgtctctccgtctcggtgtgtgtgaca 2477

```

```

DB 301 CTGCCCTACAGTGAATCCAGCGGTGGTGTCTCTCCCTGCTCGGTGTGCTGTGACA 360
QY 2478 atccctgagctcttcctgattagcaactctctccagagcaaccctggagcagctgt 2537
DB 361 ATCCGTGAGTGTCTTCTCTATATGACACTCTTCTCCAGAGCAACCTTGGACAGCTGT 420
QY 2538 ggggagcatcattacttcaacgctgtacccctacgctcgtgtgtgtgtgtgtgtgtgt 2597
DB 421 GGGGAGCATCATCTACTTACCGCTGACCTGACCGCTACGCTGCTGTGTGAGCATGACAGAC 480
QY 2598 taacgtggcttcaactcaaatatcttgtagcgtgctgtctgtgtgtgtgtgtgtgt 2657
DB 481 TACGTGGCTTCACTCACTAAGATCTTCCGTAGCCCTGCTGTCTGTGGCTTTTGGGTTT 540
QY 2658 ggcctgtagtacttgcctcttttgagagagagagcatttgagtgagctggagacaactg 2717
DB 541 GCGTGTGATGACTTGTGCCCTTTTGGAGGAGCAGGCGCATGTGAGTGCAGTGGACACCTG 600
QY 2718 ttgagagctcctgtgag-aggagatgcttcaatcaccactgcatccatgatgct 2776
DB 601 TTTGAGACTCTCTGTGAGAGGAAGATGGCTTCAATCAGCACTTGGCTTCCATGATGCT 660
QY 2777 gttgagaccttctctat-agggtgatgacctgtatgacattgagcgtgtcttccagg 2833
DB 661 GTTTCACACTTCTCTATGAGGGGTGATGACCTGTGATGAGGCTGTCTTTCAGG 718

RESULT 3
BG482804 705 bp mRNA linear EST 21-MAR-2001
LOCUS 602502594F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4616207 5',
DEFINITION mRNA sequence.
ACCESSION BG482804
VERSION BG482804.1 GI:13415083
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 705)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1370 row: k column: 24
High quality sequence stop: 688.
Location/Qualifiers
1..705
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4616207"
/clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site:1:
SfiI (ggcgctcgcc); Site:2: SfiI (ggcattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTTAGGCG-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGGCGGACATG-dr(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
Ca). Note: this is a NIH-MGC Library."
BASE COUNT 255 a 109 c 86 g 255 t

```

ORIGIN

Query Match 6.3%; Score 656.8; DB 10; Length 705;
Best Local Similarity 98.6%; Pred. No. 1.9e-61;
Matches 694; Conservative 0; Mismatches 7; Indels 3; Gaps 3;

QY 8753 gaaaatataaacaacaataacttccatcatgagcatttccagagtttctaccoca 8812
DB 1 GAAAAATATMAAAACAAATACTTCATATGAGCATTTTTCAGAGTTTCTTAACCA 60
QY 8813 gcttaattttctagtcagtaacatttgtaaaatacgttccactaactactcgtt 8872
DB 61 GCTTATTTTCTAGTACAGTAAACATTTGTAAAAATFACTGTTTCACTAATCTACTGTT 120
QY 8873 aactgtcttgagagaaaaaataatagagagactatgtttggggaagtcaagtat 8932
DB 121 AACTGCTTGAGAGAAAAAATAATAGAGACTATGTGGGGAAGTTCAAGTGAT 180
QY 8933 ctttaataatcattactactctccacttttccaaaattgtaataatacgttaag 8992
DB 181 CTTTCAATATCACTACTACTCTTCCACTTTTCCAGATTTGAATTAAGCTAAAG 240
QY 8993 ggttaagactcaagattcaaatatcttcatatttttaatttacaagatattat 9052
DB 241 GGTAGAGACTTCAAGATTCAATTAATCTTCTATATTTTAAATTTACAGAAATATAT 300
QY 9053 ataaccactgctgtaaaaaaaga-aaatgattgttttagaagttaaagtaataatgat 9111
DB 301 ATMACCCACTGCTGAAAAAGAAACAAATGATGTTTGAAGTTAAAGTCAATATGAT 360
QY 9112 ttttaataagtaagagagcatalttccaactagtagtagagcagtcgttcaatt 9171
DB 361 TTTAAATTAATGAATGAAGAGCATATTTCCAAATACATGATGATGAGCATCTGCAATT 420
QY 9172 taacagatctcaaaaatacagaatttataagaataaattctccactaataatttca 9231
DB 421 TACAGATCTTCAAAATAACAGATTTATAGAAATATTTCTCCTCATTAATATTTTCA 480
QY 9232 aaatcaaatatgatgttccctcaatttactaaatcgttacttaacttccatatagta 9291
DB 481 AATCAATCAATTAATGATGTTTCTCTCTTACTTAAATGATTTCTTCAATTAATAGTA 540
QY 9292 aatctatgagcaactcctactactcgttctcctcgtatgattca-aggccatatttcaaaat 9350
DB 541 AATCTTATGAGCACTCTTACTTCTGTTCTCTGATTTTCAAGGCCATATTTTACAAAT 600
QY 9351 caaaagcactgtgaactatttgaagaacaacagacatttataacagattgaagac 9410
DB 601 CACAAGGCACTGTGACATATTTTGAAGAAACACACATTTTAATACAGATTGACAGGAC 660
QY 9411 cctctctgaagctagaacaacatcatagttatacatctcatca 9454
DB 661 CTCTCTTGAAAGCTAG-ACCAATCTATAGTTAATCTTCAATTA 703

RESULT 4

LOCUS B1854140 854 bp mRNA linear EST 10-OCT-2001
DEFINITION 603381449F1 NIH_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5388972 5',
ACCESSION B1854140
VERSION B1854140.1 GI:15994887
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 854)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL1991 row: b column: 13
High quality sequence stop: 801.
Location/Qualifiers
1..854

FEATURES

source

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5388972"
/clone_1b="NIH_CGAP_Mam4"
/tissue_type="tumor, gross tissue"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: oligo dT.
Average insert 2.5 kb. Library constructed by Life
Technologies, catalog # 12018-016. Investigators providing
samples: Lothar Hennighausen/Priscilla Furth, NIH
Reference for transgenic model: Li et al., Cell Growth and
Differentiation 7, 3-11 (1996). Note: this is a NCI_CGAP
Library."

BASE COUNT 238 a 198 c 227 g 191 t
ORIGIN

Query Match 6.1%; Score 639.8; DB 10; Length 854;
Best Local Similarity 88.1%; Pred. No. 1.1e-59;
Matches 753; Conservative 0; Mismatches 97; Indels 5; Gaps 5;

QY 6040 tgaagaagatataatagaagaagcgaagcctgtctgttgaagagttgcgtggca-tt 6098
DB 4 TGACCAAGATCATATATGAGAGAGAGGAGGAGCCTGCAGTCGACAGATGTCATCGCAGTC 63
QY 6099 cctctgtgagtgcttctgggctcctgggagttatagggcttgaataatacataacttc 6158
DB 64 CTTCCCGAGAGAGTGTTTGACTCCTGTGGAGTTAAGGAGCTGGGAAGTCAACACTTTTC 123
QY 6159 aagatgttaacagagatataccactgttaccagagagatgttcccttaacaataatagt 6218
DB 124 AAGATCTGACTGGAGAACCCCTGTGACAGAGGAGATGGCTTCTTAACAAAAACAGC 183
QY 6219 atctataaacaatcatalgaatatacagaacalgggctactgcccctcaattgtagcc 6278
DB 184 ATCTATCAAAATATATCATGAAGTACACCAACATGGGCTACTGCCCTCACTTTGAGGCC 243
QY 6279 atcaagagcctgtgactcgggagagaaacagtggaattcttgcctttgaagaagagtc 6338
DB 244 ATTCACAGAGCTGCTGACGGAGAGAGCATGTGGAGTTCTTTGGCCTCTAGGGAGTCC 303
QY 6339 ccagagaagaagttggaagttgtagtgggagcttgcgaactlbggctcgtgaag 6398
DB 304 CCAGAAAAGGAAGTTGGCAAGTTGTGATGGCAATTTGCCAAACTGGGCTGTGTAAG 363
QY 6399 tatgagaanaatatgctgtaactatagtggaagcaacaagcgaagcttctacagcc 6458
DB 364 TATGAGAGAAAATATATGACAGTACAGTGGCGGCAACAAACGACTCTCCACAGCC 423
QY 6459 atgagcttgatcggcgccctccctgtgtgttctcgtatgaaccacacagagcatgat 6518
DB 424 ATGGCTTTGATTGGGGGACCTTCGTGTGTGTTCTGATGAACCAACACAGGATGGAC 483
QY 6519 ccacaagccggcggttcttggaatgtgcccataatgtgttcaagaagagagatca 6578
DB 484 CCTAAAGCCGAGATTTCTTGGAATGTGCCCCCAACATTTGCAAGAGGAGGAGATCT 543
QY 6579 gtatgcttatactcatagataggaagaatggaagcttgcactagaatgagcatc 6638
||||| ||||||| ||||||| ||||||| ||||||| ||

Db 544 GTAGTCCCTACATCTAGTATGGAAGAAATGTAAGCTCTTTGTACAAAGATGGCCATA 603
Qy 6639 atgagcaatgaaggttcaagtgcttgcaagtgctcaagcattcaaaataagtttga 6698
Db 604 ATGTGCAATGGAAGGTTGAGGTGCTTGGCAGTGTCCACATCTGAAAAACAGGTTCCGA 663
Qy 6699 gatgttatacaatagtttgaagataagcaggcaccgagcctgaagcctgcag 6758
Db 664 GATGTTATCAATAGTGTGACGAATAGCAGGCTCCACCTGACCTGAAGCCTGTCCAG 723
Qy 6759 gattcttgacttgcaatctcctggaagtgcttaagaagaacacgggaacatgcta 6818
Db 724 GA-GTCTTTGAGCTTGCTTACCGGAGAGTGTCTTAAGAGAAA-ATGACACATGCTT 781
Qy 6819 caatcaagcttccatctcattatctctcgtccagagatattcaacatctcctccag 6878
Db 782 CAGTACCAAGCTTCCATC-TCCTTGTATCTCTAGCCAGATA-TCAGCATCTCTCCAGA 839
Qy 6879 agcaaaaagagactc 6893
Db 840 AGCAACAGCGGACTC 854

RESULT 5
LOCUS BG436050 640 bp mRNA linear EST 14-MAR-2001
DEFINITION 602508836F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4619552 5',
mRNA sequence.
ACCESSION BG436050
VERSION BG436050.1 GI:13342556
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 640)
NIH-MGC <http://mhc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLOMTECH Laboratories, Inc.
CDNA Library Preparation: CLOMTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1CM1379 row: g column: 09
High quality sequence stop: 635.
Location/Qualifiers
1. 640
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4619552"
/clone_lib="NIH_MGC_79"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: placenta; Vector: pDNR-LIB (Clontech);
Site.1: SfiI (ggccgctcgcc); Site.2: SfiI (ggccattatggc
) 5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGGCGCGCATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
library."

BASE COUNT 233 a 97 c 74 g 236 t
ORIGIN
Query Match 6.1%; Score 633.2; DB 10; Length 640;

Best Local Similarity 99.5%; Pred. No. 6.6e-59;
Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8718 gctcaaatcttctacatctcctcaactagcagaagaaatataaaacacaaatct 8777
Db 1 gctcaaatcttctacatctcctcaactagcagaagaaatataaaacacaaatct 60
Qy 8778 tccatattgagcattttcagagtttctcaaccagctcttatttctctagcaglaaca 8837
Db 61 tccatattgagcattttcagagtttctcaaccagctcttatttctctagcaglaaca 120
Qy 8838 ttgtcaaaaacacgcttcaactactactgttactgtctctgagagaagaagaat 8887
Db 121 ttgtcaaaaacacgcttcaactactactgttactgtctctgagagaagaagaat 180
Qy 8898 atgaagaacactgtttgtgggaagttcaagtgatctcttcaatactactactctc 8957
Db 181 ATGAGAGAACTATGTTTGGGGAAGTTCAAGTATCTTTCAATATCTACTAATCTT 240
Qy 8958 ccaacttttccaaaatttgaaatataacgctaaagtgtaagacttcaagatttcaatta 9017
Db 241 CCACCTTTTCCAAAATTGAAATATTAAAGCTAAAGGTAGACTTCAGATTTCAAATTA 300
Qy 9018 atcttctatatcttcttaattcaagatatataaccactgctgaaaaaaga 9077
Db 301 ATCTTTCTATATTTTAAATTTACAGAAATATTAATTAACCCAGCTGAGAAAAAGAAA 360
Qy 9078 aatgattctttagaagttaaagcaaatatgatttcaatataagtaagaaagcatt 9137
Db 361 AATGATGTTTTTAAAGTTAAAGCAATATGATTATTAATTAATTAAGTAAGCAAGCAT 420
Qy 9138 ttccaataactagtgatagtgatcggttgcaatttcaagtatcttcaaaaatagcaatt 9197
Db 421 TTCCAAATTAAGTATGATATGCAATGCTGCAATTTTAAAGTATTCAAAATATAGATTT 480
Qy 9198 tatagaataatttcccccattatatttcaaaatcaagtgatgcttctcatt 9257
Db 481 TATGAATAATTTCCCATTTATATTTTTCAAAATCAAAAGTTATGTTTCTCATTTT 540
Qy 9258 lactaaatcgtatctcaattctcattatagtaaatctatgagcaactcctactcgg 9317
Db 541 TACTAAATCGTATCTATCTATCTTCAATATAGTAAATCTATGAGCAACTCTTACTCGG 600
Qy 9318 ttccctgattcaagccatattttaaataataaa 9355
Db 601 TTCCTGATTTCAAGGCAATATTTTAAATATCAAAA 638

RESULT 6
LOCUS B1182779/c 878 bp mRNA linear EST 10-JUL-2001
DEFINITION UNL-P-FN-bp-c-01-0-UNL.s1 UNL-P-FN Sus scrofa cDNA clone
UNL-P-FN-bp-c-01-0-UNL 3', mRNA sequence.
ACCESSION B1182779
VERSION B1182779.1 GI:14657188
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE 1 (bases 1 to 878)
AUTHORS Caetano,A.R., Johnson,R.K. and Pomp,D.
TITLE Generation and sequence characterization of a normalized cDNA
library from swine ovarian follicles
JOURNAL Unpublished (2001)
COMMENT Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
Email: dmpomp@unl.edu
The sequence contained an oligo-dT track that was present in the

QY	8705	atgaatctgcagctcaaatcttctcaatctcaacacacagcagaagaataataa	8764
Db	194	ATTAAATCTGCAGCTCAAAATTTTTCATCTCTTCAATCACTAGTCAGAAAAATATATA	253
QY	8765	aacaacaatacttcacataatgagacatttltcaagattltcacaacagctcttaatttc	8824
Db	254	AACAACAATCTTCCATATGAGCATTTTTCAGAGTTTTCATCAACCCAGTCCTTATTTTTC	313
QY	8825	tagtcaagaaacatttgrtaaaatctgcttccaactaactactcgttcaactgcgtcag	8884
Db	314	TAGTCAGTAAACATTTGTAAAAATTCCTTTTCACATTAATCTTACTGTTACTGTTGAG	373
QY	8885	agaaaagaaaaataatgagagaactattgtttcgagggaagctc-aagltgacttcaatc	8943
Db	374	AGAAAAGAAAAATATGACAGAACCTATGTTGGGAGATTCAAATGATCTTTCAATATTC	433
QY	8944	attactaactcttcacatttltccaaaaatttgaatataaagcctaaagtgtaagactt	9003
Db	434	ATTCTACTCTTCTTCCACTTTTTCACAAATTTGAATATTAAGCTTAAGAGtgTAAAGC-T	492
QY	9004	cagatttcaaatatactcttcacataatttlttaaatlttcagaataatlatataccacatg	9063
Db	493	CAGATTTCAAATTAATCTTCTTCTATTTTTTTAAATTTACAGAAATATATATATATCCAC	552
QY	9064	ctgaaaagaagaaaaatgatgttltgaagaatgaagccaatattgattttaaataatag	9123
Db	553	CTGAAAAAGAAAAAATATGATGTTTTCAGAGTTAAAGCTTAAGCATATTTGATTTTAAATAT	612
QY	9124	taatgaagcatalatttccaatactagt-gatatagcactcgttgcattt	9172
Db	613	TAAATGAAGCATATTTCCATTAAGTAGATGATGATGATGATGATGATGATGATGATGAT	662
RESULT	8		
AU135588			
LOCUS		736 bp	linear
DEFINITION	AU135588 PLACE1 Homo sapiens CDNA clone PLACE1002437 5', mRNA		EST 24-OCT-2000
ACCESSION	AU135588		
VERSION	AU135588.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 736)		
	Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,		
	Yamamoto,T., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and		
	Isogai,T.		
TITLE	HRI human cDNA project		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Takao Isogai		
	Genomics Laboratory		
	Helix Research Institute		
	1532-3 Yana, Kisarazu, Chiba 292-0812, Japan		
	Tel: 81-438-52-3851		
	Fax: 81-438-52-3852		
	Email: genomesehri.co.jp		
	HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix		
	Research Institute; cDNA library construction; Department of		
	Virology, Institute of Medical Science, University of Tokyo, and		
	Helix Research Institute.		
FEATURES			
SOURCE	Location/Qualifiers		
	1..736		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="PLACE1002437"		
	/clone_lib="PLACE1"		
	/tissue_type="placenta"		
	/note="Vector: pMT185FL3"		
BASE COUNT	163 a 199 c 199 g 170 t		5 others
ORIGIN			

[illegible]

Db	241	TTCAAAATTTCTGCTTTTGCATCTTTGGGACACCTCAGAAAACCTATTATTAACACGTGTA	300
QY	9674	ataatgaagaatacagaagaanaataatgaagccctatacatataatgcccagacaattca	9733
Db	301	ATATGAGAAATACAGACGAAATAATATTAAGCCCTTATACATATAAGCCGACCAATTCA	360
QY	9734	tgtttaaaaaaacaacaacctcacacactgatttcatattctcgtactgtaagaacat	9793
Db	361	TTGTTAAAAAACCAACCAACCTCACACACTACGTATTTCCTTTCGTACTGAAACCAAT	420
QY	9794	gcttctgactacttaaatctgtgcacatcatcattcaactgtaagtaatcatctgactaa	9853
Db	421	GC-TTGTGACTATTAAATGTTGCACATCATTTATTTCACCTGTAAGTAATCATTTGACTTAA	479
QY	9854	gccatttg-cctgcttcttctctctcgtgntgnatata-tcaggttaaaatattttcoaaag	9911
Db	480	GCCATTGTGCTGTGTTTCTTCTGTGGTGTATATATTCAGGTAAATATTTTCCAAAG	539
QY	9912	agccatctgctaatcgtaaactcgaacccttgataltgagacaataattggaaccttgg-	9970
Db	540	AGCCATGTGTCATGTAAATACATGAACACTTTGATATTGAGACATTAATTGTACCCCTGGT	599
QY	9971	tattatctactagaataatgata-----ctnagaagaatctgctcctaattcttcaa	10024
Db	600	TATTATCTACTAGTATTAATGTAAATACTGTACGAGAACATATGGTCTATATCTTTTTCAA	659
QY	10025	aatgctcatcccccttaaanagtctattacc	10057
Db	660	AATTTGCTGCTCCCTTTTAGAATGTTCTATTTCC	692

RESULT	11
LOCUS	AL048638
DEFINITION	AL048638 631 bp mRNA linear EST 29-FEB-2000
ACCESSION	DK22P564A1364_r1_564 (synonym: hdbir2) Homo sapiens cDNA clone DK22P564A1364, mRNA sequence.
VERSION	AL048638
KEYWORDS	AL048638.3 GI:5927971
SOURCE	EST.
ORGANISM	human. <i>Homo sapiens</i> Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 631) Duesterhoefl,A., Labber,J., Mewes,H.W., Gassenhuber,J. and Wiemann, S.
TITLE	EST (Duesterhoeft, et al.) Unpublished (1999)
JOURNAL	On Apr 30, 1999 this sequence version replaced gi:5866336.
COMMENT	

Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No s1 sequence available.
This clone (DKRP564A1364) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..631

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PKR2p564A1364"
/clone_lib="564 (Synonym: hfb2) "
/risseq_type="brain"
/dev_stage="fetal"
/lab_host="X1-2bue"
/notes="Vector: pAMP1, 229 a 93 c 86 g 220 t 3 others"
BASE COUNT

```

ORIGIN

Query Match	5.4%	Score 567.8;	DB 9;	length 631;
Best Local Similarity	99.0%;	Pred. No. 6.4e-52;		
Matches 591;	Conservative	0;	Mismatches 4;	Indels 2;
				Gaps 2;

QY	8525	ttttttttttttttaaattgcaacaatgcgaagaacccaagaatgataaggttcacagt	8584
DB	28	tttttttttttttttaattgcaacaattgcgaagaacccaagaatgataaggttcacagt	87
QY	8585	ttaacaacatgaattctctcaacagggaaaaacagctagctgtgaaaactctgtgaaaaaaca	8644
DB	88	ctaaacaaatgaattctctcaacagggaaaaacagctagctgtgaaaactctgtgaaaaaaca	147
QY	8645	acttgctttatagcatttagtaaccttcaaaataattgctctgcagatatgtatacccc	8704
DB	148	acttgctttatagcatttagtaaccttcaaaataattgctctgcagatatgtatacccc	207
QY	8705	attaatctgcagagctcaaatctttcaatctcttcaatcactagcagaagaataataa	8764
DB	208	attaatctgcagagctcaaatctttcaatctcttcaatcactagcagaagaataataa	267
QY	8765	aacacaacaattccatcatatgagcagattttcaagattttcctaaccagctctaatcttc	8824
DB	268	aacacaacaattctccatcatatgagcagattttcagaattttcctaaccagctctaatcttc	327
QY	8825	tagtcaagtaacaatttgcataaaatcactgctttcactaatactactgcttaactgcttgag	8884
DB	328	tagtcaagtaacaatttgcataaaatcactgctttcactaatactactgcttaactgcttgag	387
QY	8885	agaaaagaaaatagagagagaactatgcttttgaggagaagtcagaagatcttcaataa	8944
DB	388	agaaaagaaaatagagagagaactatgcttttgaggagaagtcagaagatcttcaataa	447
QY	8945	ttaactaactctctccactctttccaaaatcttgaatataaagctaaaggtgtaagacttc	9004
DB	448	ttacttaactctctccactctttccaaaatcttgaatataaagctaaaggtgtaagacttc	506
QY	9005	agatttcaaatatccttctctatattttttaaattacagaatataataaaccactgc	9064
DB	507	agatttcaaatatccttctctatattttttaaattacagaatataataaaccactgc	565
QY	9065	tgaagaagaaaaatgcttggcttgaagaagttaaagctaaatcttgaattttaaata	9121
DB	566	tgaagaagaaaaatgcttggcttgaagaagttaaagctaaatcttgaattttaaata	622

RESULT	12
BEB79545	
LOCUS	BEB79545
DEFINITION	BEB79545 784 bp mRNA linear EST-20-OCT-2000 601491738r1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893912 5' , mRNA sequence.
ACCESSION	BEB79545
VERSION	BEB79545
KEYWORDS	BEB79545.1 GI:10328425
SOURCE	EST..
ORGANISM	human.. Homo sapiens

REFERENCE	1 (bases 1 to 784)
AUTHORS	NIH-MGC http://mgc.ncl.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Tissue Procurement: DCTD/DTF/Gazdar
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Db	368	AATACCTTCATATGAGCATTTTTCAGAGTTTTCATAACCAGTCTATTTTTCTAGTCAG	309
OY	8832	taaacatttgtaaataacatcgtttcaactaactactgtaactgcttcgtgagaaaag	8891
Db	308	TAAACATTGTGAAAATACACTGTGTTCCATTAATCTACTGTTMACTGCTTGAGAAAAAG	249
OY	8892	aaaatatgagaagaactatctgttggagggaagtcaaagtgatccttacaatcatctaa	8951
Db	248	AAAAATATGAGAGAACCTATTGTTTGGGAGATTCAAGTGAATCTTTCATATCATTACTTA	189
OY	8952	ctctccacctttccaaaaatltyaalataliaacgcclaaaggtgyaagactcacattlc	9011
Db	188	CTTCTTCCACTTTTTCCTAATATTTGAUATTAATTAACGCTTAAGAGTGTAAGCTTCAGATTTC	129
OY	9012	aaattaatcctctatatlttttaaatltaacagaatataataaccacgctgyaaaaa	9071
Db	128	AAATTAATCTTCTCTATTTATTTGTTTAAATGTACAG -ATATATATATTAACCACTGCCTGAAAAA	70
OY	9072	gaaaaaatgatgttgttagaagtttaagatcataatgttatatttaataataatgaag	9131
Db	69	GAGAGAAATGATGATGTTTATAGAAGTAAGTCATGACTGATTTTAAATATATAATATGAAG	10
OY	9132	gcataattt 9139	
Db	9	GAGATGT 2	
RESULT	14		
LOCUS	BFS74391		
DEFINITION	602131601.F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270752 5', mRNA sequence.	771 bp	mRNA linear EST 12-DEC-2000
ACCESSION	BFS74391		
VERSION	BFS74391.1	GI:11648103	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: rsraubs@mail.nih.gov Tissue Procurement: CLONETECH Laboratories, Inc. cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: LICM1082 row: b column: 01 High quality sequence stop: 637. Location/Qualifiers I..771		
FEATURES			
source			

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1IMAGE:4270752"
/clone_1ID="NH.MGC_81"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: muscle (skeletal); Vector: pDNR-L1B
(Clontech); Site_1: Sfil (ggcgctgtggcc); Site_2: Sfil
(ggcctatgtggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTTCAGAGCCCGAGGGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

```

BASE COUNT	271 a	115 c	121 g	264 t
Query Match	5.3%	Score 549.4;	DB 10;	Length 771;
Best Local Similarity	94.4%;	Pred. No. 5.4e-50;		
Matches 658;	Conservative 0;	Mismatches 26;	Indels 13;	Gaps 8;
OY 9050	tataaacccatgctgtgaaaaaagaataatgattgctttagaagtgataagtcacatg	9109		
Db 1	TATATTAACCCACTGCTGTGAAAAAGAAAAATGATTTGTTTACAACTTAAAGTCATATTTG	60		
OY 9110	atttcaatatagaatgaatgaagacatattccaaatactagatgatalgcatcgttgcaa	9169		
Db 61	ATTTTAAATATATATGAATGAAGGACATATTTCCAAATAACTAGATATGGCATTCG-TGCAT	119		
OY 9170	tttaacagatctctcaaaaaatacagaattatagaataattctcctcaatttaattttt	9229		
Db 120	TTTTACAGATCTCTCAAAAATACAGATTTATAGCAATATTTCTCTCATTTTAATATTTT	179		
OY 9230	caaatcaaatgatacgtgttcctcatlltactaaatcgtatctcaatctctcatatag	9289		
Db 180	CAAAATCAAGTATATAGTTTCTCTCATTTTACATAAATGATATTCATCTTCATATATAG	239		
OY 9290	taaatctatgagcaactcccttactcgtgtctcctgatttcaaggccatatttaaaaa	9349		
Db 240	TAAATCTATGACCAACTCTTCTTCTGCTGCTCTGATTTCAAGGCCATATTTTAAAAA	299		
OY 9350	tcaaaagcagcgtgtaactatttgaagaacaacgcacatttatacagattgaaga	9409		
Db 300	TTAAAAAGGCACCTGTGACACTA-TTTGAAGAAAAACACACATTTTATACAGATGGAAGA	358		
OY 9410	cctctctgaaagctagaacaacatctcatagatatacatcttcaataactgyltacct	9469		
Db 359	CCCTCTTCTGAACCTTGAAAAACATCATATAGTTATACATCTTCATTAATCTGTACCTT	418		
OY 9470	ttaaaatgtaattttttacattttccctgctgtaaacctaatgctgtgtagaattttacc	9529		
Db 419	TTAAAAATAGTAAATTTTTTACAATTTTCCTGTGAAACCTPA-TGTGGTGAATTTTTTAC	477		
OY 9530	aacttatctcaatcaagaacaattctcgtatattccctgctgtaagtgtacatagttag	9589		
Db 478	AA-TCTATATCTAATCAACGACAAATTTCTGTATTTCCCTGTGGAATGACTATGTGAG	536		
OY 9590	tttcsgaaattctcaaaaatcogtltgcaaaaattctcgtctttgcatcttgggacacct	9649		
Db 537	TTTTCGAAATTTCTCAAAATACGCTGTTCAAAAATTTCTCTCTT--GATTTTGGGACACCT	594		
OY 9650	cagaaacttatcaacaactgtaatactgataatgagaatcagaagaanaataataagccctta	9709		
Db 595	CAGAAATATATTT--AAAATGGGAATATAGAGAAAT-CAGAAACAAAATATATAGGCTCTATA	650		
OY 9710	tacataaatgccagacaaatcattcgttaaaaaa 9746			
Db 651	---ATTAAATGCCGCGCAAAATCTTGTTTAAAAAACAAA 684			
RESULT 15				
BS67118	BS67118	648 bp	mRNA	linear
LOCUS	602589265P1 NIH_MGC_76	Homo sapiens	CDNA	clone IMAGE:4723121 5',
DEFINITION	mRNA sequence.			
ACCESSION	BS67118			
VERSION	BS67118.1	GI:13574771		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 648)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			

Mon Sep 16 10:20:04 2002

us-09-595-526b-1.rst

Page 13

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
plate: L1CM1582 row: b column: 18
High quality sequence stop: 639.

FEATURES
source

BASE COUNT	207 a	120 c	84 g	237 t
ORIGIN				

Query Match	5.2%;	Score 545.8;	DB 10;	length 648;
Best Local Similarity	96.1%;	Pred. No. 1.4e-49;		
Matches 622; Conservative	0;	Mismatches 16;	Indels 9;	Gaps 6

QY	9457	acgctgtacccttcttaaaatgaatcttttcaatcttccggtgtaaaccaatctgtgct	9516
Db	1	ACGTGTACCTTTTAAATAGTAATTTTTTTCATTTTCCGTGTAAACCTAATTTGGCT	60
QY	9517	agaatcttaccacactatacctaataagcaaaatctctgatalatccctgtggaat	9576
Db	61	AGAAATTTTACCAACTCTATACCTCAATCAACCAAAATTTCTGTATATTCCTGTGAAT	120
QY	9577	gtaccatctgtgagcttcgagaaatctcaaaataagctgtctcaaaaatcttgcttggcat	9636
Db	121	GTACCAATGTGAAGATTTCAGAAATTTCTCAAAATACCTGTGTCAAAAATTTCTGCTTTTGCAT	180
QY	9637	ctttgggacaccccgagaaactctatcaaatgtgaaatgaaatgaagaatlaagaanaaat	9696
Db	181	CTTTGGGACACCTTCAGAAACTTATTTAACACTGTGAATATGAGAAATATACGAGAAATAAT	240
QY	9697	aataagccctctatacataaattgcgcagacaatctatgtgtaaaaaaacaacaacctc	9756
Db	241	AATPAGCCCTCATATATTAATATGAGCCAGACAAATTCATTGTTACAAAACCAACCAACCTC	300
QY	9757	acacactcgtattctatctctgtacgtgaagcaaatgctttgtgactataaatgttgc	9816
Db	301	ACACTACTGTATTCTCATTTCTGTACTGGAAGCAAAATGCTTTGTGACATTAATATGTGC	360
QY	9817	acactatctatctacgtatagtaatcaatctgactaagaacattg-ctgtgttctctct	9875
Db	361	ACATTCATTCATTCACGTATGTATTAATCATTTGCAATAACCAATTTGCTGTGGTTTTCTTCT	420
QY	9876	tgtgctgtatatacatcaagtaaaatcttccaagaagccatgctgatactaaactgaa	9935
Db	421	TGTGCTGTATATATCAGSTAAATATTTTCCAAAGACCATGTGTATGTAAATACGAA	480
QY	9936	cc-cttghatctgagacatlaatttggaccttgtatcttctactag--aataatgtaa	9993
Db	481	CCACTTGTGATATGACACATTAATTTGTACCCCTTGTATTTATCTACATAGTAATATATGTA	540
QY	9994	tactgnaaataatgtctctlaatctctt--caaaaigtgcatcccccctaanaagtl-ct	10055

Mon Sep 16 10:20:04 2002

us-09-595-526b-1.rst

Page 14

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2002, 07:01:42 ; Search time 277.92 Seconds
(without alignments)
6013.566 Million cell updates/sec

Title:

US-09-595-526B-1_COPY_291_7094

Perfect score:

6804

Sequence:

1 atgcttctgttgcctcagct.....gaagaatccttcatcagc 6804

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:

383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters:

767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/prodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/prodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/prodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/prodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCRTUS.COMB.seq:*
6: /cgn2_6/prodata/2/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	430.8	6.3	5894	3	US-08-665-259-24
2	430.8	6.3	5894	3	US-08-762-500-24
3	430.8	6.3	5894	3	US-08-762-500-24
4	56	0.8	7218	1	US-08-232-463-14
5	52.4	0.8	2726	1	US-08-461-823-1
6	52.4	0.8	4646	1	US-08-181-471-2
7	52.4	0.8	4669	2	US-08-583-276-18
8	52.4	0.8	4669	2	US-08-583-276-18
9	52.4	0.8	6505	2	US-08-793-610-5
10	52.4	0.8	9318	2	US-08-793-610-5
11	52.4	0.8	4403765	4	US-09-103-840A-2
12	52.4	0.8	4411529	4	US-09-103-840A-1
13	50.8	0.7	4264	2	US-08-784-649A-1
14	50.8	0.7	4264	2	US-08-784-649A-5
15	50	0.7	4233	3	US-09-120-513-1
16	49.4	0.7	4233	3	US-09-120-513-1
17	49.4	0.7	4233	3	US-09-120-513-1
18	49.2	0.7	4669	2	US-08-752-447-1
19	49	0.7	5045	4	US-09-390-721-3
20	49	0.7	5045	4	US-09-390-721-3
21	46.2	0.7	7218	1	US-08-232-463-14
22	45.2	0.7	23673	4	US-09-773-816-1
23	44.2	0.6	1526	4	US-08-858-207A-34
24	43	0.6	15367	4	US-09-627-376-3
25	42.4	0.6	1518	2	US-08-997-080-88
26	42.4	0.6	1518	2	US-08-997-362-88
27	42.4	0.6	1518	3	US-08-873-970-88

28	42.4	0.6	1518	4	US-09-095-855-88	Sequence 88, Appl
29	42.4	0.6	1518	4	US-09-324-542-88	Sequence 88, Appl
30	40.8	0.6	1971	4	US-08-858-207A-72	Sequence 72, Appl
31	38.8	0.6	1260	2	US-08-578-158-1	Sequence 1, Appl
32	38.8	0.6	1815	4	US-09-042-785A-24	Sequence 24, Appl
33	38.8	0.6	2186	3	US-08-959-382-1	Sequence 1, Appl
34	38.8	0.6	2612	4	US-09-042-785A-3	Sequence 3, Appl
35	38.8	0.6	2638	4	US-09-042-785A-22	Sequence 22, Appl
36	38.8	0.6	3474	4	US-09-527-236A-11	Sequence 11, Appl
37	38.6	0.6	6909	4	US-09-199-637A-111	Sequence 111, App
38	38.2	0.6	3924	2	US-08-996-644-3	Sequence 3, Appl
39	38.2	0.6	3924	3	US-09-352-552-3	Sequence 3, Appl
40	38.2	0.6	3927	2	US-08-996-644-1	Sequence 1, Appl
41	38.2	0.6	3927	3	US-09-352-552-1	Sequence 1, Appl
42	38	0.6	1209	4	US-08-936-165A-55	Sequence 55, Appl
43	37.8	0.6	732	4	US-08-919-573-3	Sequence 3, Appl
44	37.8	0.6	735	4	US-08-919-573-1	Sequence 1, Appl
45	37	0.5	6688	4	US-09-381-862-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-665-259-24
Sequence 24, Application US/08665259
Patent No. 6028173
GENERAL INFORMATION:
APPLICANT: Landes, Gregory M.
APPLICANT: Burn, Timothy C.
APPLICANT: Connors, Timothy D.
APPLICANT: Dackowski, William R.
APPLICANT: Van Raay, Terence J.
APPLICANT: Klinger, Katherine W.
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
NUMBER OF SEQUENCES: 73
COMPOSITIONS, METHODS OF MAKING AND USING SAME
CORRESPONDENCE ADDRESS:
ADDRESS: GENZYME CORPORATION
STREET: One Mountain Road
CITY: Framingham
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,259
FILING DATE: 17-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
TELEPHONE: (508) 872-8400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 872-8400
TELEFAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 5894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2..5053
US-08-665-259-24


```

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,500
FILING DATE: 09-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,259
FILING DATE: 17-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10469
FILING DATE: 17-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: IGS-9.3
TELEPHONE: (508) 872-8400
TELEFAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 5894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2..5053
US-08-762-500-24

```

```

Query Match      6.3%; Score 430.8; DB 3; Length 5894;
Best Local Similarity 56.1%; Pred. No. Se-122;
Matches 944; Conservative 0; Mismatches 692; Indels 48; Gaps 5;

```

```

QY 1760 ggaagctcgggggggcttcgacttgcagatgtgtgtgagcaggaatcattcagg 1819
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 555 ggagacatcgggggagagccttcctgcccgtcacagatcgttggacgggcatcagagt 614
QY 1820 tgcagcgggcaacagaga-----agaaaactgtgtctatcagcaaga 1864
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 615 accatgccgatgccgcacacacgcacgctgtccagagactgacgggtgacatcaggagt 674
QY 1865 tggccatccctcgttaacgttgatgaatcttcttcgagtgatgagcggatcagccc 1924
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 675 tcccgacccggcgttcacacgacaccccttctcgtgcacatccacagacagcggc 734
QY 1925 tctcatgacgctgacctgagatttactcagtgctgctgatacacaaggcactgtatg 1984
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 735 tgcctcgtcgtcgtcagcttccacacacgctcctcaccattgcccgtcgtcgtgacag 794
QY 1985 agaagagagcagcgtcgaagaagacatcagatcagcctgagccctggaacacagacatc 2044
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 795 agcaagaaagagcgttgaaagagatgacgcatgagggcgtcagcagctgctgacact 854
QY 2045 ggtttagctgtgtctttagttagcctcattcctctctgtgagcgtgagcctgactagtg 2104
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 855 ggagtgccctggtcctcgttcttcttcttcttctcctcattgacgccccttcttcatgaccc 914
QY 2105 tcatcctgaatfta-----ggaacctctgcccctcaagtgatcccaagc 2149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 915 tgccttcttctgctcagtgaaagcgaatgtaagcctgctgtcccgacgacaccccttccc 974
QY 2150 tgggttcttctcctcgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2209
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 975 tgggtcctcgtcctcgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1034
QY 2210 gcaaccttcttcagagcacaactcgtgagagcctgtgtgtgtgtgtgtgtgtgtgtgtgt 2269
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1035 gcaccttctttagcaaaagcacaacagcagcagccttccggagggcttcttcttcttca 1094
QY 2270 tgtacctcctcctcgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2329
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

Db 1095 cctacatccctcacttcttctggtgcccctcgttacacttgatgacttgagccagaaagc 1154
QY 2330 tcttcgtacgctcgtctcgtcctcgttgggttggcgtgagtaacttgcctt 2389
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1155 tctgctcctcgtcctcgttcttcttcttcttcttcttcttcttcttcttcttcttctt 1214
QY 2390 ttgagagcagggcatttgagtcagtgaggaacacctgtttagagctcctgtgaggaag 2449
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1215 ttgagcgaagagcattggcagctcagtgaggaacacctgtttagagctcctgtgaggaag 1274
QY 2450 atggtctcaatcacaaccttgatcctcagatgagctgtttagacacctcctcctatgggg 2509
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1275 acgacttctgcttccggcagctgctgaggaatgctcctcctgagacgtgctgtatggcc 1334
QY 2510 tgatgacctgtgatactttagagctgttcttccagggcagtaaggaatcccaagcctgtgt 2569
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1335 tggtagcctggtacatgagagccgttcttccagggcagctgagacgtgctgtatggcc 1394
QY 2570 atttcccttcacacagctcactgctgttctgaggaagtgatg-----agaaga 2620
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1395 acttcttcatcatgccccttcttcttcttcttcttcttcttcttcttcttcttcttctt 1454
QY 2621 gccacctggttccaaacagagagaatgtaagaatctgcatgaggaaggaacccacc 2680
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1455 aagaagacagctgaccccccagaaagcactcagaaagcagcttcttgaacccagccagag 1514
QY 2681 actgaagctgagcgtgctcctcctcagaaacctgtgtaaaagcttacagagatgagatga-- 2738
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1515 acctggtgcccgggagatcagatcagatcagatcagatcagatcagatcagatcagatcag 1574
QY 2739 ----gtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 2794
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1575 acagggcggcggcgtcagaaacactgaaacctgacagagagcagatcaccctctgctc 1634
QY 2795 ttggcacaatggagcggggaagaacacacatgtaactcctgacgggtgtgtctccccc 2854
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1635 tgggcacacagagtgccgggaagacacacacacacacacacacacacacacacacacac 1694
QY 2855 cgacctggcagcggcctcactcctcgtggaagaagacatcgtctcgtgagatgaagcaatcc 2914
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1695 ccacagtgagcagggcagatcagatcagcagggatgaaatctccagacatggttccagatcc 1754
QY 2915 ggcagaacctgggggtcgtcctccacagataacgtgctgttgaacatgctgactgtgaag 2974
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1755 ggaagagcgttggtgctgtgctgctgctgctgctgctgctgctgctgctgctgctgctg 1814
QY 2975 aacacatcgttctatgcccgttgaagaggtctctcctcagaaacagtcagtcagtcagtc 3034
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1815 agcacctttattttctacgcccagctgaaagggcctgtcagcgtcagaaatgcccctgaagaag 1874
QY 3035 ttgagcagatgagcctcgtgagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3094
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1875 tcaagcagatg----ctcacatcattcggccttgagagcaatggaatcagagagcggct 1931
QY 3095 agctgcaagtgtgaatgcaagaagatcctgtgagccttgagcctgtgtgtgtgtgtgtgtgt 3154
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1932 tcttgcagagggggcagatgagcgcagcttctcattccgcatccctcctatgcagagctcca 1991
QY 3155 aggttgcatcttgatgaaacccaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3214
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1992 aggtgctgatactgagagcagacacacacacacacacacacacacacacacacacacac 2051
QY 3215 gggagcgtgctgagaaatcaccagcaagccgacacatattctcctcacaacacacag 3274
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2052 gggatcttcttccagcgaacaaagtgacccgacacacacacacacacacacacacacacac 2111
QY 3275 atgaagcagcgtcctcgtgagagagatgcaatactcccaatgggaagcgtgtgtgtgtgtgt 3334
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2112 acgagcgtgacgtcgtgagagacccgacacacacacacacacacacacacacacacacacac 2171
QY 3335 ttgggtcctcctcgttcttctgaagaacacagcgtggaacagcctactacagccttggatca 3394
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2172 gcgggtcctcgtcgttcttctcagacagaaatagcgtccggcgtatcagatgacgctgtgca 2231

```

OY 3395 agaa 3398
111
Db 2232 AGGA 2235

RESULT 3
US-08-762-500-74

: Sequence 74, Application US/08762500
: Patent No. 6030806

GENERAL INFORMATION:

: APPLICANT: Landes, Gregory M.

: APPLICANT: Burn, Timothy C.

: APPLICANT: Conners, Timothy D.

: APPLICANT: Dackowski, William R.

: APPLICANT: Van Raay, Terence J.

: APPLICANT: Klinger, Katherine W.

: TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,

: NUMBER OF SEQUENCES: 83

: CORRESPONDENCE ADDRESSES:

: ADDRESSEE: GENZYME CORPORATION

: STREET: One Mountain Road

: CITY: Framingham

: STATE: Massachusetts

: COUNTRY: United States of America

: ZIP: 01701

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent Release #1.0, Version #1.30

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/762,500

: FILING DATE: 09-DEC-1996

: CLASSIFICATION: 435

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 08/665,259

: FILING DATE: 17-JUN-1996

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: PCT/US96/10469

: FILING DATE: 17-JUN-1996

: ATTORNEY/AGENT INFORMATION:

: NAME: Dugan, Deborah A.

: REGISTRATION NUMBER: 37,315

: REFERENCE/DOCKET NUMBER: IGS-9.3

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (508) 872-8400

: TELEFAX: (508) 872-5415

: INFORMATION FOR SEQ ID NO: 74:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 6525 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: MOLECULE TYPE: cDNA

: FEATURE:

: NAME/KEY: CDS

: LOCATION: 573..5684

: US-08-762-500-74

: Query Match

: Best Local Similarity 56.1%;

: Matches 944; Conservatively 0; Mismatches 692;

: Indels 48; Gaps 5;

: Length 6525;

: Pred. No. 5.4e-122;

: DB 3;

: Score 430.8;

: DB 3;

: Length 6525;

: Pred. No. 5.4e-122;

: DB 3;

: Score 430.8;

: DB 3;

: Length 6525;

: Pred. No. 5.4e-122;

OY 1865 tgcctatccctgttactgtatgacatcttctgcgggtgtagaaccggtatcagccccc 1924
1306 TCCGTAACCCGCGCTTCATGACAGACCCCTTCTCTGCGCATTCAGTACAGCGCCCC 1365
OY 1925 tcttcataagcctgctgattactcagtgctgtagatcaatcaaggatcgtatg 1984
1366 TGGTGGCGCTGCTACCTTACCTACACCGCGCTCACATGCGCCGCTGCTGTCAGG 1425
OY 1985 agaaagagcagcgtgaaagagacatcgtgtagatcagcctgagcagacatcct 2044
1426 AGAAGAAAG 1485
OY 2045 ggttagagctgattcattagagcctatccctctctctctgagcgtgctgtag 2104
1486 GGAAGTGGCTGCT 1545
OY 2105 tcatcctgaagta-----ggaacctgctgacctcagtgatcccaag 2149
1546 TCGCTCTGTCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 1605
OY 2150 tgggtgttct 2209
1606 TGGTGTGCGCTGCT 1665
OY 2210 gcaacctcttcacagacacacacacacacacacacacacacacacacacacac 2269
1666 GCACCTTCTTACGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1725
OY 2270 tgaactgacctacgctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2329
1726 CCAATACCT 1785
OY 2330 tcttcgtacgctgctgtctctctctctctctctctctctctctctctctct 2389
1786 TGTGCTCTGCT 1845
OY 2390 ttagagagcagcgtatgagatgagatgagatgagatgagatgagatgagatg 2449
1846 TTGAGGCGAAAG 1905
OY 2450 atggttcaatcacaacacacacacacacacacacacacacacacacacacac 2509
1906 ACGACTTCTGCTGCGCGAGGCTGCGGAGGAGTCTGCTGCTGCTGCTGCTGCT 1965
OY 2510 tgaactgctgtagatgagatgagatgagatgagatgagatgagatgagatg 2569
1966 TGGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2025
OY 2570 atttccttgacccaagcctcactggttgcgaggaagtgtg-----aga 2620
2026 ACTTCTTATCATGCGCTCTATTTGTTGGAGAGAGAGAGAGAGAGAGAGAGAG 2085
OY 2621 gcaacctggttccaacagagagatgtagaattcgtatgagagagagagagag 2680
2086 AAG 2145
OY 2681 acttgaagctggtggtggtggtggtggtggtggtggtggtggtggtggtg 2738
2146 ACTGTTGGCGGGGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCA 2205
OY 2739 ----gttgctgtgtagtgcctgacatgattttagagagcagatcactctcc 2794
2206 AAG 2265
OY 2795 tgggcaacaatgagcggggaagagacacacacacacacacacacacacacacac 2854
2266 TGGGCGCAAG 2335
OY 2855 cgaactcgggacacgctacatcctcgtggaagaacatcgtccttgaagttag 2914
2326 CCACAGTGGAG 2385

```
0Y      2915    ggcgaaccbbggggtcttgccccagcaaaagtgttgttaacbtgatcvtcgagg   2974
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2386    GGAAGACGCTGGGCCCTTGCCCGCAGCACACTTCGTITTTAACAACTTGGACGTGCAG   2445
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      2975    aaacaatctgttcatatgatcccgctltgaagaagtcctctaagaagcaactlgaagcgagga   3034
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2446    AGCAACCTTTATTTTCTACGCCCACTGAAGGGCCTGTACAGTCAAGAAGTACCCTGAAGAAG   2505
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      3035    tlgagcagatatgcccttgatalgtttgtttgcatacaaagcttgaanaagcaaacagccc   3094
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2506    TCAAAGCAAGATTG--CTGCACATCATCGGCTGGAGGACAAGTAGAACAATCACGAGCCGCT   2562
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      3095    agctgtcaagtgtgaattgcagaagaactatctgtgaccttgaccettgttcgysggatta   3154
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2553    TCCTGAGCGGGGGGATTAAGCGCAAGCTCTCCATCGGATCGCCCCCTCATCGAGGCTCCA   2622
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      3155    agutgtcatctcttgatgaaccaacagactgtgttgagaccttacctccgaggggaalat   3214
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2623    AAGTGTCTGATACTGGACGACCCACTCGGGCATGTGACGCCATCTCCAGAGAGGCGCATCT   2688
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      3275    atgaagcggagcgtctctgggggaagaagattgccaatctccaatyggaaagctgtgctgy   3334
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2743    ACGAGGCTGACCTTCCTGGGAGCCGATCGCCATCATGGCCAAAGGGGGGAGCGAGTCT   2802
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      3345    tggagctctccctctgtttcttaaagaacagcttggaacagcgtcacactacgttagcttgy   3394
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     2803    CGGGGTCTCTGCTTCTTCCTAACGACAAAATACGGTTCGGCTATCATGACCTGTGTGA   2862
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      3395    agaaa   3398
          ||| |
Db     2863    AGGA   2866

RESULT       4
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
```

```

: TELEPHONE: (703)836-9300
: TELEFAX: (703)683-4109
: TELEX: 899149
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7218 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: CLONE: PTZgpt-F15
: US-08-223-463-14

Query Match      0.8%, Score 56, DB 1, Length 7218;
Best Local Similarity 5.6%; Pred. No. 4, 9e-06;
Matches 23; Conservative 221; Mismatches 166; Indels 0; Gaps 0.

QY 4930 taagagtgagcctctatgaccacatcagtgagatgtccctgtgtlccatctggtlcatctt 4989
      || || || || || : : : : : : : : : : : : : : : : : : : : : : : :
DB 1050 TCGAGGAGCCTTGCATATATATATATATATATATATATATATATATATATATATATATAT 1109
QY 4990 gcaatgctctgtccacagcagcttgtcgtatccatccagagcgggtcagcaaa 5049
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1110 YTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1169
QY 5050 gcaaaacactgcagltcatcagtgagtgaaagcctgcatctactgactctaaattt 5109
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1170 YTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1229
QY 5110 gctctggatattgcaataagctgtccctgccacactggtcatatatactctcaatcgc 5169
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1230 YTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1289
QY 5170 ttccagcagaagctcctatgtgtccctccaccatctgcctgtcagcctctactttg 5229
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1290 YTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1349
QY 5230 ctgtatgggtggtcacaacacctcctcatgtaaccagcctccttltgttcaagatcccc 5289
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1350 YTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1409
QY 5290 agcacaacctatgtgtgtctcaccacgctgaacctcttcatgtgcattaa 5339
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1410 YTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTATCTCTTTAA 1459

RESULT 5
US-08-461-823-1
: Sequence 1, Application US/08461823
: Patent No. 5593840
: GENERAL INFORMATION:
: APPLICANT: Bhatnagar, Satish K.
: APPLICANT: George Jr., Albert L.
: APPLICANT: Nazarenko, Irlina
: TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACID SEQUENCES
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: OncorPharm, Inc.
: STREET: 200 Perry Parkway
: CITY: GaitHERsbury
: STATE: Maryland
: COUNTRY: USA
: ZIP: 20877
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/461,823
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 435

```

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/168,621
 FILING DATE: 16-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/010,433
 FILING DATE: 27-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Karla, Glenn E.
 REGISTRATION NUMBER: 30,649
 REFERENCE/DOCKET NUMBER: PA-0012 CIP 2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301 208-6997
 TELEFAX: 301 208-6997
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2726 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 US-08-461-823-1

Query Match 0.8%; Score 52.4; DB 1; Length 2726;
 Best Local Similarity 46.7%; Pred. No. 3e-05;

Matches 253; Conservative 0; Mismatches 271; Indels 18; Gaps 2;

QY 2750 atggcctgacatgaattttatgagggccagatcacctcctctcctgagccacaatgag 2809
 Db 1665 AGGAGCTGAGCTGGAGAAAGAGGCGGACGCTGCTGAGGAGGAGGAGGAGGAGGCT 1724
 QY 2810 cggggaagaagcagaccatgcaatcctgacgggtgtgttccccccgagcagcagc 2869
 Db 1725 GTGGGAAAGACAGTGTCTCAAGCTCTGAGGCGGTTCTAGACACCCCTTGGCAGGAAAG 1784
 QY 2870 cctacatcctggaagaagacat--tcgctctgagatgagcacaatccgagcagcctg 2926
 Db 1785 TGCTGCTTGAATGGCAAGAAATAAAGGACTGAATGTTCAAGTGGCTCCGAGCAGCCTGG 1844
 QY 2927 gggctgtccccagacatacgtgtgttgacatgctgactgtcgaagaacacatcgtg 2986
 Db 1845 GCATCGTGTCCAGAGACCCATCCTGTTTACTGACAGCATTTGCTGAGAACATTGCCCTATG 1904
 QY 2987 tctatgcccgttgaagaagcctctctgagaagcagctgaaagcgagatgagcagatg 3046
 Db 1905 GAGCAACACAGCCGGGTGTGTACAGAGAGATCGTGAAGGAGCAAGAGGAGGCCAACA 1964
 QY 3047 ccttgatgtgtgttgccatcaagcagctgaaag-----caaaacaa 3091
 Db 1965 TACATGCCCTTCAATCGACTGCTGCTAATAATATAGCACTAAAGTAGAGACAAAGGAA 2024
 QY 3092 gccagcgtcagatgagatgacagaaagctatctgtgagccttgagccttgttcggggat 3151
 Db 2025 CTGAGCTCTGTGGGCAAAACAAACGCAATGCTGCTGCTGCTTTTGAAGCAGC 2084
 QY 3152 ctaaggttgcatctgagatgaaccccaagcgtgtgtgagcccttactcccgagaggaa 3211
 Db 2085 CTGATATTTGCTTTTGGATGAAGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2144
 QY 3212 tatggagcgtcgtcgtgaataacagacaagccgacacattatctcttaacacacaa 3271
 Db 2145 TCCAAAGAGCCCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2204
 QY 3272 tg 3273
 Db 2205 TG 2206

RESULT 6
 US-08-181-471-2
 ; Sequence 2, Application US/08181471

Patent No. 5641508
 GENERAL INFORMATION:
 APPLICANT: Li, Lingna
 APPLICANT: Ishiko, Valeryl K.
 TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL
 TITLE OF INVENTION: COMPOSITIONS TO HAIR FOLLICLES
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Thomas Fitting
 STREET: 12526 High Bluff Drive, Suite 300
 CITY: San Diego
 STATE: CA
 COUNTRY: USA
 ZIP: 92130
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/181,471
 FILING DATE: 13-JAN-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/041,553
 FILING DATE: 02-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: ANT0029P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-792-3680
 TELEFAX: 619-792-8477
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4646 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: CDS 14267
 LOCATION: 425..4267
 US-08-181-471-2

Query Match 0.8%; Score 52.4; DB 1; Length 4646;
 Best Local Similarity 46.7%; Pred. No. 4.5e-05;
 Matches 253; Conservative 0; Mismatches 271; Indels 18; Gaps 2;

QY 2750 atggcctgacatgaattttatgagggccagatcacctcctcctgagccacaatgag 2809
 Db 3585 AGGAGCTGAGCTGGAGTGAAGAGGCGCAGACGCTGCTGTGAGGAGCAGAGTGGCT 3644
 QY 2810 cggggaagaagcagaccatgcaatcctgacgggtgttccccccgaccccgagcagc 2869
 Db 3645 GTGGGAAAGACAGTGTGTCAAGCTCTGAGGCGGTTTACAGACCCCTTGGCAGGAAAG 3704
 QY 2870 cctacatcctgggaagaagacat--tcgctctgagatgagcacaatcccgagcagcctg 2926
 Db 3705 TGCTGCTTGAATGGCAAGAAATAAAGCAGCTGAATGTTCACTGCTGCTGCTGCTGCTGCT 3764
 QY 2927 gggctgtccccagataagctgtgttgatgacatgctgactgtcgaagaacacatcgtg 2986
 Db 3765 GCATGCTGTCCAGAGGCCATCTCTGTTGACTGACGATTTGCTGAGAACATTGCTTATG 3824
 QY 2987 tctatgccgcttgaagaagcctctctgagaagcagctgaaagcgagatgagcagatg 3046
 Db 3825 GAGCAACACAGCCGGGTGTGTACAGAGAGAGATCGTGAAGGAGCAGCAAGAGAGGCCAACA 3884
 QY 3047 ccttgatgtgtgttgccatcaagcagcgtgaaag-----caaaacaa 3091

Accession	Sequence	Position
Db	3885 TACATGCTTCATCGAGTACTGCTCCATAAATAATATGACCTAAAGTAGACAGCAAAAGAA	3944
Oy	3092 gccagcgcgtacagtgtaatcagaagaagctacgtggtgacctggcccttgcgcggagat	3151
Db	3945 CTCAGCTCTCTGGTGGCCAGAAACGCAATTCGCTAGCTGTGTCCTTGTGTAGACAGC	4004
Oy	3152 ctaaggtgtcattcattctgatatgaaccacaagactggtgtgtaaccttactccgcaggagaa	3211
Db	4005 CTCATATTTTGGCTTTTGGATGAAGGCCACGCTCCTGTGATTCAGAAAGTGAAGGTTG	4064
Oy	3212 tatggagagcctgcctgtaaataccgacaagacgcgacacattctctctacacacaca	3271
Db	4065 TCCAAAGAGCCCTGGACAAAGGCCAGGAAGGCCGACCTGCATTGTGTGATTGCTCACGCC	4124
Oy	3272 tg 3273	
Db	4125 TG 4126	

```

1      RESULT      7
2      US-08-583-276-18
3      ? Sequence 18, Application US/08583276
4      ? Patent No. 5837536
5      ? GENERAL INFORMATION:
6      ? APPLICANT: McDonaugh, Kevin T.
7      ? APPLICANT: Niennhuis, Arthur
8      ? APPLICANT: Tolstoshev, Paul
9      ? TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
10     ? TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
11     ? TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
12     ? NUMBER OF SEQUENCES: 19
13     ? CORRESPONDENCE ADDRESS:
14     ? ADDRESSEE: Carella, Byrne, Bain, Gillfillan,
15     ? ADDRESSEE: Cecchi & Stewart
16     ? STREET: 6 Becker Farm Road
17     ? City: Roseland
18     ? STATE: New Jersey
19     ? COUNTRY: USA
20     ? ZIP: 07068
21     ? COMPUTER READABLE FORM:
22     ? MEDIUM TYPE: 3.5 inch diskette
23     ? COMPUTER: IBM PS/2
24     ? OPERATING SYSTEM: PC-DOS
25     ? SOFTWARE: DM4.V2
26     ? CURRENT APPLICATION DATA:
27     ? APPLICATION NUMBER: US/08/583,276
28     ? FILING DATE: 05-JAN-1996
29     ? CLASSIFICATION: 435
30     ? PRIOR APPLICATION DATA:
31     ? APPLICATION NUMBER: 08/232,444
32     ? FILING DATE: 31-OCT-1994
33     ? APPLICATION NUMBER: 07/887,712
34     ? FILING DATE: 22-MAY-1992
35     ? INFORMATION FOR SEQ ID NO: 18:
36     ? SEQUENCE CHARACTERISTICS:
37     ? LENGTH: 4669 bases
38     ? TYPE: nucleic acid
39     ? STRANDEDNESS: singular
40     ? TOPOLOGY: linear
41     ? MOLECULE TYPE:
42     ? DESCRIPTION: Genomic DNA
43     ? US-08-583-276-18

```

	Query Match	Score	DB	length
Best Local Similarity	46.7%	Pred. No. 4, 5e-05		
Matches	253; Conservative	0; Mismatches	271; Indels	18; Gaps
Qy	2750	atggccctgcactgaatttttatggagggccagatacctctcttctctgggcccacatgag	2809	
Db	3585	atggactgagcccttggagagtggaaggagggccacacgcctgtgtgtggggccacacatggcgt	3644	

[illegible]

RESULT - 8
5206352-3
Patent No. 5206352
Applicant: Koninson, Igor B.; Pastan Ira H.; Gottesman,
Michael M.
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DN
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/622,836
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
FILING DATE: 28-MAR-1986
SEQ ID NO.:3
LENGTH: 4669
5206352-3

	Query Match	0.8%	Score 52.4	DB 6	Length 4669;
	Best Local Similarity	46.7%;	Pred.No. 4.5e-07;		
	Matches 253; Conservative	0;	Mismatches 271;	Indels 18;	Gaps 2
Oy	2750 atgcgctgcacatgaatttttaagaagcacaatcaccttcctcgaggccacaatggag	2809			
Dd	3585 aaggactgagccttgtaggtgaagaaggagccaaagcttgcctctgtgttgcaagcagtgcct	3644			
Oy	2810 cgggaagaagcagcacacatgtcatcctgccgggttgtccccccagacctggagaccg	2869			
Dd	3645 gggggaagcagcagtggtccagctcccttgagcgygtcttaagcacccttgcgaaggaaaag	3704			
Oy	2870 cctaacctctggaaaaagcat---tcgcttcgagatgaagcacaatccgcagcaacttgg	2926			
Dd	3705 tgcctcttatatgcgcaaaataaagcgcagctgaattgttcaatgtgctccgagcacacttgg	3764			

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,610
FILING DATE: 07-MAR-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: DE P 44 31 973.8
FILING DATE: 08-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: DE 195 03 952.1
FILING DATE: 07-FEB-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03175
FILING DATE: 10-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Berman, Richard J.
REGISTRATION NUMBER: 39,105
REFERENCE/DOCKET NUMBER: P1614-7007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9318 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA
US-08-793-610-6

Query Match 0.8%; Score 52.4; DB 2; Length 9318;
Best Local Similarity 46.7%; Pred. No. 7.7e-05;
Matches 253; Conservative 0; Mismatches 271; Indels 18; Gaps 2;
QY 2750 atggctgacacgaatttattatgagggcacaatacctccttccgcccacatgag 2809
DB 4936 agggactgacacctgagggatgaggaagggccacgacctgctggtggcagcagctg 4995
QY 2810 cggggaagacgacacacatgctacccggtgtgttcccccgcacacctcgagcag 2869
DB 4996 gtgggaagacgacaggtgctcagctcctgaggggtttacgacaccttggcagggaa 5055
QY 2870 cctacatcctggaagaagacat---tcgctctgagatgagcaccacgcggcagaa 2926
DB 5056 tgcctgctgattgacaaagaaatmaagcagctgattgttcagtggtccgacacac 5115
QY 2927 gggctgctcccgacatacgtgtgttgcacatgctgctgctgagaaacacatctgt 2986
DB 5116 gcatgctgtcccgagacccatctgtttgactgcagcattgctggaacattgcttatt 5175
QY 2987 tcatgtcccgctgaaagggctctcgaagacgtagaagcggagatggaagcagatg 3046
DB 5176 gaagacaaagccgggtggtgtcagagaaagatgctgagggcagaaagaaagccaa 5235
QY 3047 ccctgagatgtgttgcacatacgaagcctgaaag-----caaaaca 3091
DB 5236 tacatgcttgcacatgacgactgcttaataatattagcactaaatgagagacaa 5295
QY 3092 gccagctgctgagtgaaagcagaagaagctatctgtgcttgcgcttgcgagga 3151
DB 5296 ctgagcttctgtgtggccagaaacagcattgcttgcctgcttggtagacac 5355
QY 3152 ctgaagttgctatctgctgagaaacacagcctgtgtgagaccttaccgcaagggaa 3211
DB 5356 ctcatattttgttggatgaaagccacgctgcttgcattgagaaatgaaaggttg 5415
QY 3212 tatggagctgctgtaaatacgaacaaagccgacacattatctctacacacaa 3271
DB 5416 tccaaagacccctgagacaaagccagaaagccgacacgacattgtgattgtcacc 5475

QY 3272 tg 3273
DB 5476 tg 5477
RESULT 11
US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Query Match 0.8%; Score 52.4; DB 4; Length 4403765;
Best Local Similarity 47.6%; Pred. No. 0.008;
Matches 280; Conservative 0; Mismatches 290; Indels 18; Gaps 2;
QY 2776 ggcacatcacctctctctgagccacaatgagcgggaagacacacatgcatc 2835
DB 3000421 ggcgaattcttggggcttcttgaagtcacagcgccggcgaagtcacacacgaagc 3000362
QY 2836 ctgacgggtgtgttcccccgcacacctggaacgcgctacacatccttgggaagacatcgc 2895
DB 3000361 ctcatcgggctgctgacgacacacgacgacgacgacgacgacgacgacgacgac 3000302
QY 2896 tctgagatgagacacatccgagaaacctggtgtgttcccgacataagtgctgtt 2955
DB 3000301 gactgggacccgacttcttctgacgacgacgacgacgacgacgacgacgacgac 3000242
QY 2956 gacatgctgactgtcgaagaacacatctgttctatgctgacgcttgaagggctctgag 3015
DB 3000241 caaaagctcaccgsggtatgaaacctgcttctgctgctgctgctgctgctgctg 3000182
QY 3016 aagcagctgaaagcgaagatgagcagaatggccctgagatgtgtgttgcataaagaag 3075
DB 3000181 gccgacccgagatgacgctgctgacgacgacgacgacgacgacgacgacgacgac 3000131
QY 3076 ctgaaagcaaaacacagcagctgtcaggtggaatgacgaagaagctatctgtgtgt 3135
DB 3000132 ---ACACCCCTAGTGGCAAGTACTCCAAAGGCGCATGCGAGTGGCGTACGACCTT 3000077
QY 3136 gcttctgctgaggttcaaggtgtgtaattgtatgtaacacagcgtgtgtgtgacct 3195
DB 3000076 tgcctgattcaacgacccgagctgctgttcttgcagacgacccaccttccggcctg 3000017
QY 3196 taactcccgagggagataatgagctgtgtgtgaa---tacgacaagcgcgacacat 3252
DB 3000016 gtgaagcccgccagatgacagacatcatgctgacctgaaagggcgccgacagatc 2999957
QY 3253 attctctacacacacatgataagcgaagcgtctctggtggaacagatgtgcatc 3312
DB 2999956 tttctcaccacgacgacatgacgacgacgacgacgacgacgacgacgacgacgac 2999897
QY 3313 tcccatggaagctgt 3360

Db 3599 TACATGCTTCATCGAGTCACTGCCTAATTAATATAGCACTAAAGTAGAGCAAAAGAA 3658
Qy 3092 gccagctgtcagatgtgaatcagagaatcgtctgtgacctgtgtcgaggat 3151
Db 3659 CTCAGCTCTCTGTGGCCAGAAACAGCATTCATAGCTGTGCTTGTAGACAGC 3718
Qy 3152 ctaaggtgtcatctctgtatgaaccacagctgtgtgtgaccttactcccgaggagaa 3211
Db 3719 CTCATATTGCTTTGGATGATGAAGCCAGCTAGCTGTGATACAGAAAGTGAAGGTTG 3778
Qy 3212 tatggagctgtcgtcgtgaatcagacaagccgacacattctctctacacacaca 3271
Db 3779 TCAGAAAGCCCTGGACAAAGCAGAGAGCCGACCTGCATGTGTGCTCACCCGC 3838
Qy 3272 tg 3273
Db 3839 TG 3840

RESULT 14

US-08-784-649A-5
Sequence 5, Application US/08784649A
Patent No. 5830697

GENERAL INFORMATION:
APPLICANT: Sikic, Branimir I

APPLICANT: Chen, Gang

TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
CYCLOSPORIN MODULATION

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA

COUNTRY: USA
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,649A
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J

REGISTRATION NUMBER: Reg.No. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 4264 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: CDNA
US-08-784-649A-5

Query Match 0.7%; Score 50.8; DB 2; Length 4264;
Best Local Similarity 46.5%; Pred.No. 0.00013;

Matches 252; Conservative 0; Mismatches 272; Indels 18; Gaps 2;

Qy 2750 atggcctggcactgaatttattgaagggcagacacccctcctcctgagccacaatggag 2809
Db 3299 AGGAGCTGAGCCTGAGGAGGAAGAGGCGACAGCGTCTGTGGGGCAGACAGTGGCT 3358
Qy 2810 cggggaagacgacaccacatgtaatcctgacccgggtgttcccccgcgacctgggacgcg 2869
Db 3359 GTGGGAAGAGCACAGTGTCTCAGAGCTCTGAGAGCGGTTTACGAGACCCCTTGCGAGGGGAAG 3418

Qy 2870 cctacatccttggaaaagacat---tcgctctgagatgaagcaccatccggcagaacctgg 2926
Db 3419 TGCTGCTTTGATGGCAAGAAATTAAGGACGATGTTCAAGTGGCTCTCCAGACACCTGG 3478
Qy 2927 gggctctgcccaagacataacgtctgttgcacatgctgactgtcgaagaacacatcgt 2986
Db 3479 GCATCTGTCTCCAGAGCCCTCCTGTTTGTGACTGACGATTCGTCGAGACATTCGCTATG 3538
Qy 2987 tctatgccgcttgaagggtctctctgagaagcagcggaaggagggagatgagcaagt 3046
Db 3539 GAGCAACAGCGGGGTGTGTACAGAGAGGATGTGAGGGCAGCAAGAGAGCCACACA 3598
Qy 3047 cccctgatgtgttctccatcaagcaagctgaaag-----caaaacaa 3091
Db 3599 TACATGCTTCATCGAGTCACTGCCTAATTAATATAGCACTAAAGTAGAGCAAAAGAA 3658
Qy 3092 gccagctgtcagatgtgaatcagagaatcgtctgtgacctgtgtcgaggat 3151
Db 3659 CTCAGCTCTCTGTGGCCAGAAACAGCATTCATAGCTGTGCTTGTAGACAGC 3718
Qy 3152 ctaaggtgtcatctctgtatgaaccacagctgtgtgtgaccttactcccgaggagaa 3211
Db 3719 CTCATATTGCTTTGGATGATGAAGCCAGCTAGCTGTGATACAGAAAGTGAAGGTTG 3778
Qy 3212 tatggagctgtcgtcgtgaatcagacaagccgacacattctctctacacacaca 3271
Db 3779 TCAGAAAGCCCTGGACAAAGCAGAGAGCCGACCTGCATGTGTGCTCACCCGC 3838
Qy 3272 tg 3273
Db 3839 TG 3840

RESULT 15

US-09-194-905-7/C
Sequence 7, Application US/09194905
Patent No. 6306627

GENERAL INFORMATION:
APPLICANT: DECKER, Heinrich

TITLE OF INVENTION: ISOLATION OF THE BIOSYNTHESIS GENES FOR
PSEUDO-OLIGOSACCHARIDES FROM STREPTOMYCES GLAUDESCENS

TITLE OF INVENTION: GLA.O AND THEIR USE
NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/194,905
FILING DATE: 29-JUL-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP97/02826
FILING DATE: 30-MAY-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19622783.6
FILING DATE: 07-JUN-1996

ATTORNEY/AGENT INFORMATION:
NAME: Granados, Patricia D.
REGISTRATION NUMBER: 33,683

REFERENCE/DOCKET NUMBER: 026083/0193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2002, 01:19:31 : Search time 11758.7 Seconds
(without alignments)
7809.816 Million cell updates/sec

Title: US-09-595-526b-1_COPY_291_7094

Perfect score: 6804

Sequence: 1 atgcgtgtgtgcctcagct.....gaagaatcctgtcctacag 6804

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmoy:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: qb_estl:*
10: qb_estl2:*
11: qb_hlc:*
12: qb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	692.4	10.2	809	10	BI754756 603025477
2	639.8	9.4	854	10	BI854140 603381449
3	543.6	8.0	837	10	BF160011 601768192
4	536.8	7.9	652	9	BB468374 BA468374
5	532.4	7.8	724	10	BG920223 602822304
6	526.6	7.7	720	10	BI248317 602966918
7	523.4	7.7	702	10	BI658600 603284335
8	489.8	7.2	878	10	BI182779 UNL-P-FN-
9	473	7.0	515	10	BE665489 154542 MA
10	459.4	6.8	554	10	BE094524 MRO-UT004
11	447.6	6.6	515	10	BF076332 225856 MA
12	433.2	6.4	518	10	BF042703 BP2500205
13	428.8	6.3	463	10	BE715104 MK3-HT073
14	425.4	6.3	427	10	BM153383 TCBAP2D11
15	424.2	6.2	998	10	BG678861 602624760
16	411	6.0	596	9	AA063753 mJ79h09.r
17	399.2	5.9	417	9	AW362709 RC6-CT028

18	366.2	5.4	412	9	AW380897 CM3-HT028
19	365.8	5.4	441	10	BF042938 BP250002A
20	364.6	5.4	662	10	BI468033 EST000443
21	363.6	5.3	434	9	AW322680 uc051b11.y
22	362	5.3	422	10	BE329960 CM3-GN005
23	345.6	5.1	366	10	BF951740 QV1-NN121
24	340.8	5.0	717	10	BE742059 601575815
25	337	5.0	835	9	AW013420 pc015K5.W
26	327.6	4.8	351	10	BP928185 CM4-NT021
27	325.8	4.8	623	9	AW421371 fJ90e07.y
28	321.2	4.7	352	10	BE892148 QV1-MT013
29	320.8	4.7	324	9	AW845151 RC0-CT000
30	319.8	4.7	736	9	AU135588 AU135588
31	318.2	4.6	2640	11	U66691 Homo sapien
32	315.6	4.6	551	9	AL733552 y066h03.y
33	312.2	4.6	591	9	AL588915 AL588915
34	309.2	4.5	782	10	BG775975 602650251
35	308.8	4.5	381	10	BE757461 211904 MA
36	301.4	4.4	786	10	BI736551 603361011
37	301.2	4.4	699	10	BI739256 603359544
38	299	4.4	363	9	AV647223 AV647223
39	296.4	4.4	359	9	BB871492 BB871492
40	286.2	4.2	549	10	BI976880 486050 MA
41	285.4	4.2	529	10	BC883616 fp27e09.y
42	285.4	4.2	589	10	BC936214 SS1-0568
43	283.2	4.2	370	9	BB871749 BB871749
44	281.2	4.1	353	9	BB871954 BB871954
45	277.6	4.1	491	10	BB879888 RC2-ET018

ALIGNMENTS

RESULT 1
BI754756 809 bp mRNA linear EST 25-SEP-2001
603025477F1 NIH_MGC_114 Homo sapiens CDNA clone IMAGE:5195995 5',
DEFINITION
BI754756 mRNA sequence.
ACCESSION
BI754756.1 GI:15746334
VERSION
EST.
KEYWORDS
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 809)
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
DNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11490 row: 1 column: 20
High quality sequence stop: 768.
location/Qualifiers
1. 809
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5195995"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is Oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for

FEATURES

source

Db 484 CCGTAAAGCCCGAGATTTCTTGGAATGTCGCCCTAAGCATTTGTCAGAGGAGGATCT 543
QY 6289 gtagtgccttaacatcctcatagatggaagaatggaagctcttgcactagatggcaatc 6348
Db 544 GTAGTCCTTACATTCATGATGATGAGAGATGTAAGCTCTTTGACAGAGATGCGCATTA 603
QY 6349 atggtcaatggaaggttcaaggtccttgccaggtgcacagatcctaaataatggttga 6408
Db 604 ATGGTCATAGGAAGGTTCAGGTGCTTGGCATGTTCACATCTAATAAAGAGTGTCCGA 663
QY 6409 gatgtttatatacatagttgtaacgaatagcaaggtccaaaccccgagctgaagctgtccag 6468
Db 664 GATGTTATACATAGTTGTAGCAATAGAGGCTCCACACCTGAGCTGAGCTGTCCAG 723
QY 6469 gatctcttgagcttgacattcccttggaagtgtcttaaaagaagaacaccggaatgcta 6528
Db 724 GA-GTCTTGGAGCTTCCGCTTACCGGGAAGTGTCTAAAGAGAAA-ATCGACATCTGCTT 781
QY 6529 caatacagcttcacatctcatatctctctgcccagatatagcaatcctctccag 6588
Db 782 CAGTCCAGCTTCCATC-TCCTTGTATCTTAGCCAGATA-TCAGCATCTCTCCAGA 839
QY 6589 agcaaaaagcagactc 6603
Db 840 AGCAACGCGGACTC 854

RESULT 3
BF160011 837 bp mRNA linear EST 30-OCT-2000
LOCUS 601768192P1 NCI_CGAP_Lu29 Mus musculus CDNA clone IMAGE:3987503 5',
DEFINITION mRNA sequence.
ACCESSION BF160011 GI:11040118
VERSION BF160011.1 GI:11040118
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 837)
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaabp-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM9194 row: 9 column: 24
High quality sequence stop: 669.
Location/Qualifiers
1. 837
/organism="Mus musculus"
/strain="CZECH II (fetal)"
/db_xref="taxon:10090"
/clone="IMAGE:3987503"
/clone_id="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary."
Stem cell origin"
/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 226 a 188 c 230 g 193 t
ORIGIN

Query Match 8.0%; Score 543.6; DB 10; Length 837;

Best Local Similarity 88.4%; Pred. No. 6, 1e-139;
Matches 647; Conservative 0; Mismatches 79; Indels 6; Gaps 5;
QY 5963 tgggtactctgcctcagttgtagcatcacagagctgttgactggaaggaacagttg 6022
Db 13 TGGGCTACTGGCCCTCAGTGTGACGCGCATCACAGAGCTGCTGACTGAGAGACATGTGG 72
QY 6023 agttcttgccctcttg-agaagagctccagagaagaagtgtgcaagttgtgagtg 6081
Db 73 AGTCTTTGGCCCTCCTCTAGGGGAGTCCAGAAAAGAAAGTGGCAAGTTGGTGAATGG 132
QY 6082 gcaattcggaaactgggctcgtgaagtaagtaagaaataatgctgtaactatagtgga 6141
Db 133 GCAATTTGCCAANAAGTGGGCTGTGTAAGATAGAGAAAATAATATGCCAATACTACAGTGGC 192
QY 6142 ggcacaaagcgaagctctctacagcaatgcttgatcggcggctcctgtggtgtt 6201
Db 193 GGCAAACAAACGAAAGCTTCCACAGCATGGCTTGAATTGGCGGCTCTCTGTGGTGT 252
QY 6202 ctgatatgacccacacagagatgatcccaagcccgagctctgtggaattgtgc 6261
Db 253 CTGGATGACCAACACACAGCATGGACCTTAAGCCCGAGATTTCTGTGGAA-TGTGCC 311
QY 6262 ctaagtgtgtcgaagggagagatcagtagtgccttacatctcatagtaagaaagt 6321
Db 312 CTAAG-CATGTCAAGGAGAGGAGATCTGTAGTCTCTTACATCTCATAGTAAAGAAATGT 370
QY 6322 gaagctcttgcaactagatggaatcagatgcaatggaaggtcaggtccttgcaat 6381
Db 371 GAAGCTCTTGTACAAAGATGGCCATTAATGTCATAGTAAGAGTTGACGATAGCGAGT 430
QY 6382 gtccagcatctaaataatagtttggaatggtgtatcaatagttgtacgaatagcagg 6441
Db 431 GTCCAACTCTGAAACAAAGGTTGGAGATGTTATACAAATGTTGACGATAGCGAGC 490
QY 6442 tccaaacccgacctgaaagccgtccagatctcttgacttgatctcctggaagtgt 6501
Db 491 TCCAAACCTTGACCTGAAACCTGTCCAGAGATGTTTGGACTTGGTCCAGAAAGTGC 550
QY 6502 ctaaaagaagaacaccggaacatgctataacacagcttccatctatctctctg 6561
Db 551 CTAAGAAGAAACATCGAAGCATGCTTCAGTACAGCTTCATCTCTCTGTCATCTA 610
QY 6562 gccagatatcagatcctctccagagcaaaagcagccaca-tagaagactcctc 6620
Db 611 GCCAGATATTCAGCATCTCTCCAGAGCAAAAAGCAGCTCCACATTAGAAGACTCTC 670
QY 6621 tgttctcagaacaactgacccaagtaattgtgaacttgccaaggaaccaagtgtga 6680
Db 671 TGGTCTTCAGACACACTGACCAAGTAT--GTCAACTTGCCTCAAGGACCCCAAGTATGA 728
QY 6681 tgaccacttaaa 6692
Db 729 TTGACCTTAA 740

RESULT 4
BB468374 652 bp mRNA linear EST 25-OCT-2001
LOCUS BB468374 RIKEN full-length enriched, 12 days embryo eyeball Mus
DEFINITION musculus CDNA clone D230019D04 3' similar to X75926 M.musculus abc1
ACCESSION BB468374 GI:16427507
VERSION BB468374.2
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 652)
REFERENCE Arakawa,T., Carlnet,P., Fukuda,S., Furuno,M., Hanasaki,T., Hara,A.,
Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,

FEATURES	source
Db	6293 tgcataactcacaatagatcttgaaagaatctgaaagcctcttgacactcagatgagcaatcatg 6352
Db	246 tcccttaccatctctatgtagttagaagaatgatggaagctctcttgtagcaagagatgcccatatg 305
Qy	6353 tcaatvgaaaggtctcaggtgcttgccatgctcgcacatctctaaataataggtttgagatg 6412
Db	306 tcaatvgaaaggtccaggtgacgtcccttgccagatgctccaaacatctgaaaaaacaggttggagatg 365
Qy	6413 gttatatacaatagttacagaatagaggtgtccaaaccggagactggaagcctgccaagatt 6472
Db	366 gttattacattatgtttacgaattagcagcctccaacacctgacctggaagcctgtccagagat 425
Qy	6473 tctt-tggacttcatacttcccttgaaagtgltcttaaagaagaaacaccggagaaatgtacaa 6531
Db	426 tctttgtgacctgctgcttccggagatgctccttcaaaagaaacatcgaacacatgcttcag 485
Qy	6532 tacacgcttccatctcaatctaatctctcctcgcgcagatattta-gcatctctcccaag 6590
Db	486 tacacgcttccatctcctcttgcacatcttcagcagaatattttcagacatctctccacag 545
Qy	6591 caaaaagagactccacatagaaagactactcgttcttcagacaacacttgacaagtatt 6650
Db	546 caaaaagagactccacatagaaagactactcgttcttcagacaacacttgacaagtatt 6605
Qy	6651 tgtgaac-ttggcaagaagcaaatgtatgtatgaccacttaag--acccttcattaca 6707
Db	606 tcttgacatttttcccaagagccaaatgtatgagaccactcttcaaaagacacttgacatggc 665
Qy	6708 caaaaaccagacagtagtggagcgttgcaagtcttcacatctt 6750
Db	666 aaaaaaccagacagtagtggagcgttgcaagtcttcacatctt 708
RESULT	7
LOCUS	B1658600
DEFINITION	6032984335p1 NIH_GCAP_Mam4 Mus musculus cDNA clone IMAGE:5328392 5',
ACCESSION	B1658600
VERSION	B1658600.1 GI:15572836
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE	1 (bases 1 to 702)
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaabs-remail.nih.gov Tissue Procurement: Lochar Hemmighausen Ph.D., Priscilla Futh Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: L1AM1833 row: f column: 09 High quality sequence stop: 645.

BASE COUNT	191 a	166 c	172 g	173 t	ORIGIN
Query Match	7.7%	Score 523.4	DB: 10	Length 702	
Best Local Similarity	91.6%	Pred. No. 2.2e-133			
Matches 565	Conservative 0	Mismatches 51	Indels 1	Gaps 1	
OY 6189	lccitggtgtgtcttcctgta	tgaaaccacacacagcagcagc	atgcatcccaagccgctgctt	6248	
Db 1	TCCTGTGGTGTTTCTGGATGA	CAACCAACCAAGCATGAGCCTAA	AGCCCGAGATCTT	60	
OY 6249	gtggaatgtgtccctcaag	tgtgttcaagagagggagatcag	atgtgtctatcatctc	6308	
Db 61	GTGGAAATTTGGCCCTAACCA	TTGTCAAGAGGGGAGATCTT	TAAGTCCTTAATCTCAATG	120	
OY 6309	tatggaagaatgtgaagct	ctttgacacagatgacatc	atgtgtcaatgtgtcaatgtga	6368	
Db 121	TATGGAAGAATGTGAAGCT	TTTGTACAAAGCATGGCCATAT	TGTGCATGGAAGTTTCA	180	
OY 6369	gtgcctgtgcagtgctcag	catctaaataaggttggagatgt	gtatatacacaatgtgt	6428	
Db 181	GTGCCTTGGCAGTGTCCACA	ACTGCAAAAGAGTTTGAGAT	TGTATACAAATAGTTGT	240	
OY 6429	acgaatagcagatgtccaa	cccgagcttaagcctgtccag	atctcttggacttgc	6488	
Db 241	ACGANTAGCAGAGCTCCAA	CCCTGACCTTAAGCCTTCA	CAGAGTTCTTTGGACTT	300	
OY 6489	tccctggaagtgtcttaaa	agagaacacacggaacatgtc	ataatacaccatcttc	6548	
Db 301	TCCCGGAAGTGCTCTAAAG	AGAAATCTGAACATCGAAT	CGTTCAGTACCGCTTCCAT	360	
OY 6549	attactctctctgcccaga	tatatltaagatctctctcc	acagggcaaaaagcgatcc	6608	
Db 361	CTTTGCATCTCTACGACGA	AGATATTTCAGATCTCTCC	CAGACAAAAGCGACATCT	420	
OY 6609	agaagactactctgtgttc	tcagacaacacttgaacca	tatttgyaacttgc	6668	
Db 421	AGAAACACTACTCTGTCTC	TACAGACAACACTTGACCA	ATATTTTGTGAATTTGCCA	480	
OY 6669	ccaagaatgatatgacac	acttaaaagacctc	atcattacacaaaaacagac	6728	
Db 481	CCAAAGTATGATGTACCA	CTTAAAGACCTCTGATCTG	ACAAAAACCGACAGTTGTG	540	
OY 6729	cgttgcagttccacatct	ttttctacagagatga-gaa	agttaaaagaagcatgtatga	6787	
Db 541	TGTGGCGTTTCTCACATC	CTTTTGGCAGAGATGACGA	ACGTGACACAAAGTCATGT	600	
OY 6788	gaatcgtgtcatacgg	6804			
Db 601	GAATCCCGTTCACACAG	617			
RESULT 8					
B1182779/c		878 bp	mRNA	linear	EST 10-JUL-2001
LOCUS	B1182779				
DEFINITION	UNI-P-FN-bp-c-01-0-UNI.s1	UNI-P-FN	Sus scrofa	CDNA clone	
ACCESSION	B1182779				
VERSION	B1182779.1	GI:14657188			
KEYWORDS	EST.				
SOURCE	plg.				
ORGANISM	Sus scrofa				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
TITLE	1 (bases 1 to 878)				
	Generation and sequence characterization of a normalized cDNA				
	library from swine ovarian follicles				

JOURNAL
COMMENT

Unpublished (2001)
Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail.

Seq primer: M13 -29
POLYA=Yes.

FEATURES

Location/Qualifiers
1. . 878

```

/organism="Sus scrofa"
/strain="University of Nebraska, Lincoln Swine Selection
Lines"
/db_xref="taxon:9823"
/clone="UNL-P-FN-bp-C-01-0-UNL"
/clone_lib="UNL-P-FN"

```

/lab host="DHI08 (Life Technologies)"
/note=Vector: pRT3D-pac (Pharmacia) with a modified
polylinker. Site_1: Not I. Site_2: Eco RI. The UNL-P-FN
library is a normalized library representing porcine
ovarian follicles, ranging between 2.0 to 10.0 mm in
diameter, collected during 7 days of the follicular phase
of the pig estrous cycle. This library was derived from
the library UNL-P-F. The tag is a string of 5-6
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennan and Soares, Genome Research 6: 791-806
1996.

	TAG_SEQ=None found"			
BASE COUNT	212 a	219 c	184 g	258 t
ORIGIN				
				5 others

Query Match	7.2%;	Score 489.8;	DB 10;	Length 878;
Best Local Similarity	89.4%;	Pred. No. 5.3e-124;		
Matches 550;	Conservative 0;	Mismatches 62;	Indels 3;	Gaps 2

QY	6190	ccctggtgtttcttcgagtagaccaccacaaagagtagatcccaaaagccggggttctt	624
Db	771	CCCCGTGCTTTCTTGATGAAACCGACCAAGGAT-GATGCCAAAGCCCGGAGTTCT--	713
QY	6250	tggattgtgcccctaaatgtgtcgaaggaggagatacgaatgtagtcttacatctaagt	6305
Db	714	GTGATTGTGCCCCCTTAATATATGTCMAAGGAAGGAATGATGTGGTTACATCTATAGT	655
QY	6310	atggaagaatgtgaagctcttccttgaatgagatggaatcatgtcaatgaaagttcag	6365
Db	654	ATGGAAGAAATGTGAAGCTCTTTGCGACCGAGATGCGAATTATGTCTAATGGAGTTCAAG	595
QY	6370	tgccttgcagtgctgcagcatctcaaaaatagtttggagatggtatatacaatagtcta	6425
Db	594	TGCTTTGGCAGTGTCCAACTCTGAAAAAATAGTTTGGAGATGGTATATCGATAGTTGTA	535
QY	6430	cgaatacgaaggtlccaaaccccgagccttgaagcctgtlccagaattctcttgaacttgat	6485
Db	534	CGAATACGAGGTGCCAACCTGTGACGTGCAAGCCGTCGAGAGATGTTCTTGTGAAATGCTTT	475
QY	6490	ccttgaagatgtlctctaaagaagaacacccgaacatgctacaaataccaggtlccatcttca	6549
Db	474	CCGGGAAGCGTCTGAAGGAGAACCGGAACATGCTCGAGTACACAGTCTTCCCTGCTCC	415
QY	6550	ttatctctcttgcgcaggaatattcagatctccttccagagcaaaaagcgaactcacata	6605
Db	414	CTGTCTCTCCCGGCGCAGGATATTACAGCGTCTTTCCAGACGAAAAAGGAGCTCCACATA	355
QY	6610	gaagactactctgttcttcagacacacactgaccaaagtattgtgaacttgcgaagagc	6665

Db 354 GAAGTACTCAGTTTCTCAGACAACCTTGACCAAGTATTGTAACCTTGGCCAGAC 295

Qy 6670 caaatgtatgatgaccacttaaaagaccttcattacaacaaaacgcagacagtatggac 6729
|||||
Db 294 CAAAGTGTATGATGACCACTTTAAAGCACCTGTCATTACTATAAAAACCACACAGTAGTGAT 235

Dy 6730 gttgcagttctcacaatcttctcacagatgagaagtgaagaacgtatgatgaaga 6788
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 234 GTTGCTGTTTCTCACATCTTTTCTGCAGGATGAGAAAGTGAAAAGATTACGTGTGAGGA 175

Gy	6790	atccctgcatcacgg	6804
Db	174	ATCCTGTTCCTATGG	160

RESULT	9			
BE665489				
LOCUS	BE665489	562 bp	mRNA	linear
				EST 25-APR-2001

ACCESSION BE665489
VERSION BE665489.1 GI:10026080
KEYWORDS EST.

ORGANISM *Bos taurus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bovini; Bos

REFERENCE

AUTHORS
Smith, I. P. L., Grose, W. M., Treking, B. A., Roberts, A. J., Stone, R. J.,
Casas, E., Wray, J. E., White, J., Cho, J., Fahrenkrug, S. C., Bennett,
G. L., Heaton, M. P., Laegreid, W. W., Rohrer, G. A., Chitto-Mokom, C. G.,
Perita, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keele, J. W.

TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL	Genome Res. 11 (4), 626-630 (2001)
MEDLINE	21180013
COMMENT	Contact: Smith TPL

FEATURES

Location/Qualifiers
1. .562

```

/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_id="MARC 4BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV Sport6; Site_1: XbaI; Site_2: XhoI
library made from pooled tissue from day 20 and day 40
embryos."

```

BASE COUNT	139 a	134 c	159 g	130 t
ORIGIN				

Query Match	7.08;	Score 473;	DB 10;	Length 562;
Best Local Similarity	91.08;	Pred. No. 1.8e-119;		
Matches 503; Conservative	0;	Mismatches 50;	Indels 0;	Gaps 0;

```

0y      3531 catcgatgtctctcgtatatctccaaccatcagaagcatggtcttgaaagccgcgtgg 3590
          |||||
Db      10  CATTGATCTCTCTGTGATCTCCACCATTCATCAGGAACATGTGGCTGAGGCCCGGCTGGT 69

```

QY 3591 ggaagacataggagcagctgacgtacgtatgtctgcatatgaagctgcaagagagagc 3650
|||||
Db 70 ggaagacataggagcagctgacgtacgtatgtctgcatatgaagctgcaagagagagc 129
QY 3651 ctgttggaactcttccatgagatgatgacggcctcgaagctgagcattctagta 3710
|||||
Db 130 ctgttggaactcttccatgagatgatgacggcctcgaagctgagcattctagta 189
QY 3711 tggcatctcagagacagcctggaagaatattcctcaaggtgagcgaagagatggagc 3770
|||||
Db 190 cggcatctcagagacagcctggaagaatattcctcaaggtgagcgaagagatggagc 249
QY 3771 ggtatgtgagacactcagatgagtgatcttgcagcaagaagaagcggcgttgggga 3830
|||||
Db 250 ggtatgtgagacactcagatgagtgatcttgcagcaagaagaagcggcgttgggga 309
QY 3831 caagcagagctgtcttcgcccgttcacgtgaagaatgagtgatctgcatccaaatgattctga 3890
|||||
Db 310 caagcagagctgtcttcgcccgttcacgtgaagaatgagtgatctgcatccaaatgattctga 369
QY 3891 catagaccagaaatccagagagacagactgtctcagtgagatgagatgagcaagagtccta 3950
|||||
Db 370 catagaccagaaatccagagagacagactgtctcagtgagatgagatgagcaagagtccta 429
QY 3951 ccaggtggaagagctggaagaatcacaagaacagatgttggccttcttggaagagact 4010
|||||
Db 430 ccaggtggaagagctggaagaatcacaagaacagatgttggccttcttggaagagact 489
QY 4011 gctaatctcagagacagagagctggaagaatcttctgcatgagatgtctgcatgagctggt 4070
|||||
Db 490 gctaatctcagagacagagagctggaagaatcttctgcatgagatgtctgcatgagctggt 549
QY 4071 tgtctgcatggtc 4083
|||||
Db 550 tgtctgcatggtc 562

RESULT 10
LOCUS BF094524 515 bp mRNA linear EST 19-OCT-2000
DEFINITION MR0-UT0047-170900-202-f10 UT0047 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF094524
VERSION BF094524.1 GI:10900234
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 515)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Birones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.U.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
CONTACT: Simpson A.U.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0-UT0047-170
900-202-f10&ts=2000-09-17&at=1)
Seq primer: puc 18 forward

High quality sequence start: 15
High quality sequence stop: 515.
Location/Qualifiers
1. 515
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="tgm0047"
/dev_stage="Adult"
/note="Organ: uterus-tumor; Vector: puc18; Site_1: Smal;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 143 a 125 c 132 g 115 t
ORIGIN

Query Match 6.8%; Score 459.4; DB 10; Length 515;
Best Local Similarity 98.4%; Pred. NO. 1e-115; 6; Indels 2; Gaps 2;
Matches 485; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

QY 1049 ctacacactcctactgcaatgattgatatgaagaattgagctagctcctctccgca 1108
|||||
Db 15 ctacacactcctactgcaatgattgatatgaagaattgagctagctcctctccgca 74
QY 1109 ttatctggaagctctgagcgcgtgtctgttgggaagatcctgtatcacctgacac 1168
|||||
Db 75 ttatctggaagctctgagcgcgtgtctgttgggaagatcctgtgtatcacctgacac 134
QY 1169 cagccacaagcagatgctgagtgctgagtggaacagacctccaggaactgctgttc 1228
|||||
Db 135 cagccacaagcagatgctgagtgctgagtggaacagacctccaggaactgctgttc 194
QY 1229 atgactctggaagcagatgctgagtggaacagacctccaggaactgctgttc 1288
|||||
Db 195 atgactctggaagcagatgctgagtggaacagacctccaggaactgctgttc 254
QY 1289 gccagaagatgagcctgtccgagatgctgttggagcagcaggaagacacttggg 1348
|||||
Db 255 gccagaagatgagcctgtccgagatgctgttggagcagcaggaagacacttggg 314
QY 1349 aacagcagtgatgctgagtgatgagacagcccaagacatcgttggccaagc 1408
|||||
Db 315 aacagcagtgatgctgagtgatgagacagcccaagacatcgttggccaagc 374
QY 1409 acccagagatgctcagtcacgtatggttctgtgtaacctgagagagcttcaag 1468
|||||
Db 375 acccagagatgctcagtcacgtatggttctgtgtaacctgagagagcttcaag 434
QY 1469 agactaa-cagagcaatccgagacatatcctgcttcagtgagtgctcaacctgaag 1527
|||||
Db 435 agactaa-cagagcaatccgagacatatcctgcttcagtgagtgctcaacctgaag 493
QY 1528 ctagaaccatag 1540
|||||
Db 494 ctagaaccatag 506

RESULT 11
LOCUS BF076322 554 bp mRNA linear EST 25-APR-2001
DEFINITION 225856 MARC 2BOV Bos taureus cDNA 5', mRNA sequence.
ACCESSION BF076322
VERSION BF076322.1 GI:10870075
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taureus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovine; Bos.
1 (bases 1 to 554)

OY	1528	ctaggaccccatcgacacagaagctctggtccatcaacaagttcaatgagctgctatgag	1587
Db	61	CTAGAACCAAGTACGCACAGAGGTTCTGCTCATCAACAAAGTCCATGGAGCTTTGGATTGAG	120
OY	1588	aggaagttctggtcgtgtatgtgttcaactgtaattaccagagcagcatagctgccc	1647
Db	121	CCCAAAATTCTGGGCTGGGGTAGTGTTCACATGGAATTGCTCCGGCAGCGCTCAGTTACCG	180
OY	1648	catcatgtcgaagtacagaatccgaatgtgacatltgacaatgttgagagaggaataaatc	1707
Db	181	CATCATGTCAATACAAAGATCCGGATGCGACATTTGACAAAGTGGAGAAGCGAATTAAGATC	240
OY	1708	aaggaatggtacttggaacctgtctctcgactctgagctgaccccttggagacatcgtgaagtc	1767
Db	241	AAGGAGGGGTACTGGGACCCCTGCTCGGGCTGTGACCCTTTGAGCATATGGCGTATGTC	300
OY	1768	tggggggagcttcgcctactcttcaggaatgtgtgtgagcaagcaatcatcaaggctgacg	1827
Db	301	TGGGAGGGCTTCGCTTACTTTGCAGGATGTGGTGAGACAGGCATATCATCGSGCTCGAGCG	360
OY	1828	ggcaccggagaagaactcgtgtctctatagaagaagaatggccctatccctgaagtlgat	1887
Db	361	GGCACAGAGAGAAACTGGCGCTGTACATGACGCGAGATGCTTTACCCCTGTATGTTGAT	420
OY	1888	gacaccttctcgtcgggttatagaccggtcaatgaccccttcaatgaagcttgccgattat	1947
Db	421	GACATCTTCCTCGGGTATGAGCCGGTCCAGTCCCTTCCTTCATGACGCTGGCGTCGATAC	480
OY	1948	tactcagtgctcgttatcatcatcaaggcatcgtgtatga	1995
Db	481	TACTCGTGCGCTGTGATCATCAAGGCGCATTTGTTGCGA	518

RESULT 13			
LOCUS	BE715104	463 bp	mRNA
DEFINITION	MR1-H0737-060700-004-b09	H0737	linear
ACCESSION	BE715104		Homo sapiens CDNA, mRNA sequence.
VERSION	BE715104.1	GI:10103369	
KEYWORDS	EST.		
SOURCE	human.		

REFERENCE
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A.J.G.

Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-MR3-HT0737-0660>)
 700-004-B09&t3=2000-07-06&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 24
 High quality sequence stop: 461.
 Location/Qualifiers
 1..463

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0737"
/dev_stage="Adult"
/name="Organ: head,neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
fused into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      147 a      105 c      111 g      100 t
ORIGIN

```

Query Match	6.3%	Score 428.8	DB 10	Length 463
Best Local Similarity	97.3%	Pred. No. 2.9e-107		
Matches 436	Conservative 0	Mismatches 12	Indels 0	Gaps 0

Q7 4480 gcagatataccttcaggaccttcagagagaacacattccgattatctcgtgtgaaagctat 4539

Db 6 GTAGATATCCTTCAGGACCGGCACAGGAACATTCGGATATCATGGTGAAGACCTAT 65

QY 4540 gtgcagatcatagccaaagcttaagacaagaatctggtagatgaattagratgac 4599

QY 4600 ggctttccctgggtgtcagtaataactcaagcacttcctccgaagtcgaagaagttaatgat 4659

DD 126 GGCCTTCCCGGGGTCGTAGTAATACCTCAAGCACTTCTCCGAGTCAAGAATTAATGAT 185
 QY 4660 gccatcaacaatlgaaagaacacttaagctcggccaagacagttctgcagatcgatt 4719

Db	186	GCATCAACAAATATAGAAACACCTTAAGCTGCGCCAAGGACAGTTCCTCAGATCGATT	245
Ov	4720	ctcacacagcttgcgaagattatagacagacactgcagacacccaagaataatctcaagctgcg	4779

Db 246 CTCACAGCTAGGGAAGATTATGACAGGAGCTGACACCGAATAATCTCGAGGTGTG 305

Db 306 TTCTAATACCAAGGGCTGGCATGCATTCAGCTCTTTCTCTGAATGTCATCAACATGCATT 365

4840 ctctggggccaacccgcgaagaaggaggaacccctagccactatggaatcaatcgtcttcaat 4899
4841 |||||
4842 |||||
4843 |||||
4844 |||||
4845 |||||
4846 |||||
4847 |||||
4848 |||||
4849 |||||
4850 |||||
4851 |||||
4852 |||||
4853 |||||
4854 |||||
4855 |||||
4856 |||||
4857 |||||
4858 |||||
4859 |||||
4860 |||||
4861 |||||
4862 |||||
4863 |||||
4864 |||||
4865 |||||
4866 |||||
4867 |||||
4868 |||||
4869 |||||
4870 |||||
4871 |||||
4872 |||||
4873 |||||
4874 |||||
4875 |||||
4876 |||||
4877 |||||
4878 |||||
4879 |||||
4880 |||||
4881 |||||
4882 |||||
4883 |||||
4884 |||||
4885 |||||
4886 |||||
4887 |||||
4888 |||||
4889 |||||
4890 |||||
4891 |||||
4892 |||||
4893 |||||
4894 |||||
4895 |||||
4896 |||||
4897 |||||
4898 |||||
4899 |||||
4900 |||||
4901 |||||
4902 |||||
4903 |||||
4904 |||||
4905 |||||
4906 |||||
4907 |||||
4908 |||||
4909 |||||
4910 |||||
4911 |||||
4912 |||||
4913 |||||
4914 |||||
4915 |||||
4916 |||||
4917 |||||
4918 |||||
4919 |||||
4920 |||||
4921 |||||
4922 |||||
4923 |||||
4924 |||||
4925 |||||
4926 |||||
4927 |||||
4928 |||||
4929 |||||
4930 |||||
4931 |||||
4932 |||||
4933 |||||
4934 |||||
4935 |||||
4936 |||||
4937 |||||
4938 |||||
4939 |||||
4940 |||||
4941 |||||
4942 |||||
4943 |||||
4944 |||||
4945 |||||
4946 |||||
4947 |||||
4948 |||||
4949 |||||
4950 |||||
4951 |||||
4952 |||||
4953 |||||
4954 |||||
4955 |||||
4956 |||||
4957 |||||
4958 |||||
4959 |||||
4960 |||||
4961 |||||
4962 |||||
4963 |||||
4964 |||||
4965 |||||
4966 |||||
4967 |||||
4968 |||||
4969 |||||
4970 |||||
4971 |||||
4972 |||||
4973 |||||
4974 |||||
4975 |||||
4976 |||||
4977 |||||
4978 |||||
4979 |||||
4980 |||||
4981 |||||
4982 |||||
4983 |||||
4984 |||||
4985 |||||
4986 |||||
4987 |||||
4988 |||||
4989 |||||
4990 |||||
4991 |||||
4992 |||||
4993 |||||
4994 |||||
4995 |||||
4996 |||||
4997 |||||
4998 |||||
4999 |||||
5000 |||||

QY	4900	catccctgaatctccacgaagcagcagc	4927
Dp	426	catccccgggaatctccacccctagagagac	453

RESULT 14

ACCESSION	sequence.
VERSION	BM153383
KEYWORDS	BM153383.1
SOURCE	GI:17178477
ORGANISM	EST.
	human.
	Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (pages 1 to 427)
Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R. Jr.,
Gunarathne,P.H., Muzny,D., Bouck,Y.J., Gibbs,R.A. and Margolis,J.F.
Pediatric leukemia cDNA Sequencing Project (2001)
neoplasmdb (2001)

COMMENT
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine

1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clonesetxccc.org
Seq primer: M13 primer.

FEATURES

source

1. 427
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TCBAP162"
/clone_lib="Pediatric pre-B cell acute lymphoblastic
leukemia Baylor-HESC project-TCBA"
/sex="male"
/tissue_type="Leukopheresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
/note="Vector: lambda psb; Site_1: BamHI; Site_2: EcoRI;
First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer [5'GAGAGCTGACGCGCGGAGAGAG(T)VN
3'; V-A/C/G; N-A/C/G,T] and then dg tailed. Second strand
was primed with a BamHI-dC primer
[5'ACAGAGCTCGGATCCGCGCGCGCATATATATAT(C) 3].
Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamHI and SalI sites of
lambda psb vector. Library went through one round of
normalization. Library was constructed by Mei Yu at RIKEN
of Japan (Carinici P. Westover A, Nishiyama Y, Ohsumi T,
Itoh M, Nagaoka S, Sasaki, Okazaki Y, Muramatsu M,
Schneider C, Hayashizaki Y, High efficiency selection of
full-length cDNA by improved biotinylated cap trapper.,
DNA Res 4: 1, 61-6, Feb 28, 1997)."

BASE COUNT 85 a 104 c 126 g 112 t
ORIGIN

Query Match 6.3%; Score 425.4; DB 10; Length 427;
Best Local Similarity 99.8%; Pred. No. 2.4e-106;
Matches 426; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1740 tgaaccttgaggagacatgctgctgaggggcttcgctacatgagatgtgt 1799
|||||
DB 1 TGACCCCTTGAGACATCGGTACGTGGGGGCTTCGCGCTTGCACAGATCGT 60
QY 1800 ggaagcaggaatcatcaggtgctgacgggacccgagaagaactggtgtatata 1859
|||||
DB 61 GGAAGCAGCAATCATAGAGGTGCTGACGGGACCGAAGAAACCTGGGTATATGCA 120
QY 1860 acagatgcctatccctgttactgtatgacatcttctgcgggtgatgacggatca 1919
|||||
DB 121 ACAGATGCCCTATCCCTGTACGTGATGACATCTTCTGCGGGATGATGACGCGGTCAAT 180
QY 1920 gcccctctcatgagcgtgctgctgattacatgctgctgctgctgctgctgctgct 1979
|||||
DB 181 GCCCTCTTCATAGACGCTGCTGATTCATCAGTGGCTGATCATCAAGGATCGT 240
QY 1980 gatatgaagaagcagcagcgtgaaagacacatgcatgagggcctgagaaacagat 2039
|||||
DB 241 GATATGAAAGAGGCGCGGCTGAAAGACATCGGATCATGGGCTTGAAACAGCAT 300
QY 2040 actctggtttagctgttcatatagatgacatctcctctctgtgagcgtgctgct 2099
|||||
DB 301 CCTCTGTTTACCTGTTTATAGTATGCTCATCTCTCTCTCTGAGGCTGGCTGCT 360
QY 2100 agtggatcaccgaagttaggaactgctgctacatgctgctgctgctgctgctgct 2159
|||||
DB 361 AGTGGTATCTGAAAGTGAAGAAACCTGCTGCTTACAGTATCCACAGGTGTTTGT 420
QY 2160 ctctctctg 2166
|||||
DB 421 CTTCCTG 427

RESULT 15

B678861 998 bp mRNA linear EST 01-MAY-2001
LOCUS 602624760F1 NCI_CGAP_Skn4 Homo sapiens cDNA IMAGE:4749735 5',
DEFINITION MRA sequence.

ACCESSION

B678861
VERSION B678861.1 GI:13910258

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS

1 (bases 1 to 998)

TITLE

NIH-MGC http://mgs.nci.nih.gov/.

JOURNAL

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM10603 row: 9 column: 16
High quality sequence stop: 860.

FEATURES

source

1. 998
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4749735"
/clone_lib="NCI_CGAP_Skn4"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 285 a 233 c 244 g 236 t
ORIGIN

Query Match 6.2%; Score 424.2; DB 10; Length 998;
Best Local Similarity 93.8%; Pred. No. 9.3e-106;
Matches 485; Conservative 0; Mismatches 28; Indels 4; Gaps 4;

QY 33 gtgaagaacctcattcagaagaagaacaatgctgctgctgctgctgctgctgctgct 92
|||||
DB 169 GAGAAAGAGAGCAACCAAAAGTGAAGAAACAGTGCAGCTGCTGGAAGGCGCTG 228
QY 93 gacctattatcttccgcatcctgcatctctgctgctgctgctgctgctgctgctgct 152
|||||
DB 229 GCTCTATTATTCTTCGATCTGATCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 288
QY 153 acatgaatgcatcttcccaataagcattccctcgcaggaacattcctctgctgct 212
|||||
DB 289 ACATGAATGCCATTTTCCAAATAAGCATG-CCTTGCAGAGAACATCTCTTGCTTCA 347
QY 213 ggggaattatctgtaatgcaacaacccctgttccgttaccggaatccctgaggagctcc 272
|||||
DB 348 GCGGATTATCTGTATATGCAACCAACCCCTGTTTCCGTTTACCCGCTCTGCGAGGCTCC 407
QY 273 cggagttgttgaaa-cttaacaataatccatttggctgctgctgctgctgctgctgct 331
|||||
DB 408 CGGAGTGTGGAACCTTTTAAACAAATCATTTGAGCTGCTGCTGCTGCTGCTGCTGCTGGA 467
QY 332 ggcctctttaaagcagaagaacacagcagcagcagcagcagcagcagcagcagcagcagc 391
|||||
DB 468 GCGTCTTTTATACAGCGCAGAAAGACACAGCATGAAAGAGCATGCGCAAGTTCTTGAA 527
QY 392 cattaagcagataaagaatccagctc-aaacttgaagcttcaagattccctggtgac 450
|||||

```

Db      528 CATTACGACGATCAGAAATCCAGCTCAAAACTTGAGCTTCAGATTTCCTGGTGAC 587
QY      451 aa- tgaacctctctgtggttcctatatcacaacctctctctcccaagtlactgtgga 509
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      588 AATTGAACCTTCTCTGTGGTTCTCTGTATCACAACCTCTCTCTCCCAAAGTCTACTGTGGA 647
QY      510 caagatctgagggctgatatcatcttcaccaagta 546
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      648 CAAGATGCTGAGGCTGTGATTCATTTCACCAAGTA 684

```

Search completed: September 14, 2002, 01:20:00
 Job time: 54683 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2002, 12:54:11 : Search time 20.07 Seconds
(without alignments)
2751.683 Million cell updates/sec

Title: US-09-595-526B-2

Perfect score: 11797

Sequence: 1 MACWPQLLMLMKLFFRRR.....VDVAVLTSFLQDEKESYV 2261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/pdata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/pdata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/pdata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/pdata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/pdata/2/1aa/6C.COMB.pep:*
6: /cgn2_6/pdata/2/1aa/6D.COMB.pep:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6931	58.8	1375	3	US-08-665-259-26 Sequence 26, Appl
2	6931	58.8	1375	3	US-08-762-500-26 Sequence 26, Appl
3	3129.5	26.5	1457	3	US-08-665-259-27 Sequence 27, Appl
4	3129.5	26.5	1457	3	US-08-762-500-27 Sequence 27, Appl
5	2642.5	22.4	1684	3	US-08-665-259-25 Sequence 25, Appl
6	2642.5	22.4	1684	3	US-08-762-500-25 Sequence 25, Appl
7	2642.5	22.4	1704	3	US-08-762-500-75 Sequence 75, Appl
8	340.5	2.9	1280	2	US-08-583-276-19 Sequence 19, Appl
9	339.5	2.9	1280	6	5206352-4 Patent No. 5206352
10	337	2.9	1279	2	US-08-784-649A-2 Sequence 2, Appl
11	330.5	2.8	1280	2	US-08-752-447-2 Sequence 2, Appl
12	311	2.6	1275	3	US-09-120-513-2 Sequence 2, Appl
13	311	2.6	1275	4	US-09-450-105-2 Sequence 2, Appl
14	301.5	2.6	1302	1	US-08-232-537-2 Sequence 2, Appl
15	288.5	2.4	1349	2	US-08-612-734B-2 Sequence 2, Appl
16	285.5	2.4	233	4	US-09-627-376-12 Sequence 12, Appl
17	283	2.4	1408	1	US-08-612-521-2 Sequence 2, Appl
18	275	2.3	1307	1	US-08-395-246C-2 Sequence 2, Appl
19	261	2.2	1334	2	US-08-996-545-2 Sequence 2, Appl
20	261	2.2	1334	4	US-09-328-320-2 Sequence 2, Appl
21	250	2.1	376	2	US-08-997-080-89 Sequence 89, Appl
22	250	2.1	376	2	US-08-997-362-89 Sequence 89, Appl
23	250	2.1	376	3	US-08-873-970-89 Sequence 89, Appl
24	250	2.1	376	4	US-09-095-855-89 Sequence 89, Appl
25	250	2.1	376	4	US-09-324-542-89 Sequence 89, Appl
26	240	2.0	1528	1	US-08-463-092B-6 Sequence 6, Appl
27	240	2.0	1528	2	US-08-462-109A-6 Sequence 6, Appl

28	240	2.0	1528	2	US-08-460-907B-6 Sequence 6, Appl
29	240	2.0	1528	3	US-08-463-179A-6 Sequence 6, Appl
30	240	2.0	1528	3	US-08-461-384B-6 Sequence 6, Appl
31	230	1.9	711	3	US-08-772-270A-12 Sequence 12, Appl
32	224.5	1.9	1621	4	US-08-972-927-3 Sequence 3, Appl
33	224.5	1.9	1622	4	US-08-972-927-6 Sequence 6, Appl
34	221	1.9	1531	1	US-08-463-092B-4 Sequence 4, Appl
35	221	1.9	1531	2	US-08-462-109A-4 Sequence 4, Appl
36	221	1.9	1531	2	US-08-460-907B-4 Sequence 4, Appl
37	221	1.9	1531	3	US-08-463-179A-4 Sequence 4, Appl
38	221	1.9	1531	3	US-08-461-384B-4 Sequence 4, Appl
39	218	1.8	244	4	US-08-919-573-2 Sequence 2, Appl
40	218	1.8	244	4	US-08-919-573-2 Sequence 2, Appl
41	217.5	1.8	1476	4	US-09-256-703-2 Sequence 2, Appl
42	217.5	1.8	1480	1	US-07-637-621-2 Sequence 2, Appl
43	217.5	1.8	1480	2	US-08-951-912-2 Sequence 2, Appl
44	217.5	1.8	1480	2	US-08-463-179A-2 Sequence 2, Appl
45	217.5	1.8	1480	3	US-07-890-609-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-665-259-26
Sequence 26, Application US/08665259
Patent No. 6028173
GENERAL INFORMATION:
APPLICANT: Landes, Gregory M.
APPLICANT: Burn, Timothy C.
APPLICANT: Connors, Timothy D.
APPLICANT: Dackowski, William R.
APPLICANT: Van Raay, Terence J.
APPLICANT: Klinger, Katherine W.
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES.
TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: One Mountain Road
CITY: Framingham
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,259
FILING DATE: 17-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: ICS-9.1
TELEPHONE: (508) 872-8400
TELEFAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-665-259-26
Query Match 58.8%; Score 6931; DB 3; Length 1375;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1336; Conservative 20; Mismatches 19; Indels 0; Gaps 0;

QY 887 CMEEPHTHLKLGVSIONLYKVRDGMKVAVDCLALNFEGOTTSLFNGAGKTTMTSL 946
 DB 1 CMEEPHTHLRIGVSIONLYKVRDGMKVAVDCLALNFEGOTTSLFNGAGKTTMTSL 60
 QY 947 TGLPPTSGTAYILKDRSEMSITRONLGVCPQHNVLFDMLTVEHMFARLKGJSEK 1006
 DB 61 TGLPPTSGTAYILKDRSEMSITRONLGVCPQHNVLFDMLTVEHMFARLKGJSEK 120
 QY 1007 HVAKEEMQALDVGILPSSKLSKTSQSLSGMQRLSVALAFVSGKVYLDEPTAGVDPY 1066
 DB 121 HVAKEEMQALDVGILPSSKLSKTSQSLSGMQRLSVALAFVSGKVYLDEPTAGVDPY 180
 QY 1067 SRGIMELLKXRGORTIILSHHDEADYIGDRITAIISHGKLCVSGSLFLKNOLGXY 1126
 DB 181 SRGIMELLKXRGORTIILSHHDEADYIGDRITAIISHGKLCVSGSLFLKNOLGXY 240
 QY 1127 YLTLYKDVESLSSCRNSSSTVSYLKKEDSVSSDAGLSDHESDTLIDVSAISNL 1186
 DB 241 YLTLYKDVESLSSCRNSSSTVSYLKKEDSVSSDAGLSDHESDTLIDVSAISNL 300
 QY 1187 IKKHVSEARLVDDIGHELTYYLPEAKEGAFVELFHEIDRLSDLGISSTGISETTLEE 1246
 DB 301 IKKHVSEARLVDDIGHELTYYLPEAKEGAFVELFHEIDRLSDLGISSTGISETTLEE 360
 QY 1247 IFLKVAESGVDAFTSDGTLPARRRRRAFGKOSCLRPTEDDADPNDSIIDPESRPTD 1306
 DB 361 IFLKVAESGVDAFTSDGTLPARRRRRAFGKOSCLRPTEDDADPNDSIIDPESRPTD 420
 QY 1307 ILSGMDGSGTOYKGMKLTQOQFVALMKRLLIARRSKRGFFAQIVLPAVFCIALVPSL 1366
 DB 421 ILSGMDGSGTOYKGMKLTQOQFVALMKRLLIARRSKRGFFAQIVLPAVFCIALVPSL 480
 QY 1367 IYPPGKXPSELOPMWNTNEOYTFVSNDAPEDTGFLNLTDPGSGTCMCEBNLPD 1426
 DB 481 IYPPGKXPSELOPMWNTNEOYTFVSNDAPEDTGFLNLTDPGSGTCMCEBNLPD 540
 QY 1427 TPCQAGEEMTAPVPOTIMDLFONGNWTMONPSPACOCSSDKIKKMLPVCPPGAGILPP 1486
 DB 541 TPCQAGEEMTAPVPOTIMDLFONGNWTMONPSPACOCSSDKIKKMLPVCPPGAGILPP 600
 QY 1487 PQRKONTADILODLGRNISDIYVKTYYOIIAKSLKKNLWNERPFGFSLGVSNTQALP 1546
 DB 601 PQRKONTADILODLGRNISDIYVKTYYOIIAKSLKKNLWNERPFGFSLGVSNTQALP 660
 QY 1547 PSQEVNDAIKQMKHLAKDSADRFLNSLGRFMTGLDTRNNKYKVMNNKGWHAISSEFL 1606
 DB 661 PSQEVNDAIKQMKHLAKDSADRFLNSLGRFMTGLDTRNNKYKVMNNKGWHAISSEFL 720
 QY 1607 NVINNAIIRANLOKGENSHYGITAFNHPMLTKOOLSEVALMTTSDVLYSICVIFAMS 1666
 DB 721 NVINNAIIRANLOKGENSHYGITAFNHPMLTKOOLSEVALMTTSDVLYSICVIFAMS 780
 QY 1667 FVPASFFVFLIOERYSKAKHLOFISGVKPVLYWLSNFWDMCNYVVPATLITITFCIQO 1726
 DB 781 FVPASFFVFLIOERYSKAKHLOFISGVKPVLYWLSNFWDMCNYVVPATLITITFCIQO 840
 QY 1727 KSYVSSTMLPVATLILLYGMSITPLMATPASFVKIPSTAVVLTSVNLFINGSVATF 1786
 DB 841 KSYVSSTMLPVATLILLYGMSITPLMATPASFVKIPSTAVVLTSVNLFINGSVATF 900
 QY 1787 VLEIPTDNKLNINDILKSVFLIPHPCLGRGLIDMYKNQAMADALEFGNRPVSPISW 1846
 DB 901 VLEIPTDNKLNINDILKSVFLIPHPCLGRGLIDMYKNQAMADALEFGNRPVSPISW 960
 QY 1847 DLVGNLPEMAVEGVFFLIVLIQYRFFIRPRPVNAKLSPLNDEDEVDREORILDDG 1906
 DB 961 DLVGNLPEMAVEGVFFLIVLIQYRFFIRPRPVNAKLSPLNDEDEVDREORILDDG 1020
 QY 1907 GONDILEIKELTKYRKRRAKPAVDICVIGIPGECFGLLGVNGAGKSTFKMLTGDVTVT 1966
 DB 1021 GONDILEIKELTKYRKRRAKPAVDICVIGIPGECFGLLGVNGAGKSTFKMLTGDVTVT 1080

QY 1967 RGDAFLAKNLSITSHIHVHONMGYCPQFOAITELLTGREHVERFALLRGVPEKEVGKE 2026
 DB 1081 RGDAFLAKNLSITSHIHVHONMGYCPQFOAITELLTGREHVERFALLRGVPEKEVGKE 1140
 QY 2027 WAIKRLGLVYGEYAGNYSGGKRRKLSITAMALIGBPVYFLEPTTGMDPKARRFLAMC 2086
 DB 1141 WAIKRLGLVYGEYAGNYSGGKRRKLSITAMALIGBPVYFLEPTTGMDPKARRFLAMC 1200
 QY 2087 ALSVYKESRVSILTSHSMECEALCTRMALVNGRFRCLGSVOHLKNRFGDGYTIVVRIA 2146
 DB 1201 ALSVYKESRVSILTSHSMECEALCTRMALVNGRFRCLGSVOHLKNRFGDGYTIVVRIA 1260
 QY 2147 GSNPDLPKVOEFGFLAPPGSVLKEKHNNMLOVLPSSLSLAFISILSOSKRLHIEDY 2206
 DB 1261 GSNPDLPKVOEFGFLAPPGSVLKEKHNNMLOVLPSSLSLAFISILSOSKRLHIEDY 1320
 QY 2207 SVSQTTLDQVFVNFPAKQSDDDHLKDLSTLRKNOTVVDVAVLTSFLODEKVESYV 2261
 DB 1321 SVSQTTLDQVFVNFPAKQSDDDHLKDLSTLRKNOTVVDVAVLTSFLODEKVESYV 1375

RESULT 2
 US-08-762-500-26
 ; Sequence 26, Application US/08762500
 ; Patent No. 6030806
 ; GENERAL INFORMATION:
 ; APPLICANT: Landes, Gregory M.
 ; APPLICANT: Burn, Timothy C.
 ; APPLICANT: Connors, Timothy D.
 ; APPLICANT: Dackowski, William R.
 ; APPLICANT: Van Raay, Terence J.
 ; APPLICANT: Klinger, Katherine W.
 ; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
 ; NUMBER OF SEQUENCES: 83
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: GENZYME CORPORATION
 ; STREET: One Mountain Road
 ; CITY: Framingham
 ; STATE: Massachusetts
 ; COUNTRY: United States of America
 ; ZIP: 01701
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/762,500
 ; FILING DATE: 09-DEC-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/665,259
 ; FILING DATE: 17-JUN-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US96/10469
 ; FILING DATE: 17-JUN-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dugan, Deborah A.
 ; REGISTRATION NUMBER: 37,315
 ; REFERENCE/DOCKET NUMBER: 1G5-9.3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (508) 872-8400
 ; TELEFAX: (508) 872-5415
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1375 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-762-500-26

Query Match 58.8%; Score 6931; DB 3; Length 1375;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1336; Conservative 20; Mismatches 19; Indels 0; Gaps 0;

QY 887 CMBEETHLKLGVSIQNLVYKVRDGMKVAVDGLALNFEYEGQITSTFLGHNGAKTTWMSIL 946
DB 1 CMBEETHLKLGVSIQNLVYKVRDGMKVAVDGLALNFEYEGQITSTFLGHNGAKTTWMSIL 60
QY 947 TGLPPTSGTAIILKDRISEMSTIRONLGVCPQHNVLFDMLTVEEHIMFYARLKLSEK 1006
DB 61 TGLPPTSGTAIILKDRISEMSTIRONLGVCPQHNVLFDMLTVEEHIMFYARLKLSEK 120
QY 1007 HYKAEEMQALDVGLPSSKLSKTSQLSGMRKLSVALAFVGSKVVILDEPTAGVDPY 1066
DB 121 HYKAEEMQALDVGLPSSKLSKTSQLSGMRKLSVALAFVGSKVVILDEPTAGVDPY 180
QY 1067 SRRGIWELLKTRGRTIILSTHMDADVLDGRLAIIISHGKLCCVSSSLFKNOLGTGY 1126
DB 181 SRRGIWELLKTRGRTIILSTHMDADVLDGRLAIIISHGKLCCVSSSLFKNOLGTGY 240
QY 1127 YLTIVKDVESLSSGRNSSSTVYLKREDVSQSSDAGLSDHESDTLTIDVSAISNL 1186
DB 241 YLTIVKDVESLSSGRNSSSTVYLKREDVSQSSDAGLSDHESDTLTIDVSAISNL 300
QY 1187 IRKHVSEARLVEDIGHLELYVLPYEAKGAEVLFHEIDRLSDLGISYISSETTLEE 1246
DB 301 IRKHVSEARLVEDIGHLELYVLPYEAKGAEVLFHEIDRLSDLGISYISSETTLEE 360
QY 1247 IFLKVAESGVDAETSDGTLPARNRRAFGDKOSCLRPETEDDAADPNDSIDPESRETD 1306
DB 361 IFLKVAESGVDAETSDGTLPARNRRAFGDKOSCLRPETEDDAADPNDSIDPESRETD 420
QY 1307 LLSGMDGKSYOVKGMKLQOQFVALIMKRLLIARRSRGFEAQTVPAPVFCIALVSL 1366
DB 421 LLSGMDGKSYOVKGMKLQOQFVALIMKRLLIARRSRGFEAQTVPAPVFCIALVSL 480
QY 1367 IYVPEFGKYSLELOPMWMEQTYEVSNDAPEDTGTLELNLATKPGESTRCMEGNPIPD 1426
DB 481 IYVPEFGKYSLELOPMWMEQTYEVSNDAPEDTGTLELNLATKPGESTRCMEGNPIPD 540
QY 1427 TPCQAGEEBMTAPVPOTIMDLFQNGNMTQNPSPACQSSDKIKMLPVCPPGAGLPP 1486
DB 541 TPCQAGEEBMTAPVPOTIMDLFQNGNMTQNPSPACQSSDKIKMLPVCPPGAGLPP 600
QY 1487 PQRKQNTAIIODLIGRINSDLVKTYVQIIAKSLKNITWNEPRKGGSLGVSTQALP 1546
DB 601 PQRKQNTAIIODLIGRINSDLVKTYVQIIAKSLKNITWNEPRKGGSLGVSTQALP 660
QY 1547 PSEVNDATIKOKKHLLKLAKDSSADREFLNSLGRFMTGLTRNNVVKWFMNKGMAHIISSFL 1606
DB 661 PSEVNDATIKOKKHLLKLAKDSSADREFLNSLGRFMTGLTRNNVVKWFMNKGMAHIISSFL 720
QY 1607 NYINNALILRANLQGENPSHYGITAENHPLNLTKOOLSEVALMTTSVDVLSICVIFAMS 1666
DB 721 NYINNALILRANLQGENPSHYGITAENHPLNLTKOOLSEVALMTTSVDVLSICVIFAMS 780
QY 1667 FVPASVVFVLIQERVSKAHLOFISGVKRYIYWSLNFVMDKNNYVPATLVITITICFOQ 1726
DB 781 FVPASVVFVLIQERVSKAHLOFISGVKRYIYWSLNFVMDKNNYVPATLVITITICFOQ 840
QY 1727 KSVYSTNIPVATALLLGLGMSITPLMPYPASVEFKIPSTAYVVLVSYNLFIGINSVATF 1786
DB 841 KSVYSTNIPVATALLLGLGMSITPLMPYPASVEFKIPSTAYVVLVSYNLFIGINSVATF 900
QY 1787 VLELFTDNKLNNINILDKSVFLIPFHCIGRLIDMKVKNQAMADALEREENRFPVSPISW 1846
DB 901 VLELFTDNKLNNINILDKSVFLIPFHCIGRLIDMKVKNQAMADALEREENRFPVSPISW 960
QY 1847 DLVGRNLFMAAVGVFFLITVLIQYRFTIRRPVNAKSLPLNDEDEYRERORILDOG 1906
DB 961 DLVGRNLFMAAVGVFFLITVLIQYRFTIRRPVNAKSLPLNDEDEYRERORILDOG 1020

QY 1907 GQNDILEIKELTKLYRRRRKPAVDRIQVGPBGCFGLGVNAGKSTFKMLTGDTPVT 1966
DB 1021 GQNDILEIKELTKLYRRRRKPAVDRIQVGPBGCFGLGVNAGKSTFKMLTGDTPVT 1080
QY 1967 RGDAFLKNSILSNIEHYHQMGYCPQPDATITELLTGREHYEFALLRGVPEKGVGGE 2026
DB 1081 RGDAFLKNSILSNIEHYHQMGYCPQPDATITELLTGREHYEFALLRGVPEKGVGGE 1140
QY 2027 WAIRKGLVYKGEKYAGYAGSGNKRKLTAMALIGBPVYFLDEPTTGMPPKARFLMNC 2086
DB 1141 WAIRKGLVYKGEKYAGYAGSGNKRKLTAMALIGBPVYFLDEPTTGMPPKARFLMNC 1200
QY 2087 ALSVYKGRSVVLTSHSMECEALCTRMALIVNGRFCLGSVOHLKKNRFGDYTIIVRIA 2146
DB 1201 ALSVYKGRSVVLTSHSMECEALCTRMALIVNGRFCLGSVOHLKKNRFGDYTIIVRIA 1260
QY 2147 GSNPDLKPVQDFGLAPPGSVLTKKHHNMLOYOLPSSLSTARFFSLSSKKRLHIEDY 2206
DB 1261 GSNPDLKPVQDFGLAPPGSVLTKKHHNMLOYOLPSSLSTARFFSLSSKKRLHIEDY 1320
QY 2207 SVSQTTLDOVFVNFPAKQSDDDHLKDLSTLHKNOTVVDVAVLTSFLODEKKESEYV 2261
DB 1321 SVSQTTLDOVFVNFPAKQSDDDHLKDLSTLHKNOTVVDVAVLTSFLODEKKESEYV 1375

RESULT 3
US-08-665-259-27
Sequence 27, Application US/08665259
Patent No. 6028173
GENERAL INFORMATION:
APPLICANT: Landes, Gregory M.
APPLICANT: Burn, Timothy C.
APPLICANT: Connors, Timothy D.
APPLICANT: Dackowski, William R.
APPLICANT: Van Raay, Terence J.
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: One Mountain Road
CITY: Framingham
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,259
FILING DATE: 17-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: IG5-9.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 872-8400
TELEFAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-665-259-27

Query Match 26.5%; Score 3129.5; DB 3; Length 1457;


```

: TELEFAX: (508) 872-5415
: INFORMATION FOR SER ID NO: 27:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 1457 amino acids
:   TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
US-08-762-500-27

```

Query Match	26.5%;	Score 3129.5;	DB 3;	Length 1457;
Best Local Similarity	46.0%;	Pred. No. 1.5e-288;		
Matches 676;	Conservative 207;	Mismatches 377;	Indels 211;	Gaps 28

QY	888	MEEPETHLKIGVSTONIVKRYKGMVAADGALNVEEQIISFPHGNAGKTTMSTLT	947
Db	1	MEEPETHLPVYCVDKLTKYKXKDKKLALNKLISLNIJENQVVSFIHGNAGKTTMSTLT	60
QY	948	GLPPTSGATVILGKDIRSEMSTIRONLGVCPDHNVLFDMLVVEHEHWARLAKLSBK	1007
Db	61	GLPPTSGATVIGHDIRTEMDERIKRNLCPDHNVLFDRLVVEHEHWARLSKSMAGE	120
QY	1008	VKAMEOMALDVGLPSSKLSKTSIQLSGQMOKRLVALAFVGSKVYIIDEPTACVDYS	1067
Db	121	IRKETDKMIDLEL-SNKRSHISQVLTSQGMKRLSVAFVGVGSRAIITIDEPTACVDYEA	179
QY	1068	RGGVITLLEYROGRTIITLSTHMDADVGDGDAIATISHGKLCYGVSSILFLKNOUGTGY	1127
Db	180	RRAIMDLILKTKRRTILTLSTHMDADLGDRIATISHGKLCGGSPLFLKGAIXDGR	239
QY	1128	LTVLKKDVESLSRCRNSSTVSYLAKEDVSQSSSDAGLIGSDHESDTLTDIVASISNLI	1187
Db	240	LTVLKPAPBGTSGPEPLASPGCPRLSSCPEQ-----VSGPT	279
QY	1188	RKHYSERLVEDIGHETLYLPLPEAKEGAFVELFHEIDRLSDIGISSYGISSETTLEBI	1247
Db	280	RKHVASSILVSDTSTELSTYLLIPSEAVKKAQFEBFLFOOLSHSIDALHLSFGLMTDLEEV	339
QY	1248	FLKVAEE-----SGVYA-ETSDGTLPARNRRAFDKQSCRLPTE-----	1287
Db	340	FLKXSEEDOSLENSEADVYKSRKDYLPAGABGLTAVGGQGNLARCSLQAOSASLOSASS	399
QY	1288	-----DDADPNDSDIDESRETDLLSGMDGSGSYQVYKAKL	1324
Db	400	VGSARGEGTGYSDGYDYLFDNLQDPD--VNSIQBAEMELANQV--GQSGRKLEGMWL	456
QY	1325	TQOQFVALLKRLLIARSRKGFPAQIVLPAVFCIALVPSLIVPFGKYPSELQPMY	1384
Db	457	KMRPFGHLVRFHCARNRKALCSOILLPAFVFCYAMVALSVPEIGDLPVLVPSQY	516
QY	1385	NEQYT-----FVSDAPE-----DGTLELNLATKDPGEGTRCM-----	1419
Db	517	H-NTTORGNFIPIANEERBEYRLRLSPDASPOQVLSTRLPDSGVGATVCLKSPANGSLG	575
QY	1420	-----EGNPI-----PD-----	1428
Db	576	PMLNLSGSESLLAARFDSMCLESLFTQGLPLSNFVPPPPAPSDSPVXPDEDSLOAMN	635
QY	1427	-----TTCQAGBEEMTPAR-VPTIMDLFQNGWMTQMNSPACQSSDXIKKMLPVCPPGAG	1488
Db	636	MSLPRTGAPETWSAPSLPLRVHEPVR-----CTCSAQOTGFS---CPSSVGG	680
QY	1484	LPPROKONTADILIODITGNISIDYLVKTYVQOITAKSLKNKILWNEFRGFGESLVSNTQ	1543
Db	681	HPQMRVYVGDILITDTIGNVSEYILFLTSDR-----RLHKGATTFG--NVQ	726
QY	1544	ALPSPQEVNDAIKOMKHHKLAKDSSADRELNSLGRFMTGLDTRNNVYKWFNNKGWHAIS	1603
Db	727	KSIPAS-----FGARVPPMVKRIARVRVAYQVLVNNKGYSHP	763
QY	1604	SFLVNNATILIRANLQGE-NPSHGITAFNHNPLNLTKOQLSFVALMTTSVUVLVISYI	1662

```

Db 764 TYUSLNNALLIRANLPKRSKGNPAAXYITVTNHPMKNKTSASLS-LDYLLQGTQDVIAIFII 822
Qy 1663 FAMSFPVASFVVELIDERSKAHLOFISGVKPYITWLSNFWMDMCINVPATLVITIIIFI 17222
Db 823 VAMSFVPAFSEVVFVFLVAKSRKAKHLOFVSGCNPIVIWMLNMYWMDMLNYLVPATCCVITLF 882
Qy 1723 CFQOKSVVSSNLPVLAALLLLLGWSTPFLMPASVFEKIPSTAVVVLTSVLFGIINGS 17823
Db 883 VFEDLPATSPFNEPAVLSLFLLLGWSITPIMTPASFWFEVPSAVVFLVILNLFGITAT 942
Qy 1783 VAFVLELFT-DNKLNNINDILKSVFLIPHFCLTGLIDMKNOMAMADALERFGE-NRF 18400
Db 943 VATLLOLFHEFDKDLKAVNSYLSKSCFLIPPNYMLGMLKEMAYNEINIFYAKIGQFDKM 10020
Qy 1841 VPSLSMDLVGRNLFAMAVEGVFFLITVLIOYRFFIRPPVNAKLSPLNDEDEDVRRERQ 19000
Db 1003 KSPFEMDITVRGLVAMTVEGFVFGLTIMQYNFLRQPLRPVSTRPYED-DVVASERQ 10610
Qy 1901 RILDGGGONDLLEKELTKTYRRK---RKPAVDRTCVGI-PRGECTGLGVAGAKSSTF 19566
Db 1062 RVLGGLADNDNMVKLENTITKYKRSKIGRILLADRLDGLVCVGECEFGLLGVAGAKTSTF 11220
Qy 1957 KMLGGDTTVTRGDFLKNKSLINIHNEHOMNMGCPQPAITFELLTGREHVEFFALLGCV 20160
Db 1122 KMLTGDSESTTGGAEFVNGHSLVDLLOVOOSLGTCQOFDPVDELTAHRLDLTYRLKCI 11810
Qy 2017 PEKEVGVGEMVAIFKGLGVYGEKRGVAGNYSGKNRKRLLSTAMALIGGPVYFLDEPTTGM 20760
Db 1182 PMKDEAQVWKALEKELTLYADKPAGTYSGCKRRLSTALMALIGVPAITFLDEPTTGM 12410
Qy 2077 PKARFLMNCALSVYKGRSVLTSHSMECEPALCTRAIMVNGRFLGSOHLKNRFG 21360
Db 1242 PKARFLMNLILDLIKTGRSVLTSHSMECEPALCTRLAIMVNGRHLGISOHLKNRFG 13010
Qy 2137 DGYITVIRAGSNBDLCPVODFGFLAPGSGVLEKEHRNMLYOLOPSSLSLARIPSIJSQ 21960
Db 1302 DGYITVIR-TKSSONVADVVRFFNRNRPPEAHAGKTPYKVOTLOLSEHLSIOVSKMEO 13600
Qy 2197 SKKRLHIEDYSVSQTLDOYVFNPAKDQSD 2227
Db 1361 VGVGLGIEDYSVSQTLIDNVFNPAKKQSDN 1391

RESULT 5
US-08-665-259-25
: Sequence 25, Application US/08665259
: Patent No. 60281173
:
: GENERAL INFORMATION:
: APPLICANT: Landes, Gregory M.
: APPLICANT: Butru, Timothy C.
: APPLICANT: Connors, Timothy D.
: APPLICANT: Dackowski, William R.
: APPLICANT: Van Raay, Terence J.
: APPLICANT: Klingert, Katherine W.
: TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
: TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING SAME
: NUMBER OF SEQUENCES: 73
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: GENZEYS CORPORATION
: STREET: One Mountain Road
: CITY: Framingham
: STATE: Massachusetts
: COUNTRY: United States of America
: ZIP: 01701
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/665,259
: FILING DATE: 17-JUN-1996
: CLASSIFICATION: 435

```

ATTORNEY/AGENT INFORMATION:
 NAME: Dugan, Deborah A.
 REGISTRATION NUMBER: 37,315
 REFERENCE/DOCKET NUMBER: 1G5-9.1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (508) 872-8400
 TELEFAX: (508) 872-5415
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1684 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-665-259-25

Query Match 22.4%; Score 2642.5; DB 3; Length 1684;
 Best Local Similarity 35.7%; Pred. No. 6.8e-242;
 Matches 639; Conservative 300; Mismatches 523; Indels 327; Gaps 48;

QY 534 AGIYFTGTPGSI-LEPHHYKIRMDIDNVERTN-----KIKQYV----- 574
 DB 111 AAVFEHPFNKBEPLPLAVKYHLRF--SYTRNNYMTQTSFPLEKETEGMTTSLFPL 167
 QY 575 --DRGPRADPED--MRYVWGFAVLQDVVEQALIVLTGTE----KKGVYVMOQMPY 624
 DB 168 FPNQPRFLITSPDGGEPYIREGFLAVOHAVDRALMEYHADATROLFORLTVYIKRPY 227
 QY 625 PCYVDLFLRYMSRMLFMTLAMYSAVILKIGIYERKARLEKTRIMGLDLSIMFS 684
 DB 228 PPFIDPFLVAIQOLPFLLLSTYALTATARAVOEKERRLKEKRYMGLSWMHMSA 287
 QY 685 WFISSLILVYASGLIVYIILKLG-----NLPSDPSVYEVLSVFAVITLQCFILSTL 739
 DB 288 WFLLEFLLEPLLAASFMTLLFCVKVKNVAVLSRSDPSLVLAFLCFAISTISEFSFMTF 347
 QY 740 FSRANLAAACGIIYFTLYPYLVCAVADYVGTFLKIFASLSPVAFGFCFEFALFEE 799
 DB 348 FSKANMAAFGFLFYIYIFVAPRYNNMTLSOKLCSLLSNVAMACQILGFEA 407
 QY 800 QGIGVQMDNLFESPE-EDGFNLTTSISMLEDFTLVYGVMTVYLAEPVQYGIIPRWYF 858
 DB 408 KGMGIQWMDLT-SPVNVDDDFCGQVGLMLLDSVLGLVYWEAVFPGQVPGWYF 466
 QY 859 PCTSYWGE-----ESDEKSHPSGNSOKRMSCEMEEPHLKLGSIONLVYVYDGM 912
 DB 467 FIMPSYWGKPRAVAGKEEDSDP--EKALRNEYFEEPEPDVAGIKIKHLSVFPVGN 523
 QY 913 K--VAVDGLALNFYEQITTSFLGNAGAKTTMSITLGPPTSGATYIILKDIRSEMST 970
 DB 524 KDRAAVRDLNLNVEGQITVLGNHAGAKTTLSMLTGLPPTSGRAVYISGSEISQDMVQ 583
 QY 971 IRONLVCPOHNVLFDMITVEEHMFYARLKLGISEKHVAKMEOMALDVLGIPSSKLKSKT 1030
 DB 584 IRKSLGICPOHDLIFDNLTAENHLYFAOLKGLSRCKPREVKOMLHIGL-EDKWNMSR 642
 QY 1031 SOLSGMORKSVLAFVAGSKVITLDEPTAGVPSYSRGIMWELLTYRGGRTIILSTHH 1090
 DB 643 RFLSGMRKRIKSTIGALIASGVKVLIDEPPTSGMDAISRRALIDLOKOSDRITVLTTHF 702
 QY 1091 MDEADVLDRIATISHKLCVSSSFLKMQDLGTGYVLTIVKPKDVESLSSCRNSSTVS 1150
 DB 703 MDEADVLDRIATIMAKGRLQCCSSSFLKQYAGYHMTLYKE-----P 746
 QY 1151 YLKKEDESSQSSDAGLGSHESTLTITIVSAISNLIRKHVSEKRIYEDIGHETLYVLPY 1210
 DB 747 HCNEDP-----ISQLVHNNVPAJTLSSAGAEISFTLPR 780
 QY 1211 FAKKGAFAVELFHEIDRLSDLGISYSYISSETLEELFLKVAE--ESGVAETSDGTLPA 1268
 DB 781 ESTHR--FEGFLAKLEKKOKELGASFGASITTMEEVFLKGVKLVDSMDIQAQ--LPA 836
 QY 1269 ---RRNRRAFG--DKOSCLRPFTEDDAADPND--SDIDPESRETDLLSGMDQKGSYOV 1319

DB 837 LOYHERRASDMAVDSNLC-----GAMPDSDGIGALLIEERTAVKINTGL----- 881
 QY 1320 KGWKLTOQOQFVALLMKRLLIARRSRKGFPAQIVLPAVEFCIALVSLVPPRGKYPSLEL 1379
 DB 882 ---ALHCQOFKAMFLKKAAYSREKMAVAQVLPVLTCTTALL----- 922
 QY 1380 QPMWNEQYTPVSNDAPEDTGTELLINALTKDPGFETRCMEGNPIPDTPCOAGEEWTYA 1439
 DB 923 -----AINYSSELEFDDPML--RLTLA-----EYGR 946
 QY 1440 PVPQITMDLFONGNMTNOMPSPACOCSSDKIKKMLPYCPGAGGLPPOGRKONTADIID 1499
 DB 947 VYFVSYPGSQLQOULSEHLKDALQAE-----DEPREVLCD 983
 DB 984 L-----EEFLI-----FRASYEGGFN----- 1000
 QY 1556 KQKKHLKLAKDSSADRFNLISGREMTGIDTYRNNKVMFNNKGWHAISFLVANNALLR 1615
 DB 1001 -----ERCL--VAASEFDVGEFTVNALEFNNQAYHSPATALAVDNLLEK 1043
 QY 1616 ANLQKGENPSHYGITAFNRP-----LNLTKQOLSEVALMTTSVDVLSICVIFAMSFPYA 1670
 DB 1044 --LLCG--PHASIVSNFPQPRSAIOAKDQPN-----GRKFDTALNL--LFMAAFILAS 1093
 QY 1671 SFVFLIQRERVSRAKHLQFISGVKPYIWLNSFWDMCNVYVPAVLVIIIFCQOKSYV 1730
 DB 1094 TFSITLAVSERAAQAKHVGCVGHVASFWSLMDLILSFLIPSLILLVFAKAFVRAFT 1153
 QY 1731 SSTNLEVALALLLWQWSTPLTPMPASFVKIPRATVYVLTISVNLFIGNSVAFVLEL 1790
 DB 1154 RQGHMADTLLLLLGWALIPLMYLNFEFLCAATVATRLTIFNLISG---ATFLWVT 1209
 QY 1791 ---FTDNKLNINIDILKSVFLIFPHRCLEGRGLIDWKN-----QAMADALERGP 1836
 DB 1210 IMRIPAVKLEELSKTLTDHFIVLPNHCIGMAVSSFEYENETRYCTSSVAAHYCKKNI 1269
 QY 1837 ---ENRFVSPLSMDL--VGRNLFMAVAGSVFELTVLIIQYFFTRIPRPVNAKL----- 1885
 DB 1270 QYOENFY-----AMSAFVGPRFVAFMAASCAYLILFLEITMLRLKILCALRRRTL 1325
 QY 1886 -----SPINDEDEDYRRRORLIDOGGOND---LEIKELKIRYRRKKP--AVDRICV 1934
 DB 1326 TELYTMFVLPEDQVADERTKILASPDSLLHTPLIILKELSKYV--EQRVPLIANDRLSL 1384
 QY 1935 GIPPGECFGLLVGNAGKSTFKMLTGTVTYRGDAFLKNLSILSNIHEVHONMGYCPQF 1994
 DB 1385 AVQKGCFCFLGNAGAKTTTFKMLTGEESLTSQDAFVGHRISSDVGKVRORIGYCPQF 1444
 QY 1995 DATTELLTGREHVEFPALLRGVPEKEVGVGMALIRKLGIVYGGKYAGNSGGKKRLS 2054
 DB 1445 DALDHMTGREMLVMYARLGIPIERHIGACVENTLRLGLEPHAKRLVTRTSGGKKRLS 1504
 QY 2055 TAAALIGCPVYVLEIDPTGMDPKARFLPMNCALSVYEGKGVNLTSSMECEALCTRM 2114
 DB 1505 TGIALLIGBAVIFLDEPSTGMDPVARRLMDVYARAREGAKIITTSISMCECALCTRL 1564
 QY 2115 AIMVNGFRICGSVOHLKNRFGDGYTIVRI--AGSNPDLPVQDFGLAPPGSVLYLKEH 2172
 DB 1565 AIMVQOQFCLGSPQILKSGSGYSLRAKVQSEGOQEALEFKAFVDTLFGSVLEDEH 1624
 QY 2173 RNMLQVQLPSSLSLARITSIISQSKKRLIHEDYVSQTTLDQVNVNA 2221
 DB 1625 QGVVHYHLGRDLSMAKYFGILLEKAKKEYGVDDYSQISLEQVPLSPA 1673

RESULT 6
 US-08-762-500-25
 ; Sequence 25, Application US/08762500
 ; Patent No. 6030806
 ; GENERAL INFORMATION:

QY	1332	LMKRLLLARRSRKGEFAOVLVAVVCALVPSLIVPFGKYPSLQLQPMWYNQYTFV	1339
Db	708	--WFFYV-----GVFCALINGGLQAPAFILFISKII	736
QY	1392	SNDAPEDTGTELELINALTKDPGFGTRCMGNPIPDTPCAGEEWTAPVQTLMDLFRON	1451
Db	737	-----GVETR-----	741
QY	1452	GNMTMOMPSPACOCSSSIKKMLPVCPPGAGLPPRQKRONADLIQDLTGNISIDLYK	1511
Db	742	-----IDDETROKSNFSSTL-----FLAL	762
QY	1512	TYVOIIAKSLKNIWNEFRYRGFSLGSVSTQALPESQEVNDAIKQMKHLKLADSS-A	1570
Db	763	GIISFII-----FLQGFITTGKA-----GELTTRIKRYMVRSLRDQSWMF	804
QY	1571	DRLPNSIGREPMTGIDTRNNYKVFNNKGWHAISSELMVITNNAILRANLQKGENPSHYIT	1630
Db	805	DDPKNTTGALTRRL-ANDAQQV-----KG-AIGSRILAVITTONI--ANLGTGI-----II	849
QY	1631	AFNPNMLTQQLSEVALMTSDVLVSLVCVIFAMSFEVASTVVFLEDRYSKAKHLOFI	1690
Db	850	SFIQWOLT-----LHLIAVIPITAIAGVEMK-----MLSGALDKKKELE--	891
QY	1691	SGVAPVITWLSNFWMDMCNVVPATLVIIIFICFOOK-----SYVSTNLPEVALL--LLLY	1745
Db	892	GAGKATEALEIENF-----RTVSLIHQOKFEHMYAQSIQVYPRNSLRKAHIF	938
QY	1746	G--WSTIPPLMPASFPVKIKISTAVVVLTVSNLFIGINSVAIFVLELPTDNKLNNINIL	1803
Db	939	GITSPFOAMMYVSYSACGFRFGAVLVA-----HKLMSFEVVL	975
QY	1804	KSVFLIEPHFCILGKLIDMYKNQAMADALEREFGENRFV-----SPLSMDLVGRNLFAMAV	1858
Db	976	---LVESAVVFGAMAVGVQVSPADPYAKAKISAHIIMITEKTPLDISYREGIMPNTL	1031
QY	1859	EGYVFLITVLIOYRFETRFR--PVNAKLSPLNDEDEDVAREQRILLDGGQNDILETEL	1917
Db	1032	EGNVTEEEVV---FNYTRPDIVLOGLS-----LEVKK--	1062
QY	1918	TKIIRRRKPAVDNRICIGIPGECFGLGVNAGKSSPFKMLTGDVTYRGDAFLNKSI	1977
Db	1063	-----GGTLALVSGSGGKSTVQJLLERFYDPLAGKVLLDKGEI	1101
QY	1978	LS-NIHEYONMGYCPQ---EP-----AIEELLGRHEVFFPALLGV	2016
Db	1102	KRLWOMRRLKGLGVSEPIPLFCSSIAENIAYGDNRSRVYSOEIIYAAKEANIHAIFISL	1161
QY	2017	PEKEVGVGEMALIKRLGLVYKEGYAGNYSQGNKRKLSTAMLLIGGPVVFLEDEPTGMD	2076
Db	1162	PNKISTVYGDKGTQ-----LSGGKKQKALALARALVAKQPHILLDEKTSALD	1207
QY	2077	PKARFLMNCALSVYKGRSVLTSMSMECECALCTRMAIMWNGREFLCGSYQHLKNFG	2136
Db	1208	TESKRVQVQ--ALDKARREGFTCIIVIAHRLSTIQN-ADLIVFQNGRYKHEGTHQQLLAQK	1265
QY	2137	DGYTIVVRIAGS	2148
Db	1266	LYFSMVSQAGT	1277
RESULT	9		
5206352-4			
Patent No. 5206352			
APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,			
Michael M.			
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA			
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS			
NUMBER OF SEQUENCES: 4			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/07/622, 836			
FILING DATE: 24-SEP-1990			
PRIOR APPLICATION DATA:			

```

: APPLICATION NUMBER: 892,575
: FILING DATE: 01-AUG-1986
: APPLICATION NUMBER: 845,610
: FILING DATE: 28-MAR-1986
: SEQ ID NO:4
: LENGTH: 1280
5206352-4

Query Match      2.9%; Score 339.5; DB 6; Length 1280;
Best Local Similarity 18.7%; Pred. No. 4,2e-22;
Matches 272; Conservative 201; Mismatches 470; Indels 509; Gaps

QY 776 KIFSLSPAFGCGCEYFALFEEOGIGVOMDLFESPVEEDGFNLUTSISMLEDTEFL- 834
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 256 EVLAIRITVIAFGQKKELRYNK-----NLEEA--KRIGIKALTANISICARLL 305
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

QY 835 ----YGVMTW-LEAVPQOYIGLR--PWYFCTSYFGEES----- 870
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 306 IVASYALAFWGTLLVLSGEGSIGOVLTVFFSVLLIGAFVGOASPSEAFANAGAAYEI 365
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 871 ----DEKSHPSNOKRMASEICEEPEPTHLKIGVIONLVKVRDGGKKYAV-DGLALNFE 925
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 366 FKIIDNKPISDYSK-----SGHKRDNIKGNLEFNHVFSPSRKREYVILKGLNLXQVS 419
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 926 GQITSELGHNAGKTTMTSLITGLPPTSTAYILGKDIRS-EMSTIRONLGVCPQHNVL 984
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 420 GQFVALVNGSCGCGSTVOLMORLPLPTEGMVSVDQDRIITNVRLREIIGVSOEPLV 479
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 985 FDMLTVEHITWYFVRKLGSSEKHYKAMEQMALD--VGLP---SSKLKSTQSLSGGMQR 1039
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 480 F-ATTIAENT-RYKRENVMTDELEKAYKKNAYDFIMKLPHKFDPLVGRGQLSGGQKQ 537
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 1040 KLSVALAFVGGSKYVILDEPTAGVDPYSRKGIWELLKTRGRTIILSTHMD--EADY 1096
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 538 RIATARALVRNPKLILDEATSAIDTESEAVVOVALDKARKRTIYLAHRLSTVRNDV 597
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 1097 LG--DRIATISHGKLCVGSSEFLKNOLOGVLYTLTKADV---SSLSGCCNSSSTFVS 1151
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 598 TAGDDGVIVYBK-----NDELIMKER--GIYFKLYVMQTGNVEYLENADDEKS--- 646
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 1152 LKKEDEVSOSSSDAGLGSDEHSPTLTITVSAISNLRKIVASEARLVEDIGHELYTVLPE 1211
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 647 --EIDALEMSSNDSR-----SSLRK----- 665
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 1212 AAKGAVELFHEIDRLSDLGISSYGISPTTLEEIFLKVAEESGVDAETSDGTLPARRN 1271
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 666 ----- 668
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 1272 RRAFQDKQSLRPTEDDAADPNDSDIDPESRETDLLSGMDKSGSYOKGWLQOQFVA 1331
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 669 RRSVRGSOAQDRKISTKEAL--DESIIP-----VSFWIMKMLNLTE 707
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 1332 LLMKRLILARSKRGFPAQOVLPAVPCIALVSELVPPFGKYPSLELDQPMWYNQGYTFV 1391
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 708 --WYFVYV-----GVCAIINGLOPAPAFILSKII----- 736
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 1392 SNDAPEDTGLELLNALTKDPGGRROMEGNPIPTPCOAGEEWTTAIVPOTIMDLFON 1451
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 737 -----GVETR----- 741
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 1452 GNMWIMQNPSPACQSSDIKKMLPVCPRPAGAGLPORPORONTADILQDLTGNISIDLYLK 1511
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 742 ----- 762
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 1512 TYVOIIAKSLKNIKWNEFRRGFSIGVSNTOALPQSOEVDANIKOMKHLKLANDSS-A 1570
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 763 GLISFIT-----FFLGQETRGKA-----GELITRRLRMVPRSMRLRDVSWMF 804
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 1571 DRPLANSIGREWTGDTLRANNKYVFPNNKGHAISSPLANVINNALIRANLQKGNPBYGTF 1630
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 805 DDPKNTGALTTTRL-ANDAADV---KG--ALGSRLAVITTONI--ANLGTGI-----II 849
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

```

```

1631 AFNHPNLTKOOLEVALMTTSVDVLSICVIFAMSFVPSFVFLIOERNSAKHLQFI 1690
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
850 SFIQWQLT-----LLLAIVPIAIGVEMK-----MLSGALMKKKELE-- 891
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1691 SGKPVITWLSNFWDMCNVVPVTLVITIFIFCPOCK--SYVSTNPLVALL--LLLY 1745
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
892 GAGKATEAEINNF-----RTVVSILQEOKEFHMAVQSLQVPRNSLRHAHLE 938
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1746 G--NSTIPPLMYPASEVFKEIPSTAVVLTSLVNLFIGINSVATEFVLELTDNKLNINDIL 1803
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
939 GITTSFTQAMMYPSYACGFRGALVA-----HKLMSEFDVL 975
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1804 KSVLIFPHFLGLGLDMVKNQAMADALEFGENRV-----SPLSWLVGNLFLAMAY 1858
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
976 ---LVFSAVVEGAMAVGVSSFAVDYAKAKISAAHIMIIEKPLIDYSTEGLEMPNTL 1931
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1859 EGVPELTLVLIQYREFRPR--PVNAKLSPLNDEDEDVRRRQRILIDGQNDILETEL 1917
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1032 ESNVTFGEVY--FNYPRIPIVLOGLS-----LEVKK- 1062
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1918 TKIYRRKKRPADVRLICVGIIPGECFGLGVNAGKSSTFKMLTGDVTVTGDAFLNKSTI 1977
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1063 -----GQTLALVSSGCGKSTVWVOLLERFYDPLAGKVLLDGEKI 1101
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1978 LS-NIHEVHONMGYCPQ-----FD-----ATTELLTGREHVEFFALLRGV 2016
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1102 KRLNVQWMLFAHLGIYSEPILEFDCSIAENIAYGDNRSVSOEELIVRAKENIAHAFIESL 1161
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2017 PEKEVGKVEEMAIRKLGIVKYEKAYAGNYSGGNKRKLTSTAALLIGPPVAVLEDEPTGMD 2076
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1162 PNYSTKVGDDKGTQ-----LSGQKORIALAVALRQPHILLDLDATSLD 1207
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2077 PRARFLMNCALSVYKEGRSVVLTSHSMECEALCTRNAIVNGRFRCLSGVQHLKRNFG 2136
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1208 TSEKXVVOE-ALDKAREGRTCIIVIAHRLSTION-ADLIVFQNGRKHGHTHOOLLAQK 1265
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2137 DGTIVVRIAGS 2148
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1266 IYFSMVSVOAGT 1277
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 10
US-08-784-649A-2
; Sequence 2, Application US/08784649A
; Patent No. 5830697
; GENERAL INFORMATION:
; APPLICANT: SIKIC, Branimir I
; APPLICANT: Chen, Gang
; TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
; CYCLOSPORIN MODULATION
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/784,649A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: Reg No. 5830697 36,677
; REFERENCE/DOCKET NUMBER: 06037/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070

```

```

TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1279 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-784-649A-2

```

```

Query Match 2.9%; Score 337; DB 2; Length 1279;
Best Local Similarity 18.7%; Pred. No. 7, 2e-22;
Matches 272; Conservative 200; Mismatches 471; Indels 508; Gaps 56;

```

```

776 KIFASLSIPVAFGRGCEFFALFEBOGIGVQMDNFFESPVEDGQNLUTSISMFLFTFL- 834
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
256 EVLAIRIVIAFGQKLELYRNK-----NLEEA--KRIGIKRATINISGAFL 305
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
835 ---YGVMTWY-IEAVFGYQIPR--PWYPPCTKSYWFGES----- 870
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
306 ITASTALAFWYCTTLVLSGEYSIGQVLTVFSLIGARVSGQASPISIBAFANRGAAYEIP 365
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
871 ---DEKSHPGSNQKRMSETCMEEPHLKLCVSTQNLVKYIRQGMKAAV-DGLALNFEY 926
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
366 KIIDNKPISIDYSK-----SGHKPDNIKMLERFNHFSYPSRKEVLIKGLNLKVQSG 419
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
927 QITSPFIGNHAKRTTMTSLTGLFPPTSGTAVITGKDIRS-EMSTIRONLGVCPQHNLF 985
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
420 QTVVALVNGSGCKSTTVQIMORLYDPTGAWSVSDQDIRTINVFLEILIGVYSQEEVLF 479
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
986 DMLTVEEHIMFYARLKGISEKHVKAEMQMLD--VGLP--SSKLKSTQSLSGQMK 1040
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
480 -ATTIENI-RRGRENVIMDEIEKAVKEANAYDFIMKLPKHFDTLVGERGAQLSGGQK 537
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1041 LSYALAFVGSKVYIIDEPTAGVDYSRRGITWELLKTRQGRITILSTHMD--EADVL 1097
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
538 IAIARALVNRNPRIILLDEATSAIDTESEAVVOVALDKARKRRTVIVIAHRLSTION 597
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1098 G--DRAITISHKGLCCVSSFLKNOLGTGYLTLVKKDV--ESSLSGCRNSSSTVSYL 1152
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
598 AGFDGCVIYERK-----NHDELMEKE--GIYFKLVMTQAGNEVELNMADESKS---- 645
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1153 KKEDSVSOSSDAGIGSDHESDTLFDVSAISNLRKHVSEARVEDIGHELITYLPLEA 1212
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
646 -EIDALEMSNDR-----SSLRK----- 664
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1213 AKGAFVELFHEIDRLSDLGISYGISFTLEIFIKVAEESGVDAFTSDGTLPARNR 1272
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
665 -----RSTR 668
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1273 RAFGDKQCLRPPTEDDAADPNDSIDIPESRETDLSDMGKGYQVKGWKLTOQOVAL 1332
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
669 RSVRGSQADQRKISTKEAL--DESLP-----VSFWRIKMLNLT- 706
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1333 LMKRLLIARRSRKGFPAQIVLPAVEVCIALVSLVPPGKPSLELOPMWIMBEYTPVS 1392
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
707 -WPFYV-----GVPCAILNGILOPAFAIIFSIL----- 735
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1393 NDAPEDTGLELNLALTKDGFGRCMGNPIPDTCQAGEEEMTAPVPQTIMDLFONG 1452
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
736 -----GVFTR----- 740
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1453 NMTQNPSPACQCSSDKIKKMLPVCPPGAGLPPQPKQNTADIIDLTGRNISDYLYKT 1512
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
741 -----IDDPETKQNSMLPSL-----FLALG 762
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1513 YVQITAKSLNKTIWNEFRYGSLSGVSNQALPPEQEVNDATIKQKKHLKLAKDS--AD 1571
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
763 IISFT-----FLQGFPPGKA-----GEILKRLRIYVFFSMRLRODYSWFD 804
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1572 RFLNSLGRFMTGLDTRNNVWVFNNKGMAISSLVFNINALLRANLQGEHPSHYGITA 1631
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```



```

Db 805 DPKNTGALTTRL-ANDAAOV-----KG--AIGSLAVITQNT--ANLGTCI-----11S 849
QY 1632 FNPPLNLTQOLSEVALMTTSVDVLVSCVTFAMSFVPAFVFLILOERSAKHLOFTS 1691
Db 850 FIVGWOLT-----LLLAIVPIIAIAGVEMK-----MLSGQALKKCKEIE--G 891
QY 1692 GVPKPVLYMNSFWDMONVVPVPTLVITIFICQOK---SYVSTNLPVLAII--LLYG 1746
Db 892 AGAIAEALENF-----RTVSLTQOKFHEMYAQSLOVPRNSIKRAHIFG 938
QY 1747 --WSTPLMYPASVEFKIPSTAVVLTISVNLFIGINGSVATFVLELTQNKLNINDIK 1804
Db 939 IYFSFTQAMMYFSYAGCFRFGATLVA-----HKLSFEDVL- 974
QY 1805 SVFLIPPHRCIGRLIDMKKNQAMADALFRGENRFV-----SPLSWDIVGNLPMAYE 1859
Db 975 ---LVSAVVFQAMAVGOVSSFPADYAKAKISAHIIMIEKTPILDSYSTEGLMPTLE 1031
QY 1860 GVAFELLITVLIOYREFIRPR-PVNAKLSPINDEDEVRERQRILDGGQNDILEIKELT 1918
Db 1032 GNVTEGEVY---FNKPTRDIPVLQGLS-----LEVKK-- 1061
QY 1919 KIYRRKRAVADRICVIGIPGCEPGLLVGNAGKSTFKMLTGDVTYRGDAFLNKNSTL 1978
Db 1062 -----GQTLALVSSGCGKSTVOLLERFYDPLAGKLLDGEIK 1101
QY 1979 S-NIEVHONMGCPQ---FD-----AITFLRGHEVEFPALLRGVP 2017
Db 1102 RLVNOMLRHIGIVSOEPLTDCSIAENIAYGDSNRVYSGEIVAAKEANIHAFIESLP 1161
QY 2018 EKEVGKVEPMARIRKILGYKGYKAGYAGNSGKRRKLTAMALIGGPVFLDEPTGMDP 2077
Db 1162 NKYSKVGKGTQ-----LSGQOKRIATARALVROPHILLDEATSAIDY 1207
QY 2078 KARFLMNCALSVYEGRSVVLISHMECEALCTRMAIIVNGRRCJGSVOHLKRRGD 2137
Db 1208 ESEKVOE-ALDKAREGTCIVIAHRLSTQN-ADLIYVFPNGKVKEGHTHQLLAGKI 1265
QY 2138 GTTVVRIAGS 2148
Db 1266 YFSMVSVQAGT 1276

RESULT 11
US-08-752-447-2
: Sequence 2, Application US/08752447
: Patent No. 5994088
: GENERAL INFORMATION:
: APPLICANT: Mechmetner, Eugene
: APPLICANT: Roninson, Igor B
: TITLE OF INVENTION: Methods and Reagents for Preparing and
: TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.
: STREET: 300 South Wacker Drive, Seventh Floor
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/752,447
: FILING DATE: 15-NOV-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5994088han, Kevin E
: REGISTRATION NUMBER: 35,303
: REFERENCE/DOCKET NUMBER: 95,1121

```

```

: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-913-0001
: TELEFAX: 312-913-9808
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1280 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-752-447-2

```

```

Query Match 2.8%; Score 330.5; DB 2; Length 1280;
Best Local Similarity 18.5%; Pred. No. 3e-21;
Matches 269; Conservative 197; Mismatches 476; Indels 511; Gaps 54;

```

```

QY 776 KIFASLSPAVAFGCGCEYFALFEQIGIGVOMDILFESPEDEGFNTLTSISMILPFTFL- 834
Db 256 EVLAIRTVIAFGQKKELERYNK-----MLEEA--KRIGIKKATANISGAAPLL 305
QY 835 ---YGVMTWY-IEAVPGQYIPR--PWYFQTSYMGES----- 870
Db 306 IYASYAFAFWYGTTLVLGSEXTIGQVLTFFSVLIGAFSGQASPSIEAFANAKGAAEYI 365
QY 871 ---DEKSHGSGNOKRMSIEICMEDEPTHLKLVGSIONLVKVVYDQKQVAV-DGLALNFEY 925
Db 366 FKIIDNKPISIDYSK-----SGHKPDNIKGNLEFNHVSYPSSRREVKILKGLNKKVQS 419
QY 926 GQITSPFNGAGKQTTMTSILTLFPPTSGTAVIILKDIRS-EMSTIRONLVCPCQHNVL 984
Db 420 GQVYALVNGSGCGKSTTVQLMQRLYDPTEGMVSVDQDITIRVRLKREIIGVSOEPLV 479
QY 985 FDMITVEHEITFAFLKLGISEKHYAKEMQMALD--VGLP---SSKLKSTQSLSGQMR 1039
Db 480 F-ATTTAENI-RYGRNVMTDEIEKAVKEMANVDEIMKLPKFFDLVYGERGQLSGGQK 537
QY 1040 KLSVALAFVQGSKVVLIDEPCTAGVDPSRSGIMWELLKXROGRTIILSTHH--HDEADY 1096
Db 538 RIAIARALVANKIILLDEPESALDTESEAVOVADLRKARKRTTIVIAHREATVAMDV 597
QY 1097 LG--DRIATISHGKICLVSSSLFLKNQLOGTGYLLLVKKDV--BSSLSSCRNSSSTVSY 1151
Db 598 IAGFDDGVIVKQ-----NHDELMKER--GIYFKLVMTQGTAGNEVELENADSKS--- 646
QY 1152 LKEDSVSSQSSDAGISGHESDITLIDVSALSNILRKVSEARLVEDIGHELYVLPYE 1211
Db 647 ---EIDALEMSSNDSR-----SSLIRK----- 665
QY 1212 AAKGAFVELFHEIDRLSDLGISYISSETLLEIFLKVAESGVDAETSDGTLPARRN 1271
Db 666 -----RST 668
QY 1272 RRAFGDKQSCLPFTEDDAADPNDSIDIPESRETDLLSGMDKGSYOVKKKLTQOQFVA 1331
Db 669 KRSVRSQAOHQHRLSTKEL--DESIPP-----VSFWRIMKLNTE 707
QY 1332 LMKRLILARSRKGFPAQIVLPAVEFCIALVESLIIVPPGKPSLDELPMMYBQTFV 1391
Db 708 --WPFYFV-----GVFCALINGGIQPAFALIFSKIIIVFTRI----- 742
QY 1392 SMDAPEDGTLELLNALAKDPGFGTRCMENPDPDPCQAGEEMTAPVPQITMDLFON 1451
Db 743 --DDPE-----TKRQNSMLFSLFLALGIIISFTF----- 770
QY 1452 GWTWQNSPACQSSDKIKKMLPVCPGAGGLPPQKQNTADILDDLGKRNISDYLVK 1511
Db 771 -----FLDGFTEGKAGEITLK 786
QY 1512 TYVOLIAKSL--KNKIWNEFRYGGFSLGVSNTOALPSPQEVNDALIKOMKHLKLANDSS 1569
Db 787 RLRYWVFRSMRLQDVSWFHD-----PKNTIGALTTRLANDAAOV----- 825
QY 1570 ADRLNLSIGRPMGLDTRNNYKVFENKGMHAISSFLNVLINNALIRANLQGENPSHYGI 1629

```

```

Db      826 -----KG--AIGSLAVITONI--ANLGTGI-----1 848
QY      1630 TAFNHPDLNLTQOLSEVALMTTSVDVLVSCIVFAMSFPAFVYVFLIERVSKAKHLOF 1689
Db      849 ISFTYOMOLT-----LTLAIVPIIAIAGVENKMFAG-----QALTKKELE- 891
QY      1690 ISGKRPVYIWLNSFVDMCNVYVPATLVIIIFCFOOK---SYVSTNLPVALT--LTL 1744
Db      892 -GAGKLTATEIENF-----RTVSLTQOKFEHMYAQSLQVYRNSLRKAI 937
QY      1745 YG--WSITPLMPASFAVEKIPSTAYVLTSVNLFIGINSVATFVLELFTDKLNINDI 1802
Db      938 FGITFSTQAMMYFAYAGCFRFGAYLVA-----HKLMSFEDV 974
QY      1803 LKSVFLIFPHFCLRGILDMYKNQAMADLERGENRY-----SPLSMDLYGRNLFAMA 1857
Db      975 L-----LVFSAYVFGAMAVQVSSFPADYAKAKISAHHIIMIEKPLIDSYSTEGIMPNT 1030
QY      1858 VEGVFFLITVLIOYFFFIKPR--PVNAKLSPLNDEDEDEVREORRLDGGGQNDILEIKE 1916
Db      1031 LBNVTFGEVY---FNYPRPDIPVLOGLS-----LEVAK 1062
QY      1917 LFKYRRKRPAVDRIQVGIPECEPGLLVNGAGKSTFKMLTGDTVTYRGDAFLNKNS 1976
Db      1063 -----GQTLALVSSGCGKSTVYOLLERYDPLAGVILLDGKE 1100
QY      1977 ILS-NIHEVHONMGYCPD---FD-----AITELLTGEHVEFFALLNG 2015
Db      1101 IKRLNVOMLRAHLGIYQSEPILEDCSIAENIAYGDNRSVYQSEIYRAKKEANIHAFFIS 1160
QY      2016 VPEKEGKVGEMAIKRLGLVYKGEKAYAGNYSGNKRLSTAMALIGPVPVFLDEPTTGM 2075
Db      1161 LPKKYSTKVGDKTO-----LSGQKORIAARLVAQPHILLDEFTSL 1206
QY      2076 DPRARFLMNCALSVYKESRVVLTSHSMECEALCTRMALVNGFRCLGVSVOHLKNRF 2135
Db      1207 DTSEKRVQOE-ALDKAREGRTCIYIAHRLSTION-ADLIVFONGSVKBEHGHQOLLAQK 1264
QY      2136 GGGYTLVRIAGS 2148
Db      1265 GIYFSMVSVQAGT 1277

RESULT 12
US-09-120-513-2
; Sequence 2, Application US/09120513
; Patent No. 6025160
; GENERAL INFORMATION:
; APPLICANT: Brun, Kimberly
; APPLICANT: Chenery, Richard
; APPLICANT: Ellens, Harna
; APPLICANT: Field, John
; TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE
; TITLE OF INVENTION: SEQUENCES ENCODING RAT MDRLB2 AND
; TITLE OF INVENTION: SCREENING METHODS THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY:
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,513
; FILING DATE: 22-JUL-1998

```

```

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T
; REGISTRATION NUMBER: 30,954
; REFERENCE/POCKET NUMBER: GP50008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5015
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1275 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-120-513-2.

```

```

Query Match      2.6%; Score 311; DB 3; Length 1275;
Best Local Similarity 19.0%; Pred. No. 2.2e-19;
Matches 281; Conservative 180; Mismatches 437; Indels 580; Gaps 62;

```

```

QY      743 ANLAACGGIYFTLYLPEYLCVAMQDYVGFLLKIFASLSVPAFGCEYFALFEQGI 802
Db      293 ANIST---GIATLVYASYAL-----AFWYGTSLVLSNEYSI 326
QY      803 GVQWMDNLFESPVEEDGFMLTTSISMMLFDITLYGVMTYIEAVFPGQYGIIPRPY----- 857
Db      327 G-----OVLTVFFSILGTGTFSGHLPNIEA-PANAGAAYVEIFKIIDN 369
QY      858 PFCSTKSYMFGESEDEKSHPGSNOKMSEICMEEPHTLKLGVSIONLVKVV--RDGKVA 915
Db      370 EPSIDSF-----STKGH-----KDSIMGLERKNYFNPSPSEVKI- 407
QY      916 VDLGLNFEYEGQITPSLHNGAGKTTTMSILTGLFPPTSGTAYILGKDIRS-EMSTIRON 974
Db      408 LKGLMLKVKSGQVALVNSGCGKSTVOLLRLYDPIEGEVSIDGQIFRTINRYLEI 467
QY      975 LGCPQHNVLDPLMTEVEHIMFYARLKLSEKHVKAEMQALD--VGLP---SSKLKSK 1029
Db      468 IGVYQSEVPLF-ATTIAENI--RYGRENVTMDIEKAAVEANAAYDFIMKLPRKFTVLGER 525
QY      1030 TSOISGGMOKLSVALAFVSGSKVYLIDEPYAGVPSRRCIMELLLKRYRGRTIILSTH 1089
Db      526 GAOISGGOKORIAARLALVNRPKIILLDEATSAIDTSEAVYQALDKARCGRTIYIAH 585
QY      1090 HMDADVLDRIALISHGKLCCVGSSEFLKNQOLGTGYLLVKKDVESLSSCRNSSTV 1149
Db      586 R-----LSTVNRADVIA 597
QY      1150 STLKEDSVSSSSDAGISGDSHESDTLTIIVSAISNLIRKHYSEARLYEDIGHLLTYLP 1209
Db      598 GF-----DGVY-----IVEQGNHE----- 611
QY      1210 YEAAKE-GAFVELF-----HEIDRLSDLGISY-----GISETTELEIFLVAEESG 1256
Db      612 -ELMKEKGIYKLVMTQTRGNIEP-----GNNAVESDTCASLELT----- 652
QY      1257 VDAETSDGTLPARRNRRAFGQKQSCLRPFTEDDAADPNDSDIDESPRTDLLSGMDKGS 1316
Db      653 --SEKSKSPLIIRSIIRSIHRQDERLSKE-----DVDEDPV----- 690
QY      1317 YQVKGWKLTOQGFVALLMKRLLIARSKKGFPAQIVLPAVYVCLALVFSLLVPPFGKYP 1376
Db      691 -WVSFWOILKLNISE--WPYLAV-----GVLCAVINQCIDPVAIFSKLIVGF----- 736
QY      1377 LELQPMWYNEQYTFVSNDAPEDTGTELLNALTRDPGRTGCMGNDLPDTPCOAGBEEM 1436
Db      737 -----SRDDHET----- 744
QY      1437 TTPAVPQTIMDLFONGNMTQNPSPACQCSSDKIKKMLPVCPGAAGLPPQRRONTADI 1496

```

```

Db 745 -----KORNCNLSL 754
QY 1497 LQDLTGRNISLYKTYVQIIAKSLKNTIWNNEFRYGGFSLGVSNTQALPPSQEVNDAIK 1556
Db 755 L-----FLVGMISFVT-----YFQGFTEFGKA-----GEILTRRLR 786
QY 1557 QMKHKLAKDS-ADRFNLISLGRFMTGL-DTRNNVYKWFNNKGMHAISFLVNNAIL 1614
Db 787 YWFKSMRLRODISWFDHKNKTGSLTRRLASDASNK-----GAMGSLAVYTQNV- 837
QY 1615 RANLQKGNPSSHGYITAFNHPNLTKOQSEVALMTTSVDLVSLICVTFAMSFVPASFV 1674
Db 838 -ANLGTG-----IILSLVGMQTLTLLLVIIPIIVIGIIEK-----874
QY 1675 FLIOERYSKAKHLOPISGVKPVIIYWLSNFVDMCNVVPALVLIIFICPOK---SYVS 1731
Db 875 -LLSQALDKKLEIS-KIATEAIENF-----RTVSLTRQKEETMAQ 919
QY 1732 STNLPVALLLLLYGWSIT-----PLMYPASFEKIPSTAYVLTSLVFLIGINSV 1783
Db 920 SLQIPYRAALKKAVFGITFAFTQAMLYFSYACFRF-----GATLV-----961
QY 1784 ATFVLELFTDKNNINDILKSVLIPPHCLGRGLI-----DMYKNQAMADALERF 1835
Db 962 ---ARELMT-----FENVMVLSAVVFGAMAGNTSSFAPDYAKAKVSASHIRI 1008
QY 1836 GE-----NRFVSLSMQDLVGRNLFAMAVEGVFELIVLQYRFPRIPR-PYNAKL 1885
Db 1009 IEKPEIDSYSTEGIKP-NW-LEGWKF---NGVMF-----NYTPRNPIVLOGL 1053
QY 1886 SPLNDEDEYVRERORILIDGGGONDLEIKELIKYRRKKRPAYDRICVGPISCEGFL 1945
Db 1054 S-----PEVKK-----GQTLRLV 1066
QY 1946 GYNGAGKSTKMLTGDTTTRGDAFLKNSILS-NIHEVQNNQYCPQ---PD-AIT- 1998
Db 1067 GSSGGKSTVOLLERFYNPAGVTFIDGKEIKQINVOMLAHGIYSQEPILDCSITE 1126
QY 1999 -----ELTGRHEHVEFFALLRGVPEKVGEMAIRKLGIVKYEKAGN 2044
Db 1127 NIAYGDNRRVYSHETIYAAREANIHOFIDSLPERKYNTRVADKIQ-----1172
QY 2045 YSGNKRRLSTAMALIGSPVVFLEDEPTTGMDPKARFRLMCAISVYKEGRSVLTJSHM 2104
Db 1173 LSGGQKRIAIARALVRQPHILLDEATSAIDTESEKVVQF-ALDKAREGRTCIIVIAHRL 1231
QY 2105 EECEALCTRMALIMVGRFCGLSQVHLKNRGDTIY 2142
Db 1232 STION-ADLIIVIQNGVKEHGHQOULLAOKGIYFSMV 1268

```

RESULT 13

```

US-09-450-105-2
: Sequence 2, Application US/09450105
: Patent No. 6169166
: GENERAL INFORMATION:
: APPLICANT: Kimberly Anne Brun
: APPLICANT: Richard James Chenery
: APPLICANT: Harna Ellens
: APPLICANT: John Anthony Feild
: APPLICANT: Lin Yue
: TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES
: TITLE OF INVENTION: ENCODING RAT MDRI1B2 AND SCREENING METHODS THEREOF
: FILE REFERENCE: GP-50008-D1
: CURRENT APPLICATION NUMBER: US/09/450,105
: EARLIER FILING DATE: 1999-11-29
: EARLIER APPLICATION NUMBER: 09/120,513
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 1275
: TYPE: PRT

```

```

: ORGANISM: HOMO SAPIENS
US-09-450-105-2

```

```

Query Match 2.6%; Score 311; DB 4; Length 1275;
Best Local Similarity 19.0%; Pred. No. 2,2e-19;
Matches 281; Conservative 180; Mismatches 437; Indels 580; Gaps 62;

```

```

QY 743 ANLAACGGITTYTLLPVLYLCVAMODYGFILKIFASLISLVAAFGCEYALPEEGCI 802
Db 293 ANISI---GIAYLLVYASAL-----ATWYGS-LVLSNESI 326
QY 803 GYQWMDLIESPVDEDFNLTTISMLFDTFLYGVMTWYIEAVFGQXGIPRPWY-----857
Db 327 G-----QVLYTFSLTGTFSIHLAPRIEA-FANARAAIEIKIIDN 369
QY 858 FPCYSYWFGEESDEKSHPSNOKRMEICEDEPTHLKLVSIONLYKY--RDGMKYA 915
Db 370 EPSIDSF-----STKGH-----KPDISINGLEFKNVFNYPSPREVKI- 407
QY 916 VQGLALNFEYGQTSFPLNGAGKTTMSILTGPEPTGTAVIIGKDIRS-EMSTIRON 974
Db 408 LKGLNLKVKSGQTVVALGNSGCKSTVOLLDRLODPIGEVSIIDQDIRITNVYIRI 467
QY 975 LGVCPQHNVLFDMLTVEEHIFARLKLSEKHVKAEMQALD--VGLP---SSKLRSK 1029
Db 468 IGVSQEPVLV-ATTIAENI-RYGRENVMTDELEKAVKEANAYDFIMKLPKFNLTGEBR 525
QY 1030 TSQLSGMOKRLSALAFVGGSKVYLDEPTACVDPYSRKGWELLKTKROGRTIILSTH 1089
Db 526 GAOLSGQKORIAIARALVRNPRIILLDEATSAIDTESAVVOALADKAREBRTIYIAH 585
QY 1090 HMEADVLDGRRIAIISHGKLCCVSSSLFKNOIGTYLTLVKKDVESSLSCRRNSSTV 1149
Db 586 R-----LSTVRNADVIA 597
QY 1150 SYLKEDSVSQSSDAGLSDEHSTLTIDVSAISNLIRKHVSEARVEDIGHELTYLVP 1209
Db 598 GF-----DCGV-----YVQGNHE-----611
QY 1210 YEAAKE-GAFVLF-----HEIDRLSDLGISY--GISETYLEITLKYAEBEG 1256
Db 612 -ELMKRGYIFKLVMTQTRGNLETP-----GNAVESQSDTASSETL-----652
QY 1257 VDLETGDTLPARRNRARFGQKOSCLRPTEDDAADPNDSIDIPESRETDLSGMDGKS 1316
Db 653 --SEKSKPLIRSTIRSHRRQDERLSKE-----DVDEYV-----690
QY 1317 YQYKGMKLTQOQFVALLMKRLIARRSRKGFPAQIVLPAVFCIALVSLYVPPGKIPS 1376
Db 691 -WYFWQILKLINISE--WPLYLV-----GYLCAYVINGCIGQVFAIVFSKIVGF-----736
QY 1377 LELQPMYNNQYTFVSNDAPEDTGTLELLNALTKDGFGRMCEGNPIPDTCQAGEEBW 1436
Db 737 -----SRDDHET-----744
QY 1437 TTPAVPQTIWDLFQNGMTWMTQNPSPACQSSDKIKKMLPVCPPAGGLPPQKOKNTADI 1496
Db 745 -----KORNCNLSL 754
QY 1497 LQDLTGRNISLYKTYVQIIAKSLKNTIWNNEFRYGGFSLGVSNTQALPPSQEVNDAIK 1556
Db 755 L-----FLVGMISFVT-----YFQGFTEFGKA-----GEILTRRLR 786
QY 1557 QMKHKLAKDS-ADRFNLISLGRFMTGL-DTRNNVYKWFNNKGMHAISFLVNNAIL 1614
Db 787 YWFKSMRLRODISWFDHKNKTGSLTRRLASDASNK-----GAMGSLAVYTQNV- 837
QY 1615 RANLQKGNPSSHGYITAFNHPNLTKOQSEVALMTTSVDLVSLICVTFAMSFVPASFV 1674
Db 838 -ANLGTG-----IILSLVGMQTLTLLLVIIPIIVIGIIEK-----874
QY 1675 FLIOERYSKAKHLOPISGVKPVIIYWLSNFVDMCNVVPALVLIIFICPOK---SYVS 1731

```



```

OY 1466 SSD-----KIRKMLPVCPPGAGLPPPOKONTADIILODITGRNISDYVITY-V 1514
      |||      |      |||      |      |||      |      |||      |
Db 827 SSDAGOLACLSGVALGTFIVCVSITIGI-----IIAHVYAKMIAVLLAAVY 875
OY 1515 QIIAKSLKRIWNERRYGGSFCVSNTOALPPSOEVDAIKOMKHLKLAODSSADRL 1574
      |||      |      |||      |      |||      |      |||      |
Db 876 MITAGVYRLV-----LALAESRHS-----AYNDAA-----IAAECRGIRI 915
OY 1575 NSIGRFMTGIDTRNNYKVMFNKKGMHAISSPLNINNALIRANLKGEMPSHYGITAFNH 1634
      |||      |      |||      |      |||      |      |||      |
Db 916 ASIGR-----ERGSRRASNAVKPEYKGI-----940
OY 1635 PLNLTKOOLSEVALMTTSDVLVSLICVIFAMSEFVPAFVFLIOERVSKAHLQFTSGVK 1694
      |||      |      |||      |      |||      |      |||      |
Db 941 -----RFTLITNT-----LLALSPTIIFYAL-----963
OY 1695 PVIYW-----LSNFVDMKNY--VVPATLVIIIFICEQOKSVSSNTLPVALLLLLGW 1747
      |||      |      |||      |      |||      |      |||      |
Db 964 --AYMGAQOVNRGTYSQDLFEIVLPAL-----FSAQS-----995
OY 1748 SITPLMYPASFEKI--PSTAYVVLTSVNLFIGNSVAFVLELFTDKNLNINDILASV 1806
      |||      |      |||      |      |||      |      |||      |
Db 996 -----AGQIFSLSPESKRAVGARNV--GLHDQKPT-----1025
OY 1807 FLIFPHCLGRGLIDMVKNOAMADALERGENRFVSPLSMDLVGRNLFAMAVEGVFFLI 1866
      |||      |      |||      |      |||      |      |||      |
Db 1026 -----IVDDAQOGSA-----LPSSITSLPTLED-----1049
OY 1867 TYLIOTRFIRPRPVNAKISPLNDEDEDERERORILDOGGONDILIEIKELTKIYRRK-R 1925
      |||      |      |||      |      |||      |      |||      |
Db 1050 -----KASP-----SSGGW-----IEPKVNSLCYPSKPO 1073
OY 1926 KPAVDRIQVIGPGCGFLIGVNGAGKSTFPMKLTGDTTVTRGDAFLKNSLTLSINIEVH 1985
      |||      |      |||      |      |||      |      |||      |
Db 1074 HPAIDVNINISIRPGEFIALVPGSGAKSTISLLQRFYDPAAGSVOLDGODIREVAVPOH 1133
OY 1986 Q-NMGVPO-----FDATTELLGRHEVEFFALLRGVPEKEVGKVEWMAIR 2030
      |||      |      |||      |      |||      |      |||      |
Db 1134 RGRGLGVPEPDLPGSISYNIGLAAPGQVLTRODRIKAKCGIHE-----1181
OY 2031 KGLVYKYGKVA-----GNYSGNKRRKLSTAMALIGGPPVFLDEPTTGMDPKARFL 2083
      |||      |      |||      |      |||      |      |||      |
Db 1182 --FISLPEGYSRTECGTNGSKLSGGOKORIAVARALIRSPVILLDEVTSLADHSEGOI 1239
OY 2084 RNCALSVKESGVYVLTSHSMECEALCTRAIMVNGFRCLGS 2127
      |||      |      |||      |      |||      |      |||      |
Db 1240 KE-AVDGASVDRITIVVAHRLSTVON-ADRIIFEDDGRVVEGS 1281

```

```

RESULT 15
US-08-612-734B-2
; Sequence 2, Application US/08612734B
; Patent No. 5914246
; GENERAL INFORMATION:
; APPLICANT: Peery, Robert B.
; APPLICANT: Skatrud, Paul L.
; APPLICANT: Tobin, Matthew B.
; TITLE OF INVENTION: Multiple Drug Resistance Gene of
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center, DC1501
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: U.S.A.
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/612,734B
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Craig, Anne I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: X-9681
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-354-9570
; TELEFAX: 617-354-4043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1349 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-612-734B-2

Query Match 2.48; Score 288.5; DB 2; Length 1349;
Best Local Similarity 16.9%; Pred. No. 3,5e-17;
Matches 289; Conservative 234; Mismatches 537; Indels 655; Gaps 61;

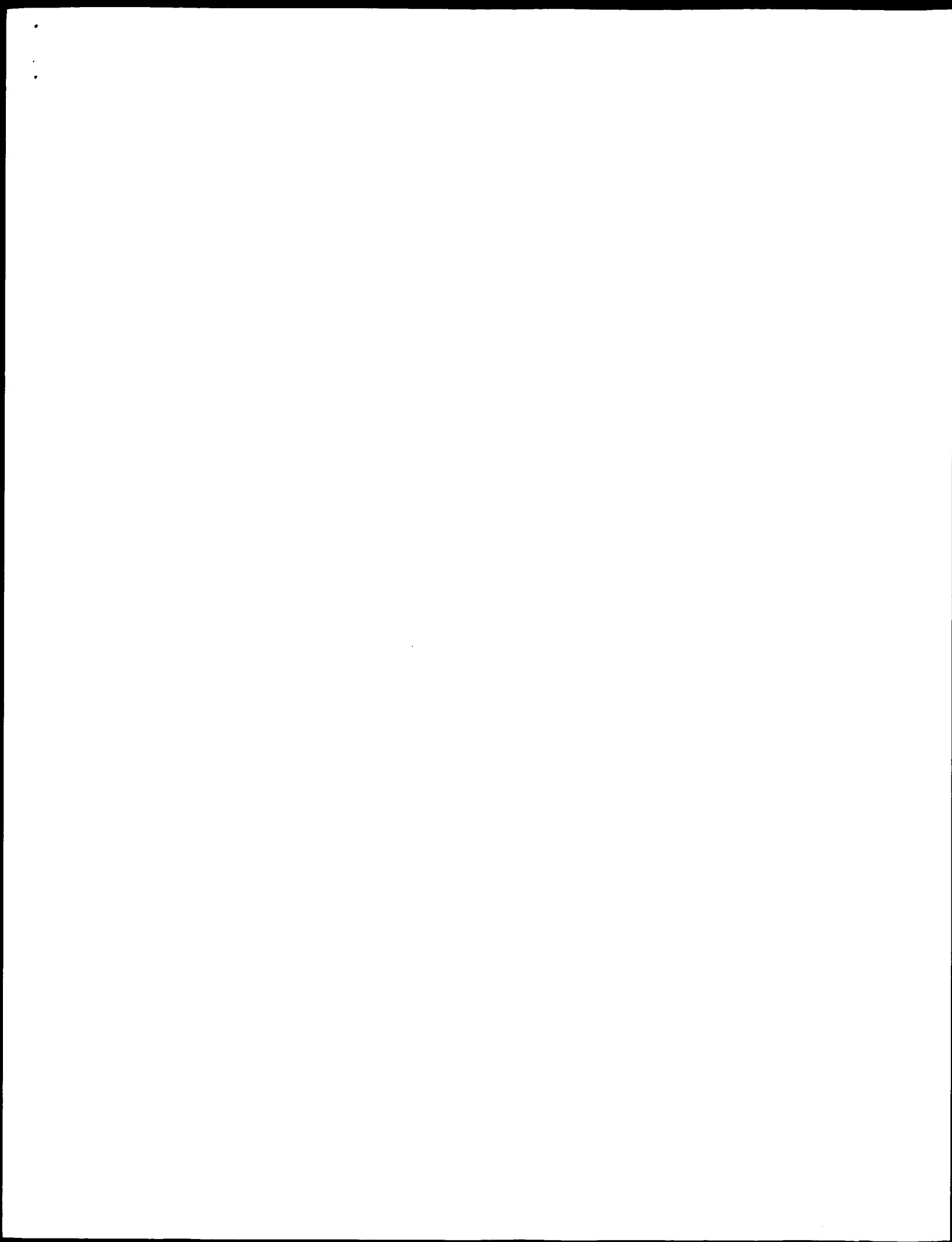
OY 575 DPGRADPEEDMRVWGMGFAYLDVNVQALIRVLTGTEKTYGYMOMPRCYVDIDIFLR 634
      |||      |      |||      |      |||      |      |||      |
Db 59 DHKRAVDLNDST-----FAHLDHEKEVLRKOLDAPSVKVS--FTLYRYASRKDILILI 112
OY 635 VMS-----RSMPLFMTLAMIYSVAVITIKGI-----VEKEBARLKETRMINGLDN 678
      |||      |      |||      |      |||      |      |||      |
Db 113 VSAICATIAAGALPLPFIIL--FGLSASAPGIGISLGTMPHYEFHK-----LTK 158
OY 679 SILMFNF--ISLIPLVSA-----GLLVVIL-----KLG-----707
      |||      |      |||      |      |||      |      |||      |
Db 159 NVLFVVLGIAEFTYVSVTFGEIYNGEHLTKIRENYLEAILRQMMAYFDKLGAGEVTT 218
OY 708 -----NLTPSDPSVVFVLSFAVVTILQCFILSTPSRAULAAC-----749
      |||      |      |||      |      |||      |      |||      |
Db 219 RITADTNLIDDAISEKVGTLTAFA--TFYATVAVV--KWKALIGSTVYALVMVG 275
OY 750 GGIYFPLLYLVYLCVAMQDY--VGFTL--KIFASLSPVAF-----788
      |||      |      |||      |      |||      |      |||      |
Db 276 GGSRFYIKYSKSI-----ESYGAGGTVAEVEVISINATAFGQDLAQYETHLAEAER 331
OY 789 -----FGCEYFALFEEQIGVQMDNLFPESVDEGDNLTTSISMLFDTFLYG 836
      |||      |      |||      |      |||      |      |||      |
Db 332 GWYKQOYILGMMIGMGFMGFIYSNYGFGFWMGSRFVVGKEVNVQVYLTVMISLIGSISG 391
OY 837 VMTWYIEAVFPGQYGIPIRPWYFPCTSYNGESEDSEKS--HGSNOKRMSELCMEEPFH 894
      |||      |      |||      |      |||      |      |||      |
Db 392 NVAPNGQAFITNG-----VAAAKIT--STIDRSPLDPSDEGKYLD-----H 432
OY 895 LKLGVSIONLVKVRDGMKVAV--DGLALNFEEQIITSPFHNGAGKTTMISLITGLFPPT 953
      |||      |      |||      |      |||      |      |||      |
Db 433 FEGNIEFRNVKHIYPRPEYTWEDVSLMPAGKTALVPGSGSGSYVGLVERFYLPV 492
OY 954 SCRAYILGDIKRS--EMSTRONIGVCPQNNVLFDMLTVE--SHIMFYANLKLSEKHVKA 1010
      |||      |      |||      |      |||      |      |||      |
Db 493 GGGVLLDGDHDIQTLNRLWRQOISLVSQEPVLFSTTIFRNIHGLIGTKEFHESKDIRE 552
OY 1011 EMEQ-----MALOVGLPSSKLSKTSQLSGGMOKRSLVALAFGSKVYILDEP 1059
      |||      |      |||      |      |||      |      |||      |
Db 553 LVNARMANAHDFIMALEBGY--DTWVGORGFLISGGOKORAIARAYSDPKIILLDBA 611
OY 1060 TACVDPYSRRGIWELLKRYRGRTIILSTHMDADVLDGRIATISHGKLCVGSLSFLK 1119
      |||      |      |||      |      |||      |      |||      |
Db 612 TSALDFKSGGVQOALDKAEGRTIIVNHRSTIKTAINIVAMVG--KLIAGQGHDELY 670
OY 1120 NQIGTGYIYTLVKKVDESSLSCRSNSSYVSTLKEDYSQSSDAGLGSDESPTLTID 1179
      |||      |      |||      |      |||      |      |||      |
Db 671 DRKGTYKKLVEAOR-----INEKEALEADADMDAD-----703
OY 1180 VSAISMLIRKHVSEARLVEDIGHELTYVLPYEAAGAFVELFHHIDRLSDLGISSYGI 1239
      |||      |      |||      |      |||      |      |||      |

```

```

Db 704 -----DFGDE-----GV 710
QY 1240 SETTEELFLVAERSVDATETSGTLPARRNRRAFGDKQCLPFTEDDAADPNDSID 1299
Db 711 T-----RIKTAVSSNSIDA-----VD 727
QY 1300 PESRETDLSGMDGSGYQVQKGMKLTQOQFVALLMKRLILARRSRKGFPAQIVLPAV-EV 1358
Db 728 EKARLEMRKTGTQKSVSAVLSKVPKPEQEKYSIMTLV-----KFIGAFNRPELGYM 779
QY 1359 CIALVSLIVPPKPKPSLELOPMWYNBOYTQVSNDAPEDEGTLELLNALTKPDGFGTRC 1418
Db 780 LIGTFEFLAG--GGQPT--QAFLYAKAISTLS--LPE-----SMFHKLHNDANF---- 823
QY 1419 MEGNPIPTPOAGEEETIAPVPOTIMDLFQNGNMTQNPSPACQCSKIKKMLPYCP 1478
Db 824 -----WSLM-----827
QY 1479 PGAGLPPPKQKNTADILDLTGHNISDYLKTYVQIIAKSLKNIWNEFRYGGFSLG 1538
Db 828 -----FVVGIAQFI-----SLS 840
QY 1539 VSNTO-ALPPOEVNDALIKQKHLKLAKDSSADRFNLSIGRFMTGLDTRNNKWFNNK 1597
Db 841 INGTAFALCSERLIRRAKSQAFRSILRODISFFDRENSGT-----881
QY 1598 GMAHISFLNVLNNAILANLOKGNPSHYGTAFNHLNLTKOOLSEVALMTSVLV 1657
Db 882 --ALTSFLS-----888
QY 1658 SICVFAMSFVASFVFLIOERVSKAKHLOFISGVKPIYWLNFVDMCNVVPATLV 1717
Db 889 -----TETKNLSGVSQV-----TLG 903
QY 1718 IIFIFCFOOKSVSSTNLPVALLLLYGW-----STPLMPASFVEKIPSTAYVL 1770
Db 904 TII-----MTSTTGAMMIIALAIQKWLALCISVVDILLACGFL-REFYMLAQFOQ 953
QY 1771 TSVNLFIGINSVATFVLETFDNKNLNNINDLKSFVFLIPHFCLGRGLIDMVKNOAMAD 1830
Db 954 KKSAYEGSASTACEATSAIRTVASLTREODW-----GYHD 991
QY 1831 ALERGENRFPVSPLSMDLVGRNLFAMAAGEVFFLITVLIQY-----RPI- 1876
Db 992 QLOKQGRKSLISVLRSSL-----LYASS-QALVFPCVALGFWGTLIGHHEYSIFRFVC 1046
QY 1877 -----RPPVNAKLSPLNDEDEDVRRERQRIIDGGQNDI-----LEI 1914
Db 1047 FSEILFGAQSAGTVSFAPDMGKAKNAAQFKLPDSKPTIDWSDEGEKLESMEGETEF 1106
QY 1915 KELTIY-RRKKRPVADRICVPIPPGECGLLGVNGAKSSTFKKMLTGDITVTRGDAF-- 1971
Db 1107 RDVHRYPTRPROPVLRGINLNSVVRKQYIALVPGSGCKSTTIALLEFPYDALAGVAVD 1166
QY 1972 -----LNKNSILSNIEHVQ-----NMGYCPOFDAITE--LITGREHVEFPAL 2012
Db 1167 GKDITKLNWNSYRSLVLSQEPITLYOGTIKENILLGVDKDVSSEETLIKVCKANITYDF 1226
QY 2013 LRGVDE--KEYGVKGEWAIRRLGLVYKGEKAYNGVSGGNKRKISTAMALLIGPPVVELD 2069
Db 1227 VMSLPEGFDTVYSGK-----GMLSGGQKORVALARALLLDDPKVLLLD 1269
QY 2070 EPTTGMDPKARFLMNCALSVYKEGRSVVLTSISM 2104
Db 1270 EATSALDSESEKVV-QAALDAAARGRTTIAVAHRL 1303

```



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2002, 12:54:11 : Search time 42.61 seconds
(without alignments)
5096.756 Million cell updates/sec

Title: US-09-595-526B-2

Perfect score: 11797

Sequence: 1 MACMPQLRLIMKMLTFRRR.....VDVAVLVSFLDEKVKESYV 2261

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR_71:*
2: PIR1:*
3: PIR2:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10922	92.6	2201	2	A54774
2	3345.5	28.4	1529	2	A59189
3	3129.5	26.5	1472	2	B54774
4	2645.5	22.4	1704	2	S71363
5	2642.5	22.4	1704	2	A59188
6	2060	17.5	1802	2	T33783
7	1984	16.8	1816	2	A84845
8	1863.5	15.8	1447	2	T15200
9	1792	15.2	1317	2	C88525
10	1542	13.1	1758	2	F88559
11	1538.5	13.0	1704	2	T42749
12	1536.5	13.0	1767	2	S60124
13	1402	11.9	1246	2	T00826
14	1158.5	9.8	1564	2	T27121
15	1013.5	8.6	373	2	T47150
16	1010.5	8.6	1431	2	T22748
17	846	7.2	269	2	T46467
18	788.5	6.7	1011	2	T07712
19	693	5.9	900	2	T07717
20	667	5.7	895	2	T07714
21	656.5	5.6	722	2	T07716
22	645	5.5	925	2	T07713
23	624.5	5.3	1336	2	T18288
24	485	4.1	196	2	T12512
25	432	3.7	339	2	S74048
26	428	3.6	664	2	T07715
27	426.5	3.6	324	2	C71081
28	421	3.6	328	2	E75108
29	411	3.5	330	2	S27707

30	410.5	3.5	310	2	C96929	ABC-type multidrug
31	410.5	3.5	327	2	D72257	hypothetical prote
32	410	3.5	314	2	D97318	ABC-type MDR trans
33	409.5	3.5	398	2	C69485	daunorubicin resis
34	403.5	3.4	297	2	AE1816	ABC transporter (A
35	396.5	3.4	333	2	D72492	probable ABC trans
36	395.5	3.4	246	2	S75436	hypothetical prote
37	390	3.3	301	2	E72384	ABC transporter. A
38	388.5	3.3	310	2	E96920	ABC transporter (A
39	388	3.3	311	2	G69803	ABC transporter (A
40	386.5	3.3	727	2	T07718	probable ABC-type
41	386	3.3	259	2	H97301	ABC-type MDR trans
42	386	3.3	331	2	D70984	probable drpA prot
43	385	3.3	350	2	B69065	ABC transporter (A
44	384	3.3	331	2	E73019	daunorubicin resis
45	380	3.2	312	2	H97342	ABC-type MDR trans

ALIGNMENTS

RESULT 1	
A54774	ATP binding cassette transporter ABC1 - mouse
C:Species: Mus musculus (house mouse)	
C:Date: 05-Apr-1995 #sequence_revision 05-Apr-1995 #text_change 02-Feb-2001	
C:Accession: A54774	
R:Luciani, M.F.; Denizot, F.; Savary, S.; Mattei, M.G.; Chimini, G.	
Genomics 21, 150-159, 1994	
A:Title: Cloning of two novel ABC transporters mapping on human chromosome 9.	
A:Reference number: A54774; MUID:94375008	
A:Accession: A54774	
A:Molecule type: mRNA	
A:Residues: 1-2201 <LUC>	
A:Cross-References: GB:X75926; NID:9495256; PIDN:CAA53530.1; PID:9495257	
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog	
C:Keywords: ATP; duplication; nucleotide binding; P-loop	
F:856-1047/Domain: ATP-binding cassette motif A (P-loop)	
F:873-880/Region: nucleotide-binding motif A (P-loop)	
F:1869-2060/Domain: ATP-binding cassette motif A (P-loop)	
F:1886-1893/Region: nucleotide-binding motif A (P-loop)	
Query Match	92.6%; Score 10922; DB 2; Length 2201;
Best Local Similarity	94.9%; Pred. No. 0;
Matches 2089; Conservative	55; Mismatches 57; Indels 0; Gaps 0;
OY 61	MSAGTLPWVGIIICNANNPCFRPTPGEPAGVGNFNKSIYARLSARLLYSQKDT 120
1	MSAGTLPWVGIIICNANNPCFRPTPGEPAGVGNFNKSIYARLSARLLYSQKDT 60
OY 121	SKDKMKVLRITLQOIKKSSNKLQDFLVNDNTPFGFLYHNLSLPSKYVDKMLRADVILH 180
61	SKDKMKVLRITLQOIKKSSNKLQDFLVNDNTPFGFLYHNLSLPSKYVDKMLRADVILH 120
OY 181	KYFLOGYQHLTSLGSKSEEMIQGDOEVELGCLPEKXLAARLYRSMDILKPL 240
121	KYFLOGYQHLTSLGSKSEEMIQGDOEVELGCLPEKXLAARLYRSMDILKPL 180
OY 241	RLNLTSPFPEKELAEATKTLHSLGTLAQELFSMRKSDMRQEVPLTNVSSSSSQI 300
181	RLNLTSPFPEKELAEATKTLHSLGTLAQELFSMRKSDMRQEVPLTNVSSSSSQI 240
OY 301	YQAVSIVGCHPEGGLKIKSLNWDENNNYKALFSGNGTEDEAEFPYNSSTPYCNDLMK 360
241	YQAVSIVGCHPEGGLKIKSLNWDENNNYKALFSGNGTEDEAEFPYNSSTPYCNDLMK 300
OY 361	NLSSPLSRITKALKPLLVGKILYTPDPATROVMAEYNAKFFQLAFAFHLEGMEEELS 420
301	NLSSPLSRITKALKPLLVGKILYTPDPATROVMAEYNAKFFQLAFAFHLEGMEEELS 360
OY 421	PKIWFPMNSQEMDLVRMLDSDRDHFWEOQLDLDTAODIVAFIAKHPEDVOSSNGS 480
361	PKIWFPMNSQEMDLVRMLDSDRDHFWEOQLDLDTAODIVAFIAKHPEDVOSSNGS 420

Query Match 28.4%: Score 3345.5; DB 2; Length 1529;
 Best Local Similarity 46.7%: Pred. No. 3.7e-208;
 Matches 721; Conservative 207; Mismatches 381; Indels 235; Gaps 33;

QY 836 GVMTHVLEAVPGQYIGRPWYEPCTKSYWFG---ESDEKSHPGSNOKRMS-----ETIC 887
 1 GILTWYIEAVHPGMYGLPRPMYFPLQKSYWLGSGRTAEAMSWPMARTRPLSYMEEDQAC 60
 QY 888 -----MEEPHKLKGVSTONLVKYYRDGKKVAVDGLALNFYGGTSTFLGN 935
 61 AMESRREETRGMEEPHKLKGVSTONLVKYYRDGKKVAVDGLALNFYGGTSTFLGN 120
 QY 936 GAGCTTMSITLGTLPSTGAYILGKDIRSEMTIRONLGVCPQHNVLVEHMLVEEH 995
 121 GAGCTTMSITLGTLPSTGAYILGKDIRSEMTIRONLGVCPQHNVLVEHMLVEEH 180
 QY 996 FYARLKLSEKHYAKEMQALDVLGPPSKLKSCTSOLOGMOKLSVALAFVGGSKVYI 1055
 181 FYARLKLSEKHYAKEMQALDVLGPPSKLKSCTSOLOGMOKLSVALAFVGGSKVYI 239
 QY 1056 LDEPTAGVDYSRGIMWELLKRYROGRTILSTHMDLADRLAIIHGLKCGVSS 1115
 240 LDEPTAGVDYSRGIMWELLKRYROGRTILSTHMDLADRLAIIHGLKCGVSS 299
 QY 1116 LFLKQGLGTGYLLTVKKDESSLSGCRNSSSTVYLLKEDSVSSQSSDAGLSDHESDT 1175
 300 LFLKQGLGTGYLLTVKKDESSLSGCRNSSSTVYLLKEDSVSSQSSDAGLSDHESDT 337
 QY 1176 LTIDV--AISNLIRKAVSEARVEDIGHETLYVPEAKKEGAFVELFHEIDRLSDLG 1233
 338 PLSSCSELOVQFIRKHVACQLVSDTSTELSYLLPSEAKKGAFFERLFOHLERSIDLALH 397
 QY 1234 ISSYGETSEETLEELFVAAE-----SGVDA--ETSDGTP----- 1267
 398 LSSGIMDTLIEEYFLVSEEDQSLSEADYKESKRDVLPGAEGPSSGCHAGNLAARCS 457
 QY 1268 -----ARRNRA--FGDKQSCLRPTEDDADPNDSIDIPESRETDLLS 1309
 458 ELTQSQSLQSSASVSGAGDEGAGYIDYGDYRPLF--DNPQDPD--NVSLOVEAEALBS 514
 QY 1310 GMDCKSGYQKGMKLTQOQFVALMKRLIARSRKGFPAQIYVPAVFCIALVFSILTP 1369
 515 RV--GQSGRKLDGGLWKLKQFGLLVKRFHCAARRSKALFQIILPAFVGVAMVALSV 573
 QY 1370 PFQGYPSLELOPMYNYBOYT-----FVSNDAPE-----DTGTELLNLTATKDPGE 1414
 574 ETGLPLPLVSPSOYH--NYTOPKGNFIPYANERREYRLSLSPASQQLVTFRLPSGV 632
 QY 1415 GTRCM-----EGNPT----- 1424
 633 GATCVLKSPPANGSLGPTLNLSSGSRLLAARFPDSMCLSEPTQGLPLSNFVPPPPAPS 692
 QY 1425 -----PD-----TPCQAGEEETAP--VPOTIMDLFONGWMTMONSPACQSSDK 1469
 693 DSPASPEDLOAMVNSLPRTAGPMMWTSAPSLPLVREPVK-----CTCSAOG 740
 QY 1470 IKKMLPVCPPGAGLPPORRONTADILDLGRNISDYVKTVOIATKSLKKIKWNE 1529
 741 TGFS---CPSSVGG--HPPOMRVVTGDLITDITGHNVSEYLLFTSDR-----RL 785
 QY 1530 FRYGFSIGVSNTOALPPSOEVDAIKOMKHLKLANLSSADRLNSLGRMTGLDTRNN 1589
 786 HRYGIFPG--NVLKSTIPASGTRAPPMVK-----IAVRA 820
 QY 1590 VKVFNKKGWHAISFLVNNALIRANLQGE--NPSHYGTITANHPNLNTKQOLEVAL 1648
 821 AOVFNKKGWHAISFLVNNALIRANLQGE--NPSHYGTITANHPNLNTKQOLEVAL 879
 QY 1649 MTSVDVAVSICVFAVSPVAFVFLIDERSKAKHLQISGVKPYIWLNSFVWDMC 1708
 880 LLOGTAVVAILFIVANSEVAFVFLIDERSKAKHLQISGVKPYIWLNSFVWDMC 939
 QY 1709 NYVPATLVIIIFICFOOKSVSSTNLPLVALLLGLGWSITPLMYPASPFKIPSTAYV 1768

Query Match 26.5%: Score 3129.5; DB 2; Length 1472;
 Best Local Similarity 46.0%: Pred. No. 3.7e-194;
 Matches 676; Conservative 207; Mismatches 377; Indels 211; Gaps 28;

QY 888 MEPEPHKLKGVSTONLVKYYRDGKKVAVDGLALNFYGGTSTFLGNAGCTTMSILT 947
 16 MEPEPHKLKGVSTONLVKYYRDGKKVAVDGLALNFYGGTSTFLGNAGCTTMSILT 75
 QY 948 GLEPPTSGAYILGKDIRSEMTIRONLGVCPQHNVLVEHMLVEEHMVFARLKLSEKH 1007
 76 GLEPPTSGAYILGKDIRSEMTIRONLGVCPQHNVLVEHMLVEEHMVFARLKLSEKH 135
 QY 1008 VKEMEQMALDVLGPPSKLKSCTSOLOGMOKLSVALAFVGGSKVYIILDEPTAGVDY 1067
 136 VKEMEQMALDVLGPPSKLKSCTSOLOGMOKLSVALAFVGGSKVYIILDEPTAGVDY 194

QY 940 NTLVATCCVILLFPEFDLPATYSPTNFPAVLSLFLYGGTSTPLMYPASPFMEVSSAYV 999
 1769 VLTSVNLFINGSVATVYLEFT--DNKLNINIDLKSVFLFPHFCGLGRGLIDMVKQA 1827
 1000 FIVINLFIGITATVATFLLQLEHDKDKLVNSYLSKSCFLFPVYNNLGHGIMEAYNEY 1059
 QY 1828 MADALERPE--NRVSPISMDLVGRNLPAVAEGVVFELITVLIORFFIRPRVNAKLS 1886
 1060 INEYAKIQOFPKMSPEEMDLYTRGIVAMAVEGVGGLTITMCOYNLRORQRPVSTK 1119
 QY 1887 PLNDEEDYRRRORLIDOGGNDILEIKELTKYIRK--RKPVDRIYCGIPRPECFG 1943
 1120 PVED--DVDAVSERORVLRGADANDMWKILENTKVKYSKIRGILLVADRLCGLVRPECFG 1178
 QY 1944 LCVNAGKSSFFKMLTGTTTGRDAPLNKSIINSIHVONNNGVPOGFALITELLG 2003
 1179 LCVNAGKSSFFKMLTGTTTGRDAPLNKSIINSIHVONNNGVPOGFALITELLG 1238
 QY 2004 REHVEFFALLRGVPEKEVKGEMAIIRKGLVYGEKYAGNYSGGNKRRLSTAMALIGP 2063
 1239 REHVEFFALLRGVPEKEVKGEMAIIRKGLVYGEKYAGNYSGGNKRRLSTAMALIGP 1298
 QY 2064 PVFLEDEPTGMDPKARPLMNCALSVMKESVYVLSHMECEALCTRAIMYNGRFR 2123
 1299 PVFLEDEPTGMDPKARPLMNCALSVMKESVYVLSHMECEALCTRAIMYNGRFR 1358
 QY 2124 CIGSVOLHKNRPGDGYTVIRTAGSNPDLKPVODFGLAFPGSVLKEKHKNLQOLPSS 2183
 1359 CIGSVOLHKNRPGDGYTVIRTAGSNPDLKPVODFGLAFPGSVLKEKHKNLQOLPSS 1417
 QY 2184 LSLARIFSLSSQSKRLHIEDYSQTLTLDQVFNFAKQSD 2227
 1418 LSLARIFSLSSQSKRLHIEDYSQTLTLDQVFNFAKQSD 1461

RESULT 3
 B54774
 A: binding cassette transporter ABC2 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 02-Feb-2001
 C:Accession: B54774
 R:Luciani, M.F.; Denlioz, F.; Savary, S.; Mattei, M.G.; Chimi, G.
 Genomics 21, 150-159, 1994
 A:Title: Cloning of a novel ABC transporters mapping on human chromosome 9.
 A:Reference number: A54774; MUID:94375008
 A:Accession: B54774
 A:Molecule type: mRNA
 A:Residues: 1-1472 <LUC>
 A:Cross-references: GB:X75927; NID:9495258; PIDN:CAA5351.1; PID:9495259
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
 C:Keywords: ATP; nucleotide binding; P-loop
 F:44-234/Domain: ATP-binding cassette homology <ABC1>
 F:61-68/Region: nucleotide-binding motif A (P-loop)
 F:1108-1300/Domain: ATP-binding cassette homology <ABC2>
 F:1126-1133/Region: nucleotide-binding motif A (P-loop)

```

QY 1068 RRGIMWLLKRYGRTIILSTHMDADVLGDRIAIIISHGKLCVSSFLTKNQLGTGY 1127
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1195 RRAIMWLILKYPGRITILSTHMDADVLGDRIAIIISHGKLCVSSFLTKNQLGTGY 254
QY 1128 LTLVKKDVSSLSGCSNNSSTVYLKEDSVSSDAGLSDHSDTLTIDVSAISNLI 1187
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 255 LTLVKKDVSSLSGCSNNSSTVYLKEDSVSSDAGLSDHSDTLTIDVSAISNLI 294
QY 1188 RHHVSEARLVEDIGHELTVVLYPEAKEGAFVELFHEIDRLSDIGISSETLEEI 1247
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 295 RHHVSEARLVEDIGHELTVVLYPEAKEGAFVELFHEIDRLSDIGISSETLEEI 354
QY 1248 ELKVAEE-----SGVDA-ETSDGTLPARNRNRAAGDKOSCLRPTTE----- 1287
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 355 ELKVAEE-----SGVDA-ETSDGTLPARNRNRAAGDKOSCLRPTTE----- 414
QY 1288 -----DDAADPNDSDIDPESRETDLSGMDGKGSYQYKGMKL 1324
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 415 VGSANGDEGTGSDGVDGRPLFDNLQDPD--NVSLOEAKEMFALQV--GQGSRLKGMWL 471
QY 1325 TQOQFVALIKRLLIARRSRKGFPAQIVLPAVFCIALVFLVPPFGKPSLELQPMY 1384
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 472 KRRQFGLVLYKRFHCAFRRSKALCSQILPAFFVCAMVALSVEIDGLPLVLPQY 531
QY 1385 NQOYT-----FVSNDAPE-----DTGTELLMLNLTDRPGTCKM----- 1419
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 532 H-NTYQPKGNFIYANEEKQETRLRLSPASPOQLVSTFRPLSGVATGCKLSPANGSLG 590
QY 1420 -----DGNPI-----DGNPI-----DGNPI-----DGNPI----- 1426
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 591 PMLNLSGSRLLAARFEDSMCLSFSTQGLPLSNFVPPPPSPAPSDPVXDBDLSLQAN 650
QY 1427 --TPQAGEEEMTAP-VQOTINDLPQNGNMTMNPSPACQSSSKIKMLPVCPPAGG 1483
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 651 MSLPPLAGEVITSAFSLPRLVHEPVR-----CCTCSAGTGSF--CPSSVGG 695
QY 1484 LPPQKONTADILQDLGRNISDLYVKTYYOIIAKSLKNKIWVEFGFSLGVSNTQ 1543
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 696 -HPQMRVVTGDIILIDIGHNVSEYLLFTSDRF-----RLHRYGATITG--NVQ 741
QY 1544 ALPPQOEVDATKQKKHKLAKLAKSSADRLNSLGRFMTGDLTRNNVAVNNKGMHAIS 1603
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 742 KSIPLS-----FQARPPMVRKLAIVRVAQVILNNKGYHSP 778
QY 1604 SFLVNIINNAIIRANLQKE-NPSHYGITAFAHPLNLTKQOLSEVALMTSVDLVLSICI 1662
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 779 TYLNSLNNALIRANLPKSGNPAAYXITVNHNMKTSASIS-LDYLLQGDVIAITTI 837
QY 1663 FAMSVPVPAFVFLIOEKVSAKHLQFISGVKPVYIWLNFVMDMGNVVPATVILIEI 1722
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 838 VAMSVPVPAFVFLIOEKVSAKHLQFISGVKPVYIWLNFVMDMGNVVPATVILIEI 897
QY 1723 CFQOKSVYSTPLVYALILLYGSIITPLMYPASFVFKIPSTVYVLTNSLFGINGS 1782
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 898 VEDLPATVSPINFPVAVLSLFLITGMSITPIMYPAFWFVESSAVFLIVNLITGITAT 957
QY 1783 VATEVLELFT-DNKLNINILDKSVLFFPHFCGLRGILIDVYKQAMADALERGE-NRF 1840
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 958 VATEVLELFT-DNKLNINILDKSVLFFPHFCGLRGILIDVYKQAMADALERGE-NRF 1017
QY 1841 VSPLSMWDLVGRNLFMAVEGVVFLITVLYRFRIRPRVNAKSLPLNDEDEDVRRERQ 1900
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1018 KSPFEMDLVITGLVAMIVEGVGFLLTMCQYNFLRQORLPVSTKPEV-DVYVASRQ 1076
QY 1901 RLLDGGGNDLLEIKELTKIYRRK---RKPVDRIQVGI-PPGCGFGLVGNAGKSTF 1956
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1077 RVLREDADNDVYKTEILKRYKSKRIIGRIILAVDRCLGVCPGCGFGLVGNAGKSTF 1136
QY 1957 KMLTGDITVTVGDAFLANNLSLINSHEVHOMNGCPOPDATTEILLTGREHVEFALLGV 2016
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1137 KMLTGDITVTVGDAFLANNLSLINSHEVHOMNGCPOPDATTEILLTGREHVEFALLGV 1196

```

```

QY 2017 PEKEVGKGEWAIKRLGLVYKGEKYNAGNSGNNRKLSTAMALIGBPVVFLEDEPTTGM 2076
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1197 FWKDEQVVKWALEKLELTLYAAKRPACTYSGGNKRKLTSTALIGVPAFLFDEPTTGM 1256
QY 2077 PKARFLMNLALSVYKGRSVLTSHEMERCEALCTMAITVNGRFRCLSGVHLKNNRG 2136
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1257 PKARFLMNLALSVYKGRSVLTSHEMERCEALCTMAITVNGRFRCLSGVHLKNNRG 1316
QY 2137 DGYTVIRIAGSNPDLKPVODFEGAPGSLVLEKERNMLOYOLPSLSIARFSLSQ 2196
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1317 DGYTVIRIAGSNPDLKPVODFEGAPGSLVLEKERNMLOYOLPSLSIARFSLSQ 1375
QY 2197 SKRLHIEDYVSQTLIDQYVNFACQSD 2227
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1376 VGVLTIEDYVSQTLIDQYVNFACQSDN 1406

RESULT 4
S71363
probable ATP-binding cassette transporter ABC-3 - human
N:Alternate names: ATP-binding cassette transporter ABC-C
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 02-Feb-2001
C:Accession: S71363
R:Kriegbauer, N., Hofmann, F.
FEBS Lett. 391, 61-65, 1996
A:Title: Primary structure of a novel ABC transporter with a chromosomal localization
A:Reference number: S71363; M0ID:96326608
A:Accession: S71363
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-11704 <KIU>
A:Cross-references: EMBL:X71367; NID:g1514529; PIDD:CA65825.1; PID:e243436; PID:g151
A:Experimental source: cell line medullary thyroid carcinoma
C:Genetics:
A:Gene: GDB:ABC3
A:Cross-references: GDB:3770735; OMIM:601615
A:Map position: 16p13.3-16p13.3
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
C:Keywords: ATP binding; nucleotide binding; P-loop; phosphoprotein; transmembrane pr
F:325-283/Domain: transmembrane #status predicted <TM1>
F:307-329/Domain: transmembrane #status predicted <TM2>
F:345-364/Domain: transmembrane #status predicted <TM3>
F:373-394/Domain: transmembrane #status predicted <TM4>
F:401-422/Domain: transmembrane #status predicted <TM5>
F:452-475/Domain: transmembrane #status predicted <TM6>
F:549-739/Domain: ATP-binding cassette homolog <ABC1>
F:566-573/Region: nucleotide-binding motif A (P-loop)
F:685-690/Region: nucleotide-binding motif B
F:1100-1120/Domain: transmembrane #status predicted <TM7>
F:1145-1169/Domain: transmembrane #status predicted <TM8>
F:1181-1207/Domain: transmembrane #status predicted <TM9>
F:1215-1236/Domain: transmembrane #status predicted <TM10>
F:1249-1264/Domain: transmembrane #status predicted <TM11>
F:1293-1324/Domain: transmembrane #status predicted <TM12>
F:1399-1590/Domain: ATP-binding cassette homolog <ABC2>
F:1416-1423/Region: nucleotide-binding motif A (P-loop)
F:1535-1540/Region: nucleotide-binding motif B
F:674, 866, 1524/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #s
F:1344/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status pr

Query Match 22.4%; Score 2645.5; DB 2; Length 1704;
Best Local Similarity 35.7%; Pred. No. 1.3e-162;
Matches 639; Conservative 300; Mismatches 523; Indels 327; Gaps 48;

QY 534 AGIVPFGITPGSTIE-LPHVYKYIRNDINVERTN-----KIKDGV----- 574
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 131 AAIVFEPHNSKEPLVLAQVHLRF---SYTRNNMTQTSFSLKTEGHTTSLEPL 187
QY 575 --DPCGRADPFED---MRYVWGFAVLDQVDEQAIIIVLTGNE-----KKTGVYMQQMPY 624
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 188 FPNRGPRTSPGCGEPGYIRREGFLAVQHAIVRAIMEVADATATQRLVITIKRPY 247

```

```

QY 625 PCYVDIFLRVSRMPLMTLMTIYVAVNIKIGIYEKARLKEPMRIMGLDNLMS 684
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 248 PPIADPFLVAIOYOLPRLLLSFTYTALTITARAVOEKERLKEKMRMGLMSA 307
QY 685 WFISSILPLVSNAGLVILKLG---NLPSDPSVVFELSVFVAVTIIQCELISTL 739
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 308 WFLFLPLFLIILAAEFMTLLGCVKPRNVAIVLSRDLPLAFELCFALISTSEFVSTF 367
QY 740 FSRANLAAACGGIYFTLPLVLCVAMODYGFILKIASLLSPARFQGEYFALFE 799
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 368 FSSANNAAFGGFLFFETIYFVAVPRYMMTLISOKLCSLLSNVAMAMGQILGFEA 427
QY 800 OGIGVOMDLFESPYE-EDGFNLTTISMLLFTFLYGMWYIEAVFGQIGIPRPF 858
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 428 KMGIGIOMRLD--SPVAVDDDFCGOVLGMLLDVLYGLVTYMEVFGQIGVQPKWF 486
QY 859 PCTKSYWGE---ESDEKSHPGSNORMSEICEEPTHLKLGVSIONLVKYYRDM 912
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 487 FIMPSYWGCKPRAVAGKEEDSDP---EKALRNEYFEAPEDELVAGIKIKHLSKYFRVGN 543
QY 913 K--VAADGLALNFYEGQITSPFGHNGAGKTTMSLTGFPPTSGATVILGDISSEMT 970
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 544 KDRAAVRLNLNLYEGQITVLLGHNGAGKTTLSMLTGLPPTSGRAYISGEISQDMYO 603
QY 971 IRONLVCPOHNVLFDMLEVEHIMFYARLKLSEKHVAKEOMALDGLPSSKLKST 1030
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 604 IRKSLDLCQHDLPNLNLYVAEHLIYTAQKLSKCKEYKQMHITGL-EDKRNNS 662
QY 1031 SOLSGMOKRLVALAFVSGSKVILDEPTAGVPYSRRGIVELLKRYRQRTIILSTH 1090
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 663 RFLSGMRRLSIGLIALNGSKVLLIDEPDGMATSRRAIDWLLROKSDRTIYLTTF 722
QY 1091 MDADVLGRIALISGKLCQVSSIFLKNOLGTYLLVLYKDVSSLSLSCRNSSYTS 1150
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 723 MDADLGRIALIMARGLQCCGSSFLKOKYGAGHMTLKE-----P 766
QY 1151 YLKEDSVSSSSDAGISGHSDELITIDVSAISNLIRKHSARLVEDIGHETVLYPY 1210
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 767 HCPED-----ISQLVHHHVPNATILESSAGAELSITLPR 800
QY 1211 EAAKEGAFVELFHEIDRLSDIGISSYGISSETLEBIFLVAE--BSGVAETSDGTLPA 1268
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 801 ESTHR--FEGFLFAKLEKKQKIGIASFGASITMEVFLRVGLVSSMDIAIQ--LPA 856
QY 1269 ---RRRRRAFG---DKQSLRPTEDDAADPND---SDIPSERETDLISMDGKGYOY 1319
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 857 LOYQHRRAASDMAVDNLC-----GAMPDSDGIALIEERTAVKLTGTL----- 901
QY 1320 KGMKLOOQOVALLMKRLIARRSRKGFPAQIYLPAPVFCIALVFLIYPPGKYPSEL 1379
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 902 ---ALHCQDFWAMFLKKAAYSREMKMAVAOVLPLCTYALL----- 942
QY 1380 QPMWNYOYTFVSNDAPEDTGTLLELNLATKDPGFGTRMCEGNIPDTPCQAGEEMTAA 1439
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 943 -----AINYSSELPDDPML--RLTLG-----EYGR 966
QY 1440 PVPQITMDLFQNGNMTMKNPSPACGSSDKIKKMLFVCPGAGGLPPRQKONTADITLD 1499
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 967 VVPSVPGTSQLQOLSEHLKDLAQEG-----OEPREVLD 1003
QY 1500 LTRGRNIDYLVKTYQIILKSLKNKIWNDFRY---GGFSLGVSNTQALPPSQEVNDAI 1555
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1004 L-----EEFLT-----FRASVGGGFN----- 1020
QY 1556 KKKKHLKAKDSSADRFNLISGRFMTGLDTRNNVYKVMNKKGMHAISSFLVNNAILR 1615
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1021 -----BRCL--VAASFRDGERIVNALFNNOYHSPATALAVDMLRK 1063
QY 1616 ANIQKGNPSHYGITAFLNP-----LNLTKQOLSEVALMTTSVDVLSVLCVIFAMSFVA 1670
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1064 --ILCG--PHASIVVSNFPQPSALQAQKDFNE--GRKGFIALNL--LFAMAFILAS 1113

```

```

QY 1671 SEVVELIOERVSKAHQLQIFSGVRPIYWLNSFWDMCNVVPATLVIIIFICEQKSYV 1730
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1114 TFSILAVSERAAVQAKHVGFSVAVHVASFWLSALLMDLISFLPLLLLVFKARDVAF 1173
QY 1731 SSTNLPLVALLLILKXGSIPLPLMPASVFKIPSTAVVLTSLVLFGLINGSVATFLEL 1790
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1174 RDGHMADTLILLILLYGMAIIPMLYLMNFFLGAAVATRLITFNILSGI--ATFLMVT 1229
QY 1791 ---FTDNKNININDILKSVFLIPFPCIGRGLIMVKN-----QAMADALERFG- 1836
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1230 IMRIPAVLEELSKTLDBVFLVLYLNHCLGMAVSSFEYENETRRCTSSFAAHCKRYNI 1289
QY 1837 ---ENREVSPLSMDL--VGRNLFAAAVEGVFLLIYLIQRFIRPRPVAKL----- 1885
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1290 QYQENFY---AMSAFGVGRFVSAAGCAVLLFLFLIENLRLRGLICALRRRTL 1345
QY 1886 -----SPLNDEDEDVRRERORILDGGQNDI---LEKELTKIYRKRKP--AVDRTCV 1934
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1346 TELYTRMFLVEDDQVADERTRIIAPSPDSLHPLIILKLSKY--RQVPLLAVDRLSL 1404
QY 1935 GIPPECGFLGVNGAGKSTFKMLTGDVTYRGDAFLNKSISNIHEVQNMGCYPOF 1994
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1405 AVQKCEGFLIGFNGAGKTTFFKMLTGEESLTSQDAFVGGRISSDQKVRQRTGCPQF 1464
QY 1995 DAITELTGRHEVERFALLRGVPEREKVKGEMAIRKLGIVKGEKYAGNYSGNKRLS 2054
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1465 DALDHMGREMLVYARLIRGIPERHIGACVENLRLGILLEPHANKLVRTYSGNKRRLS 1524
QY 2055 TAAALIGRPVYFDEPTTGMDPKARPLMNCALSVYKEGSVVLTSMECEALCTRM 2114
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1525 TGIALIGEPVAVIFDEPSTGMDPVARLLMDTVARARESGAIIITTSMECEALCTRL 1584
QY 2115 AIVMGREFRCISVOHLKNRREGDGTIVVRI--AGSNPDKLPVODFGLAPGSLKEKH 2172
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1585 AIVMGQFKCLGSSPOLHLSKFGSGTSLRAKQVSBQDPALEEFKAFVDTLTPGSVLEDEH 1644
QY 2173 RNMLQYQPPSSLSLARIFFSILSOSKRLHIEDSVSOTTLDOVFVNA 2221
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1645 QGMVHYHLPGRLSMAKVFGLIEKAKKEKYGVDVSVSISLEQVFLSPA 1693

```

```

RESULT 5
A59188
ATP-binding cassette transporter ABC3 - human
C:Species: Homo sapiens (man)
C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 04-Mar-2000
C:Accession: A59188
R:Comments, T.D.: Van Raay, T.J.; Petry, L.R.; Klinger, K.W.; Landes, G.M.; Burn, T.C.
Genomics 39, 231-234, 1997
A:Title: The cloning of a human ABC gene (ABC3) mapping to chromosome 16p13.3.
A:Reference number: A59188; MUID:97179225
A:Accession: A59188
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1704 <CON>
A:Cross-references: GB:078735; NID:g1699037; PIDN:AAC50967.1; PID:g1699038
C:Genetics:
A:Gene: GDB:ABC3
A:Cross-references: GDB:3770735; OMIM:601615
A:Map position: 16p13.3-16p13.3
C:Superfamily: ATP-binding cassette homology

```

```

Query Match 22.4% Score 2642.5; DB 2; Length 1704;
Best Local Similarity 35.7% Pred. No. 2e-162;
Matches 639; Conservative 300; Mismatches 523; Indels 327; Gaps 48;

QY 534 AGIVFTGTPGSI-E-LPHVVKYKIMDIDNVERTN-----KIKQGYW----- 574
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 AAVVEHFPNHSKEPLPLAVKYLHRF---SYTRRNYMTQGSFFLKEBGMHTTSLPPL 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 575 --DPGRADPFED--MRYWVGFAVYIADVVEQAIIRVLTGTE-----KKTGYVMQMPY 624
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

Db 168 PPNPGRRLTSPDGEPEYIRBGLAVOHAADRAIMEHAADATROLFORLTIVTKRPY 247
QY 625 PCYVDDIFLRVNSRSMPLFMTLAWISVAJIKGIVEKEARLEKTRIMGLDSTIMFS 684
Db 248 PPFIDAPFLVAIOYOLPRLILSLFTYALTITARAAYOKERERLEKYMMLGSLMHSMA 307
QY 685 WFTSLILPLASAGLIVVILKLG-----NLTPSDPSVVFELSFVAVNTLQCEFLISTL 739
Db 308 WFLFFLPLDRLAASPMILFPCVKKPNVAVLSRSDPSLVTLFLLCFALSTLSEFWMSTF 367
QY 740 FSRANMAACGGIIFLYLPLVLCVAMQDVYGFLLKIFASLLSPVAFGCEFAFLFEE 799
Db 368 FSKANMAAFAFGGELFETTYIPFEEFARVYNNMTLSQKCSLLSVNMAAQAOLIGKEA 427
QY 800 OGIGVOMNLESPYE-EDGFNLTTSISMALEPDLFVGVMTVYLEAVPQOYGPRTMYF 858
Db 428 KGMGIOMDRL-SPVAVDDDFCEGOVIGMLLIDSVLGYLVWMEAVPQGFQVPOPYF 486
QY 859 PCTKSYWFE-----ESDEKSHPGSNOKRMSSEICOMEPEPHLKGVSIQIOLVYVRGM 912
Db 487 FIMPTWCGKPRVAVGKKEEDSDP---EKALNFEFMEPEPDLVAGITIKHLSKVFYGN 543
QY 913 K--VAVDGLANFEGQITSPGLNAGKTTMTSLTGLPRTSGTAYILGKDIRSEMST 970
Db 544 KDRAAVRDLNLTNEGQITVLLGNAGKTTLSMLTGLPRTSGRAYISGEYSIDOMVQ 603
QY 971 IRONVGCPOHNVFLDMLTVEHNTWFAVRLKGLSEKHAKAMQDMALDYGRLPSKLSKT 1030
Db 604 IRKSIGLCPOHNDILFDNLTVAEHLFTYAOGLGSKQKCPREVKQMLNITGL-EDKWNRS 662
QY 1031 SOLSGMOKRLSVLAFVGVSKRVVILDEPAGVDPYSRSGIWEILLKXRGRTTILSTNH 1090
Db 663 RFLSGMRRKLSIGITALIAGSKVLLDEPTSGMDAISRRALIMDLQROKSRRTVLTTHF 722
QY 1091 MDEAVLDRILALISHGKLCVGSFLKNOIGTYUVTLLKXVYESSLSGRSSSVYS 1150
Db 723 MDEALLDRILAKKGLCCGSLFLKQYKGAGYMTLVKE-----P 766
QY 1151 YLKEDSVSSSSDAGLSDHESDPLTIDVSAISNLIRKHVSEARLEVEDIGHEILVYLPY 1210
Db 767 HCNPED-----ISQLVHNHVNMTLLESSACAEISFLIPR 800
QY 1211 EAAKGAVALFHEIDDLSDLGISYSIGSETTLEIFLKYAE--ESGVDAETSDGLPA 1268
Db 801 ESTHR--EGFLAKLEKKQELGASIFGASLTTEMEVFLRGKLVDSMDIOAQI--LPA 856
QY 1269 ---RRNRRAFg--DKOSCLPTEDEADAPND--SGIDSESETDLSGMDKGVSQY 1319
Db 857 LOYCHERRASDAVDSNLC-----GAMDPDSGIGALIEERTAVKLTGL----- 901
QY 1320 KGMKLTQOOFVALLMKRLILARSRKGFPAQIVLPAVFCIALVFSLIVPFGKYPSEL 1379
Db 902 ---ALHCQOFWAMFLKKAAYSMREWKVYAQVULVLCVTALL----- 942
QY 1380 QPWWYNBOYTVSNDAPEDTGLTLLNALITDPRGFTRCMGANTIPDTPCQAGEEWTTA 1439
Db 943 -----AINYSSELFDDPMI--RLTLG-----EYGR 966
QY 1440 VVPOTIMDLFONGMWTQNPSPACOCSSDKIKKMLPVCPRPAGGLPPQRKONTADIL 1499
Db 967 VVPFSVPTSQLGOOLSHLKDIAQABG-----QEPREVLGD 1003
QY 1500 LTGRNISDYLVKTYVQIIAKSLKKNKIVNEFRY---GGSFLGVSNTOALPPSOEVDAI 1555
Db 1004 L-----EEFLI-----FRASVEGGGFN----- 1020
QY 1556 KOMKHLKLADSDADRLNLSGRFMIGJOTRRNVKVFENKKNHAISSPLANTNNAILR 1615
Db 1021 -----ERCL--VAASFRDVGERTVYVNALFNNOAVHSPATALAVVNDLFLK 1063
QY 1616 ANLOGENSHYGIATFVHP-----LNLTKOOLSEVALMTSIVVLSICVIFAMSVPA 1670
Db 1064 ---LLCG---PHASIVSNFPPQRSALQAKQDFNE---GRKGFDIALNL--LPMATFLAS 1113

```

```

QY 1671 SEVVELIQERVSKAKHLQFISGVKPVIIYMLSNFWMCMNVVPAVLVITIFCPOOKSYV 1730
Db 1114 TFSILAVSERAVOAKKHVOFSGVHVASFMLSALIMLISFLIPSLILVFAFVDRRA 1173
QY 1731 SSTNLPVALLLILYGMSTPLPMPYASFVKIPSTVYVLTSLNLEIGINSVAFVLEL 1790
Db 1174 RQGHMADTLLLLLYGMAIIPMLTLMNFFLGAAVATYRLITFNLSG---AFFLMT 1229
QY 1791 ---FTDNKLNINDILKSVFLFPNFCIGRLIDVKN-----QAMADALERFG- 1836
Db 1230 IMRIPAKLEELSKTLDHVLVLPNHCIGMASSFEYENETRYCASSVAHCKYNI 1289
QY 1837 ---ENRVPPLSMDL--VGRNLFAMAVEGVFPLTVLLQYREFIPRVYNAKL----- 1885
Db 1290 QYQENFY---AMSAPGVGFVMAASCAVAILLLETNLLORLKGILCALRRRTL 1345
QY 1886 ---SPLNDEDEDVREERORILDGGONDI---LEIKELFKYRRKRP--AVDRICV 1934
Db 1346 TELYTRMPVLPEDQVADERTRLIARSPSLHTPLILIKELSVY--EQRVPLAVDRSL 1404
QY 1935 GIPPGCEGLLVNAGKSTFKMLTGDITVTRGDAFLKNSTLSNIEVHONMGYCPQF 1994
Db 1405 AVOKGECFGLIGFNAGKTTFTKMLTGESLTSGDAPFVGNHRISDPVGRORIGYCPQF 1464
QY 1995 DATTELTGREHEVFEALLRGVPEKEVKGEMAIRKGLVYGEKYAGNYSGGMKRKL 2054
Db 1465 DALDHAKTGEMLVYARLGRIGERHIGACVENTLGLLEPHANKLVYTTSGNKRKL 1524
QY 2055 TAMALIGRPVFLDEPTTGMDPKARFLMNCALSVYKGRSVLTSMSMECEALCTRM 2114
Db 1525 TGIALIGEPVILDEPSTGMDPVARRLLMDTVARARESGKAIITSHSMECEALCTRL 1584
QY 2115 AIVNNGREFCLGSVCHLKNRFGDGTIVRI--AGSNPLKPVODPFGIAPFGSVLKEH 2172
Db 1585 AIVNGQFCLGSPQHKLSFGSGISLRAKVOSGQOALDEEFKAVDILPFGSVLEDEH 1644
QY 2173 RNMLQYQLPSSLSLARIFSLSQSKRRLHIEDYSVQTTLDQVFNFA 2221
Db 1645 QGVNHYHLPRDLSMAKVFGLLEKAKKQGVDDYSQSILBQVFLSFA 1693

RESULT 6
T33783
hypothetical protein Y39D8C.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 17-Mar-2000
C:Accession: T33783
R:Becker, W.; Graves, T.; Yoakum, M.
submitted to the EMBL Data Library, October 1998
A:Description: The sequence of C. elegans cosmid Y39D8C.
A:Reference number: 221408
A:Accession: T33783
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1802 <BEC>
A:Cross-references: EMBL:AF101313; PIDN:AAC69223.1; GSPDB:G000023; CESP:Y39D8C.1
A:Experimental source: strain Bristol N2; clone Y39D8C
C:Genetics:
A:Gene: CESP:Y39D8C.1
A:Map position: 5
A:Introns: 45/3; 114/1; 195/1; 230/3; 543/3; 794/1; 1036/2; 1099/1; 1132/3; 11
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

```

Query Match 17.5%; Score 2060; DB 2; Length 1802;
 Best Local Similarity 27.9%; Pred. No. 1.5e-124;
 Matches 551; Conservative 338; Mismatches 630; Indels 454; Gaps 52;

```

QY 385 YPDPTRATROVAEAVKKTQELAVFHDLGMMEEISPKIWTMENSQEMDLVRMLDSRD 444
Db 119 YAPMTATATQIMDKIONRI-----TANDL-----LNP-VAAVITKGLYNTAVPVLTMTWT 167

```

QY 445 NDHEWEOOLDLMDTADIVAFIAKHPEDVOSSNGSVYTWREAFNETNOAIRTISRFMEC 504
 Db 168 YKGF-----TTEGEVSMGOFOS-----EC 189
 QY 505 VNLKLEPATEWMLINKSMELLDERKFMAGIVFTGTPGSIELPHVKKYKIMIDIDNVE 564
 Db 190 DN-----PLT-----AGIVFDDSIADKLNPKRDPETTYIRLSNTH 225
 QY 565 RTMKIKGVDMPGRADPFEDMRYNG-----GPAV 595
 Db 226 RRSR-----NAGDONSYPMDTSVFAVVOYVSGPINDDNGSGPGYMOBGFMT 273
 QY 596 LODVDEQAIIRVLTEK-----TGVMQOMPCYVDIDFLVMSRMPLEMTLAWY 650
 Db 274 VQRAVDALTEITIGEDAQITPLDSDYOVSRRFPFGTSKI-TEICAFMPVIVISFMT 332
 QY 651 SVAVIIGIYEEKARLEKEMRIMGJDNSTLMSWFTSILIPLLVAGLLVILKGNLL 710
 Db 333 SVIYIYAAVVEKEDRLKEKMYMGLSOFINVAHFILINAKLTFPAVIVILIMHFVAL- 391
 QY 711 PYSDPSVFEVLSVFAVVTILOCELISTLESANLAACGIIYFTLYL----- 759
 Db 392 -KDMTLMFEVLTITAFDVYFAFMISFPMNSATSLISVFMMLLYFWYAFSSIDOT 450
 QY 760 -PYLVCAMODYVFTLIKIFASLSP-VAFGCEYFALFEBOGIGVOMNLFESPVED 817
 Db 451 NPYPL-----GYRL-----INCINPDIALNGLQJLLAAYEQADLKKGELFTPPSPN 499
 QY 818 GFULTISIMLFDTLGYVMYIAVPPGOYGP-RWVYPPCTKSYW-GEESDEK 873
 Db 500 NTFGHALLALIVDGIIMILTYIAVIPGEGVPOKEMFW-VLPSPWPNSSGKTVDS 558
 QY 874 SHPGSNOKRMESEICMEEPETHLKIGVSIONLVY-----RDMKAVAVDL 919
 Db 559 SDQFOQIYADAHKLEKEPTDLIPTINVNLTKTYTSEFKKLDCKFEKSGEKRAVNL 618
 QY 920 ALNFYEGQITSEFGHNGACKTTMSILTLGPTSGTAYILKDKINSEKSTROMLVCP 979
 Db 619 NLMYPGOCITVLLGHNGACKSTFMSLTGVAOSSAVVNPEDITSLPKIRREMGICP 678
 QY 980 OHNVLEDMLEVEHIEFVYARLGLS--EKHVAEMQOMALDVGLBSSKLSKTSOLSGM 1037
 Db 679 QYITLGEFMTMHELEFKLEKERTWDPREARILARLIDF-----KADFNAGALSQGO 733
 QY 1038 ORKLVALAFVSGSVIILDEPAGVDPYSRGRIWELLKXROGRTIILSTHMDADVL 1097
 Db 734 KRRLSLAIALIGSEVYVMDDEPTSGMDPGARHETWLLIOREKFRITILITTFMEADLL 793
 QY 1098 GDRIALIISGKLCVGSLLFLKNQJGTGYLLLVKKDVSSLSGSSSTVSYLKKEDS 1157
 Db 794 GRIALIMAHGOIECCGSPMFLKOQYGDGYHTLV----- 827
 QY 1158 VSOSSDAGIGSDHESDITLIDVSAISNLIKRHVSEARLVEDIGHETVYVLEAKKEGA 1217
 Db 828 -----YDTTTPDYSKTTDITIREITPEAHVFTYIGDPAITLL--SATHRI 871
 QY 1218 FVELFHEIDRLSDIGISSYGISETTLEBIFLKVAE-----ESGVAETSDGTLPAR 1269
 Db 872 FPLFELKEDHQTGCGITSFVGSITTFMEVPLKVGHTADERYNHIENDISE----- 925
 QY 1270 RNRRAFGDQOSLRPTEDDADPNDSIDIDPRESTDLISGMDGSGVQVKWMLTOOOF 1329
 Db 926 -----MIEND--DPLIODI-----PAOVAVYVGTLOMOHA 953
 QY 1330 VALLMKRLIARRSRKGFQJVLPAVEFCIALVFSLIYPPRGKPSLELOQWMTNEQYT 1389
 Db 954 KAMFYKRAIFFRKMTOFLPQVLVFAVYVAVYVLSQVLPYSKE----- 997
 QY 1390 FVSNADBEDTGLLELINALTKDPGFGTRCMEGNPIPDTPCQAGEBEMWTAPVQTIMDLF 1449
 Db 998 -----QDPOTISLA-----PSSDFK--KAG-----HLVSD-- 1020
 QY 1450 QNGNMTWQNPSPACCCSSDKIKKMLPVCPRGAGGLPPORRKNQNTADILQDLTGRNISDYL 1509

Db 1021 -SGNYTTL-----LGG-----SOWLSMV 1038
 QY 1510 VKTYYOITAKSLKKNIMWNEFRYGGFSLGVSNTQALPPSOEYNDAIKOMKRLKLAKDSS 1569
 Db 1039 OGTVTQ-----LGVTOF-----VVDITSVEKFINQDTIAM 1069
 QY 1570 ADR-----FLNSLGRFTGLDTRNNVYKWFENKMKMAISSFLANINNALRANIOK 1620
 Db 1070 GSRFTGLHYALGFVPSMNEST--VSPSLKTFNNFLYIPALALITPTDSMIILSOQOKK 1127
 QY 1621 GNPFSHYGTAFNHPNLNTKQOLSEVALMTSSVDLVSGICVAFMSFVPAFVYVLEOER 1660
 Db 1128 -----QYSTAVNHPLPSTODTLKNTNRSDCAFLIAGLVASFVAGVAGSOPLITER 1182
 QY 1681 VSKARHLOFISGVKPVYIWLNSFVMDQCNVYVPATLVIIIFICEQOKSVYSTN-LPVL 1739
 Db 1183 KKSXHMQLSGIRBMMFWLTAFLINDAMFVIRLCFPAIFYIFNITAYTHDFGVMILIT 1242
 QY 1740 LLLILYGSITPLAMPASVFKRIPSTAVVLTLSVNLFTGINGSVATFVLELFTDKLNNT 1799
 Db 1243 LSFLLYGMTALPFTYWFQFFESAPKGFMMYTHILTMIGISIAVPIISOTSSIDAGYL 1302
 QY 1800 NDILKSVFLIFPHFCTLGLIDMVKNOAMADALERE-----GENRFS 1842
 Db 1303 WSLIYA--WLEFTYVISOIATVYTONENVRIACKLDCITIMFAVAVTACCTASERLYD 1360
 QY 1843 PLSDMLVGRN-----LEPMAVEGVFELITVLIOYRPF-----IRRPYNAKLSPLND 1890
 Db 1361 NVLF--VGNRKGIILYVIFLAVOGFTIWMVEMRENDQFTLPLALIRCRAKNDNIMDIT 1418
 QY 1891 -----EDEDVARRER--QRILDGGQNDILEIKELTYIRKKRPAYDRICVGIIP 1938
 Db 1419 TDKYDERVEOSDVIAEKSVOQL--ANNKTAVALSNLVWYGNFN--AVKGVNFHNS 1474
 QY 1939 GECEGLIGVNGAGKSTFKMLTGDITVTRGDAFLKNSIILNIEHVHOMQNECPQOPAT 1998
 Db 1475 KDCFELLGVNAGKSTQMLTGEMSSISGDAYVNGSVKNNMEAGANTGYCQOYDAIL 1554
 QY 1999 ELLTREHVEFFALLRGVPEKVGKVGEMAIRKGLVYKYGKAVGNTSGNKRRLSTAMA 2058
 Db 1535 KEMSGEETLYMFARLRIGPEKDIPRKVAVYIHAIGIGYASROIKTYSGNKRRLSLGIA 1594
 QY 2059 LIGGPVYVLEPPTGMPKARFLMNCALSVYEGRSVYLTISMECEPCLCTRMIMV 2118
 Db 1535 IYGLPDLVLLDEPITSGVDPKARRITIMNLNRLRDLGTALVLTSSMBCECALTEILAMV 1654
 QY 2119 NGRFRLGASVOHLKNRFGDGYTIIVARIAGSNPDLKPVODFFGLAFPGSVLKEKRRMLQY 2178
 Db 1655 YGFRFCYSCQHIKRSYGSYTLILRLKRN--DAEKTRSTIKQFRGSVIREKHVLOLNF 1713
 QY 2179 QLPSSLALAFITSLSSKKRLHIEDYSVQTTLDVQFVNFAD--QSDDD 2228
 Db 1714 DIPRDGDSMRLEFKLETIVSTLNMWDYSLSQTLLEQVIEFSRDAGVSSDSE 1766

RESULT 7

A84845
 Probable Aac transporter [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence-revision 02-Feb-2001 #text-change 02-Feb-2001
 C:Accession: A84845
 R:lin, X.; Kaul, S.; Rounsley, S.D.; Shee, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487
 A:Accession: A84845
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1816 (KSTO>
 A:Cross-references: GB:AE002093; NID:96598351; PIDN:AAC02761.2; GSPDB:GN00139

C:Genetics:
A:Gene: A12941700
A:Map position: 2

Query Match 16.8%; Score 1984; DB 2; Length 1816;
Best Local Similarity 28.8%; Pred. No. 1.3e-119; Indels 572; Gaps 60;
Matches 584; Conservative 282; Mismatches 592;

QY 489 NETNOAIRTIS-REMECVNMLK-L-EPIATEVMILINKSMELDERKFWAGIVETGTPGS 545
DB 59 DETNMMDIILSKPELRLVTKIFKDDIELEYITSANHYGVCESEVRNCSNPKIKGAVFVH 118
QY 546 IELPHNKKYKIRM-----DIDNVERTNKIKOSWMPGRADPE-----DMRY 588
DB 119 EOGHLEFDYSIRLNMHWAFAGFPVAKSIMDTN-----GPIINDLENGINTITPMTQ 169
QY 589 VMGCFAYLADVEAOAIRVLGTGTEKKTVGMQMPYPCVYDDI.FLRYMSKSMPLFMTLAW 648
DB 170 SFGSEFLTLQOVDSFII-----PASOON-----NDLPLSHSNLSALRFELPW 212
QY 649 IYSVAVITIKGIYEKARKLEKRMINGLDSILFMSFISLPLVLSAGLLVYILKGN 708
DB 213 TLFSPSVIRWVPFPTREYTDDE-----FOSIVKSMGLF----- 246
QY 709 LLPYSDSVFVFLSVFAVYVTLIOCFILSTLFSRANLAACGGIYFTLYLPLVLCVAMQ 768
DB 247 LFKSDDTLVFTYFFLGLSALIMSPMISTFTTAKTAVAGITLTLGAFPPY--TVND 304
QY 769 DYVGTFTIKIFASLSPVAFGFCCEYFALFEEOGIGVQWDLFSPVEDEGFTLTSISM 828
DB 305 ESYSMVLKVVASLSPALFALGINSFADYERAHGLRMSNIMRA-----SSGVSEFVCLLM 361
QY 829 LFDFTLGVMTWYIEANFPQOYGIIPRWYFPCTKSYWFGESEDPKSH--TG----- 877
DB 362 LLDLSILYCALGLYLDKYLPRNGVRYPMNPLFSK--YFGKKNNLOMRIFGFTDMFAD 419
QY 878 -----SNOKRMSFI-----CMEEBPTHKLKGVSIONIAKVV--RDMKAVAV 916
DB 420 IEVNGDFPDPFVSISLSEMQOELDGR-----IQVNNLKVAVASRGNCAV 468
QY 917 DGLALNFEGQITSLFHNGAGKTTTWSILTLGFPPTSGTAVYILGKDIRSEMTIRONLG 976
DB 469 NSILOTTYENQILSLFHNGAGKSTTSMYGLPLPTSGALLIGNSIITINMEIRKELG 528
QY 977 VCPQHNVLFDMLYEBEHIMFARLGLSEKKYKAKEMOMALDVLGSPSKLKSXSOLSGG 1036
DB 529 VCPQHDLFPELTYREHLEMFAYLKGVEGSLKSTVDMAEVGL--SDKINTLVRLALSGG 587
QY 1037 MOKRLSVLAFVGGSKVYIIDEPTAGVDPYRSRGITWELLKTYROGRTIILSTHMDADV 1096
DB 588 MKRKLSIGALIGNSKVIILDEPTSGMDPYSMRLTQOLIKIKKGRILLTLTHSMDABE 647
QY 1097 LGDRITAIISHKLCVGVSSFLKNOLGTYLLTVKKDVESSILSSCRNSSSTVSYLAKED 1156
DB 648 LGDRIGIMANSLKCCGSSIFLKHGYGYFTLLV-----TSPT----- 687
QY 1157 SVSOSSDAGLGSDESDTLTIDVSAISNLIRKHVSEARLVEDIGHELTYLYPEAKEG 1216
DB 688 -----VSVAHIYHRIIPSAITCYSEVGNELSEPLP--LASLP 722
QY 1217 AFVELFHEIDRL-----SDL-GISSYGISFTTLEIFLKVAAEESGVDAETSDGTLPARRN 1271
DB 723 CFENMFREIESCMKNSDSDYDGIQSYGISVYTLLEVEFLRA--GNLDIE----- 770
QY 1272 RRABDQKSCLRPTEDDAAPNDSDIDPRESRETDLSQMDGKSYQK-----GW 1322
DB 771 -----DKO-----EDIEVSPDTKSSILVCIGSMQKSSMOPKLLASGNDGAGV 811
QY 1323 KLTQ-----OOVALW-----KRLTIARRSRKGF 1347
DB 812 IITSVAKAFRLIYAAVWVILIGFISIGCCGCSITISRMFWRRCKALFIKRAASACRDKTY 871

QY 1348 FAOIVLPAVFCIALVFSILVPPFGKYSLELOPMWNEQYTFVSNAPADEDTGLELLNA 1407
DB 872 AFQITIPAVFLFLGLF-----LQKPF-----HPDQKSTITLTAAVFN 909
QY 1408 LTKDPGFGTRCMEGNPDPDPOQAGEEEMTAPYVQITMDLPONG-----NMTKONPSP 1461
DB 910 LLSGKG-----GGSPIDP-----LSVPIAKEVAOYIEGGMLOPLRNTSYKPPNP 954
QY 1462 ACQCSDDKIKKMLPCPPGAGGLPPRQKONTADLODLOTRNLSIDYUKTYQDIKSL 1521
DB 955 -----KEALDADT--DAAGPTLGPILLS----- 975
QY 1522 KKKIWNNEFRYGFSLGVSNQALPPSOEVNDALIKOMKHLKLAKSSADRFSLSLGFM 1561
DB 976 -----MSERLMSFD-----QSYQSR-----GLSHDSCNHPDGLG--- 1009
QY 1582 TGLDTRNNKVFVFNKKGMHAISFLNVLNNALIRANLOKGENPSHYGTATANNHPLTK- 1640
DB 1010 -----YTVLHNGTQOAGPIYINVMHAALIR--LATGN--KMTIOTRNHPLPPTKT 1057
QY 1641 OOLSEVALMTSDVULSICVIFAMSPVAFVFLIDERYSKAKHLOFISGVKPVLYWL 1700
DB 1058 QRIQRHDLDAFSAIITVNI-----ASFPIASPAVYIVKEREYKAKHQOLIGSVLSYWL 1113
QY 1701 SNFVDMCNVYVPAVLVILIFTCFOQKSYVSTNPLVALLLXGMSITPLMPASFVF 1760
DB 1114 STYVMDIFSLFPSPFAITLFFAAGLEOFIGIRFLPTVLMLEYGALIASSTYCLTFEF 1173
QY 1761 KIPSTP-----YVLTSVNLF-----GINSVAFVFELEF--PDNKLNN 1798
DB 1174 TEHSMQATSSYVLLPISLFEVSPSSNVILMVHFFSGLLMVLSVAGLLPATASANSY 1233
QY 1799 INDI-----LKSVELIFPFLGRLGIDM--VKNOAMADALERFGENFVSPDLVGR 1851
DB 1234 LKELLIFRALQNFRLPSGFCFSDGLASLALRGCMKDKSH-----GVFENNVAGA 1286
QY 1852 NLFAMAVEGVFPLITVLIQYFFPIRPVYNAKL----- 1886
DB 1287 SICYLGLFVRLCYCRYSMLLSFF--HGIDTKLSIYITIGASRLTELDYRVYSTSEST 1343
QY 1887 PL-----NDEDEVRERORILIDGGGONDILEIKELTYIRKR--KPAVD 1930
DB 1344 EPLKNDSTGALISTMDDDIDVOBERDRTVLSGIDNTMLYLQMLRKVYIGODKIHGKAVAO 1403
QY 1931 RLCVGIPECEFGILGVNAGKSSFTKMLTGDITYTREGDAPLANKSLSINIEHVQNMGY 1990
DB 1404 SLFFSVQAGECEGFLGTNGAGKTTLSMLSGEETPTSGTAFIFGKDIVASPAIRQIHGY 1463
QY 1991 CPOFDAITELLGREHVEFALLRGVPEKEVGKVGEMAIRKGLYKGEKAYAGNSGK 2050
DB 1464 CPOFDALFEVLVYKHELEVARIKGVADRIDNVYTEKLEVEDLLKHSKPSFTLSGK 1523
QY 2051 RKLSAMALIGPPVYFLDEPTGMDPKARFLMN--CALSVVKEGSRVLSHSEMECE 2108
DB 1524 KLSVIAIMAGDPPIYIIDEPTSGMDPAKRPMWYISLSLRSOKTAVIILTHSMNEGO 1583
QY 2109 ALCTRNALINVRGFRCLGVSVOHLKNRG----- 2136
DB 1584 ALCTRIGIMVGRICGSPHKLTRYGNHLEVEFPYNGVAPRNEVSNLENEFCOITQ 1643
QY 2137 -----DGYT-----LVVRIA----- 2146
DB 1644 WLENVPTQPSRLGLLEVCTIGVSDSITPDTASASEISLSPENVOIRAKFLGDEQVSTLY 1703
QY 2147 -----GSPN-----DLKPQDFEGLAFPGSVLKEKHR 2173
DB 1704 PPLPEEDVAFRDQSLRQLRDGGIPLPIFAEWMLTRKESALDSFIOSSFPATFKSCNG 1763
QY 2174 NMLQYLPSSL--SLARIFSLISQSKRLHLEDVSVOTITIDQYVAFNA 2221
DB 1764 LSTKYOLPFGEGGLSLADAFGLHERNRNLGIAEYISISOSTLETTFNHPA 1813


```

Db 1546 MIAHADKLVRYFSGGQKKISVGVALLAPTOMITLDEPTAGIDPKARREWEILLWCREH 1605
QY 2094 GRS-VLITSHSMCECALCTEMATMVGREFCLGSVOHLKRFEDGCTIYVIRIAGSNPD 2152
Db 1606 SNSALMTLSHMDCEALCSRIATVLRNGSLIAIGSSQELSLVNNNTMLSLTERPQORD 1665
QY 2153 KPYODFGLAFPGSVLKEKHNNM---LQYLPSSLSSU-ARISITLSQSKRLHIEDYSV 2208
Db 1666 MVVO-LVOTRLPNSVLKTTSTNKLNLKWLQPKREDCWAKFEMOALAKDLGVKDFIL 1724
QY 2209 SQTLLDQVFNFA---KDQSDDDLKDL 2234
Db 1725 AQSLEEFRLAGLDDEQDLTHSTVELS 1753

RESULT 11
T42749
ATP-binding cassette transport protein homolog - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C:Accession: T42749
R:Wu, Y.C.; Horvitz, H.R.
Cell 93, 951-960, 1998
A:Title: The C. elegans cell corpse engulfment gene ced-7 encodes a protein similar to A
A:Reference number: 222559; MUID:98297348
A:Accession: T42749
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1704 (MW>
A:Cross-references: EMBL:AF049142; NID:g3172340; PID:AMC24116.1; PID:g3172341
C:Genetics:
A>Note: ced-7
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 13.0%; Score 1538.5; DB 2; Length 1704;
Best Local Similarity 24.9%; Pred. No. 9e-91;
Matches 484; Conservative 347; Mismatches 675; Indels 441; Gaps 59;

QY 458 WTADIV-----AFIAKHREDVQSSNGSVY-----TMRFAFNEN----- 492
Db 24 WTLPELLIPCLLGLRVLVYVKKADHTSPENITDNFQVAGTVEDEVFLSNFKPIYKRW 83
QY 493 -----QAIRTL---SRFMECVNLKL-----EPITAEVWLINKS 523
Db 84 CIRSDDVVGYSKDAAKRRTVDLMKKFAERFQSAKLKLVKNSSSEQLLT---VLKRD 140
QY 524 MELIDE-----RKFMAIGIVTGTIPGSELPHVKKYKIRRDINDIVETKNIKIKGYMDPGR 578
Db 141 LPMINTEFCALINSTYAGVVEDEVDTNKKL---NRIILGKTPPEETWHLTETSYNBYGP 196
QY 579 RADPFEDM---RYVMGGAFFYLDVVDQALIRVLTGTEKKTGVMQOMPPCYVD----- 629
Db 197 SSGKYSRLSPSPPYWTSAPLFLQHAIRSSFLSSVQSGAPDLPIITLRKLPRPKRTKTSVSA 256
QY 630 --DIFLVMSRSMPLFMTLMIYSVAVITIGIYEKEARKETMRIMGLDNLSTLMSWT 667
Db 257 FIDPF-----PFIMAFYFIVNIIHITREIAENHA-VKPYLTAMGLSTFEMFYAHVY 307
QY 688 SSLPLVLSAGLLVILKLNLLPYSDPSVFEVFLSFVAFTVLTQCLISTLFSRANLMA 747
Db 308 MAPLAKFVIT--FLCSIIPLTFWVEFSPALIVTVLMTGICAGVIFGAFVASFNNMTNSAI 365
QY 748 ACGGIITFLYLPVLCVAMQDYYGFLKLPASL--LSPV-----AFGFCGEFFAL 796
Db 366 K-----ALIVAGMAMIGISYKRLPELDQSSCFELGLNINAGFALAYALSD 412
QY 797 FEEDGIGVQMDNLP-ESPVEEDGNLTSTSMMLFDIFLGVNTWYIEAV-PPGQYQIPR 854
Db 413 YMRERELNLTNNFNDSSSLH---FSLGVALVMMIVIDLWMSIGALVVDHIRTSADESLRT 469
QY 855 PWYFPCTKSYWFGESDEKSHGP-----SNOKMSEICMBEER---THL----- 895

```

```

Db 470 LDFDE-----APEDEENQTDGVTAQNTIRINEOVNRNRRSRDMETIQMNPASTSLNPDN 522
QY 896 -----KLGVSIONLVKYYRQGMKAVAVGGLNLNFEQGITFELGN 935
Db 523 ABSDSLSESTENDGARDIARADIYIRNLVYKIMSTTGEAVYDGLSLRAVRQCSITLGN 582
QY 936 GAGKTTMSILTGLPEPTSGTAYILGKDIRSEMSTIRONLGVCPQHNVLFDMLVVEEHIW 995
Db 583 GAGKSTTFESIGIIRTPNGRITIGCYDVGNBPGETRRHIGMCPQYNPLDYDLTVSEHLK 642
QY 996 FYARKLGSSEKIVKAEEMQALDVGLPSSKLSKTSQSLGQMRKLSVALAFVGSXVYI 1055
Db 643 LYVGLGAREKDFKQDMKLLSDVKL-DFKEKEKAVNISGGKRRKLCYOMALIGDSEVYL 701
QY 1056 LDEPTAGVDPYSRGIWELLKRYROGRTIILSTHMDPADVGRIRATISHGKLQVSS 1115
Db 702 LDEPTAGMDPGARODVQKLVEREKANRTIILTHYMDAEERLGDVWVIMSHGKLVAAGTN 761
QY 1116 LPLKNDLGTGYTLTVKRYVSSLSSCRNSSTVSTYKLKEDSVSSSDAGISGHESDT 1175
Db 762 QYLKQKFGTGYLLTV-----LDHNDK 784
QY 1176 LTIIDVSAISNLRKHVSEARLVEDIGHETLYVLYPEAKEGAFVLEFHEID----- 1226
Db 785 RKMAY-ILTDVCTHYVKEAREGEMHGOEILIPARKKE--FVPLPQALEIQRNRS 841
QY 1227 -----DRSLDGLISSYGISSETTLEETLEFLKVAESGVDAETSDGTLPRARRRAAF 1275
Db 842 NYEDNNPNTLKSQLATLEKRSFGLNLTLEQVITIGDK-----YKALIASRONSRI 894
QY 1276 GKQSCLRPFETDADAPNDSDIDPESRETDLSGMDKGSYQVGMKLTQGOFPALMK 1335
Db 895 HNSRNASEPSELKPAQVDIQTSSKSDSTQK--LMSQARCP-EKSGVAKMVAQFISIRK 951
QY 1336 RLLIARRSRKGFPAQIVLPAVFCIALVFSLLVPPFGKYPSTLEQPMYINQYTFVNSDA 1395
Db 952 KFLYSRRNAQLFTQVLP--IILGLVGSLT-----TLKSNT 988
QY 1396 PBDTGLLELNLNLTQDPGCTGCMGNPDPDPCQAGEEWTAPVPTINDLQNGWMT 1455
Db 989 DQ-----FVSNSL-----TP--SGLE-----PSKVWRRENGT-- 1014
QY 1456 MGNPSPACQSSDKIKMLPVCPPGAGGLPPQKQONTADILQDLTGNISDYLVKTYVQ 1515
Db 1015 -----IDVLAEPMLILIFAMVSTTFMFILIEERTCOFAHQDILGTISP 1044
QY 1516 IIAKSLAKNKIWNERRYGFSLGVSNTQALPPSQEVNDAIQMKHKLKLANDSSDRFLN 1575
Db 1045 NITKSL-----IGE-----MPA----- 1057
QY 1576 SLGRPMTGIDTFENNVKVFNNKGWHAISFLVINNALLRANLQGENPSHYGITAFAFNP 1635
Db 1058 TIGGMNNS-----DNLEALFNMRHYHVLPTLISMIRAKLTGVDAEISSGVFLSKTSN 1113
QY 1636 LNLTKQQLSEVALMTTSDVLYSTICVIFAMSFVPAFVFLIQRVYSKAKLQFISGKYP 1695
Db 1114 SNLPSQL-----IDVLAEPMLILIFAMVSTTFMFILIEERTCOFAHQDILGTISP 1164
QY 1696 VTYWLSNFMDCNVCNVVATVITIFICFQCKSVYSNTLVALLLLLYGMSITPLMYP 1755
Db 1165 ITFYASLIDYDILSLICLILFNFELAF-----HMYDHLAIVILFWLIFYSSVPFLYA 1220
QY 1756 ASFEKIPSTAVVLYVSNLFIGINGSVATVLELTQNKLNININDILKSYFL-----IF 1810
Db 1221 VSFLQSPSKANVLLIMQVYISGALLAVELIFV-----IFNIDEMKLSILVINIFEL 1275
QY 1811 PHFCIGRGLIDMVKKQAAADALERGENKRVSP-----LSMDLVGRNLPAVAVGVVFFLI 1866
Db 1276 PSYAGSAII-----TINTYG--MILPSEELNMDHCKKNMWMKMGTCVCSFAL 1322
QY 1867 TVLIQYREFIR-----PRVNAKLSPLNDE--DDVAREQRILLDGGQNDILEIK 1915

```

Db 1323 EVLLQFVRRRLSQVYVTRSSNNVCPMAGDLPVCEVSEERERHVRVNSQNSALYIK 1382
QY 1916 ELTKIYRRKRRAVDKICGIPGECFGLGVNAGKSTFPMILGDTVTBGRDAFLNN 1975
Db 1383 DLTKT -GRTAVNMLCLAVDOKECFGLGVNAGKSTFPMILGDTVTBGRDAFLNN 1440
QY 1976 SILNIEVHONMGYCPQFQDAITELLTGREHVEFFALLKGVBEKEKGAEMAKRLGLV 2035
Db 1441 DYTELI-----SIGYCPQDQALMDLTGTRESLELLAQMGMFENYKA -KAELILECVGMI 1493
QY 2036 KIGEKYAGNYSGGNKKRSTAMALIGPPVPLDEPTGMDPKARRFLMNCALSVYKEGR 2095
Db 1494 AHADKLVREYVSGGKRIKISVALLAPOTMILDEPTAGIDPKAREVWELLWCHEHN 1553
QY 2096 S-VYLLSHMECEALCTSMATMVNGRFRGLGVHLMKRFQDGYTIYVRKINSNDLKP 2154
Db 1554 SALMLTSHNDECEALCSRIAYLNKSLJAIGSQELKSLGVNNTMTLSLEPNORDVY 1613
QY 2155 VQDFGLAFPGSVLKEKHNRM--LQYQPLSSLSL-ARFISLSQSKRLHIEDVSQ 2210
Db 1614 VQ-LVQTRLPNSVLTKTSTNTKTLNKLQWIPKEKDCWAKFEVWQALAKDLGVKDELLAQ 1672
QY 2211 TPLDQVFNFA--KQSDDDLKDLIS 2234
Db 1673 SLEETFLRLAGIDEDLDTHSTVEIS 1699

RESULT 12

S60124

transport protein homolog C48B4.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 13-Jan-1996 #sequence revision 12-Apr-1996 #text change 02-Feb-2001

C:Accession: S60124; S40724; S40725

R:Kershaw, J. submitted to the EMBL Data Library, November 1995

A:Reference number: S60124

A:Accession: S60124

A:Molecule type: DNA

A:Residues: 1-1767 <KER>

A:Cross-references: EMBL:429117; NID:9439247; PID:91066912

C:Genetics:

A:Map position: III

A:Interons: 47/1; 112/3; 161/2; 220/2; 543/3; 574/3; 903/2; 1056/1; 1115/3; 1178/3; 1265/3

C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

C:Keywords: ATP; duplication; nucleotide binding; P-loop; transmembrane protein

F:628-818/Domain: ATP-binding cassette homology <ABC1>

F:645-652/Region: nucleotide-binding motif A (P-loop)

F:764-769/Region: nucleotide-binding motif B

F:1457-1642/Domain: ATP-binding cassette homology <ABC2>

F:1474-1481/Region: nucleotide-binding motif A (P-loop)

F:1586-1591/Region: nucleotide-binding motif B

Query Match 13.0%; Score 1536.5; DB 2; Length 1767;

Best local similarity 23.7%; Pred. No. 1.4e-90;

Matches 522; Conservative 370; Mismatches 735; Indels 575; Gaps 66;

QY 162 LSLPKSTVDKMLRADYILKVFLOGYQLHLTSLCNGSKSEEMQL-GDDEVSEFLCLPKE 220
Db 7 IPRHSHIVMLRRLYLONEKAKRAKESDIEGSSSENESENDSITPLDQGLAESRIPRK 66
QY 221 KLAAR-----VLRSN-----MDILKPLRLTSLNSTSPFPEKELAEATKTLHLSL 265
Db 67 KMRRLKQFILLKMDVLLKRNKVVTLFELIPL-----LI 103
QY 266 GTLAQELFSRWSMDKROEYMLPLTNSSSSSTQIYQAVSRVCGHPGEGGLKIKSLMY 325
Db 104 GPLV-----YLIVKNDHTSSPENIT----- 124
QY 326 EDNNYKALPBGNGTDEDAEFYDNSTTPPCNDLAKNLESSPLRIT--KALKPLLYGKI 383
Db 125 -DN-----FOYKGTVEV-----FLESNFKIPYKRWCLRSDDVVG-- 159

```

Db 1047 -----TLKSNNTDQ-----FRSLT-----PSGIE----- 1065
Oy 1441 VPOTIMDLFONGMWTQNPSPACQSSDKTKKMLPVCPGAGLPPQROKRNADILQDL 1500
Db 1066 -PSKVYKREFNGT-----IPEANKEKLLRS 1092
Oy 1501 TGRNISDYLVKTYVOIIAKSLKNKIWNEPRYSGFSLGVSNTQALPPSOEVDNAIKOMKK 1560
Db 1093 GGEFVLNKNRKNPLPNITKSL-----IGE-----MPPA----- 1120
Oy 1561 HLKAKASSADRLNSGRMTGIDFRNNYKWPENNKGMHAISFLVNNALIRANLQK 1620
Db 1121 -----TIGMTMNS-----DNLEALFNMYTHVLPFLSMIRARLTGTVA 1161
Oy 1621 GENESHYGTAFNHPMLNLTFRQOLSEVALMTSVLVLSICVIFPAMSEFVAPFVLIQER 1680
Db 1162 EISSGVFLYSKTSNSMLRPSQL-----IDVLLAPMLLIFAMVSTFVMEFLEER 1212
Oy 1681 VSKAKHLQFISGVKPYIYMLSNFVDMCNVVPATLVIIIFCFOOKSYVSTINLEVAL 1740
Db 1213 TCQFAHQFLLTGLSPITFYSASLIYDGLISLCLFLFEMFLAF-----HMVYDLATVIL 1268
Oy 1741 LLLYGMSTPLMYPASFVEKIPSTAVVLTSVNLFGINGSVATFVLELFTDNKNLNTIN 1800
Db 1269 FMFLYFESSVPFIYAVSEFLQSPSKANVLLIMQVVISGALLAVFLIFM-----IFNID 1323
Oy 1801 DILKSVFL-----IFPHFCIGRGLIDMKVQAMADALERFGENREVPSP-----LSMDLVGR 1851
Db 1324 EMKRSILVNFEMFLPSYAGSAII-----TINITYG-----MLPSEELNMWCHG 1370
Oy 1852 NLFMAVEGVVFLITVLIQYREFIR-----PRVNAKLSPLNDE-----DEVDRERO 1900
Db 1371 NAMLMGFGVCSRALFVLLQFKVRRFLSQVWYVRKSSHNNOVPMAGDLPVCSVSDEER 1430
Oy 1901 RILDDGGQNDILEIKELTKYRRKKRPAYDRICVGIIPGECFGLLVNGAGKSTFKMT 1960
Db 1431 RVHVNVSQNSALVYKDLTKTF--GRFTAVNELCLADVQKCEFLLVNGAKTKTTFNITL 1488
Oy 1961 GDTVTGADFLNKNSTLSINHEVHONMGYCPQFDATITELTGREHVEFPALLRGPEKE 2020
Db 1489 GQSAASGEMIGRDYTEL-----SIGCPQFDALMDLTERESIELIAHQHGENRK 1543
Oy 2021 VGVKGVEMAIRLGLVYKGEYAGNYSGGNKRLSTAMALIGBPVFLDEPTTGMPDKAR 2080
Db 1544 A--KAELILRCVGMIAHADKLVRFPYSGQGRKISVGVALLAPQMIIDEPFAGIDPKAR 1601
Oy 2081 RFLMNCALSVYKEGRS--VLTLSHMECEALCTRAIMVNGRFRCLGSVOHLKNRFGDGY 2139
Db 1602 REVMELLKCRHSNSALMTLSHMECEALCSRIAVLNGSLIAIGSSQELKSLYGNVY 1661
Oy 2140 TIVVRIAGSNPDLKPVODFGLAFPGSVLKEKERNM--LOYOLPSSLSL--ARIPSTLS 2195
Db 1662 TMLTSLTEPQNRDMVVO--LVQTRLPNSVYLKTTNTKTLNKMIKPIREKEDCMSAKTEMYO 1720
Oy 2196 QSKRHLIEDYVSQTTLDQVYVNA--KDSQSDHLKDL 2234
Db 1721 ALAKDLGVKDFILAOSSLETFRLAGLDEDDQDHTSHSTEIS 1762

```

RESULT 13
 T00826
 hypothetical protein t326g.22 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Mar-2001
 C:Accession: T00826
 R:Bounsley, S.D.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
 submitted to the EMBL Data Library, November 1997
 A:Description: Arabidopsis thaliana chromosome II BAC T326 genomic sequence.
 A:Reference number: Z14163
 A:Accession: T00826
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-1246 <R0U>
 A:Cross-references: EMBL:AC002510; NID:q2618683; PID:g2618705
 A:Experimental source: cultivar Columbia
 C:Genetics:
 A:Map position: 2
 A:introns: 33/3; 95/2; 113/3; 137/3; 168/3; 361/3; 421/2; 432/3; 493/3; 521/3; 535/3;
 A:Note: T326g.22

Query Match 11.9%; Score 1402; DB 2; Length 1246;
 Best local similarity 28.7%; Pred. No. 4, 1e-82;
 Matches 415; Conservative 195; Mismatches 388; Indels 450; Gaps 43;
 A:Note: T326g.22

```

Oy 1019 VGLPSSKLSKTSQLSGGMOKRLSYALAFVGSKVYIIDEPTAGVDPYSRRIGWELLKY 1078
Db 1 VGL-SDKINTVLRAISGGMKRLSLGIALIGNSKYIIDEPTSGMDPYSMRLTQMLIKI 59
Oy 1079 RQGTIILSTHMDADVLGDRILAIISHGKLCQVSSSLFNOLGTYLTLVKKDVSS 1138
Db 60 KKGRIILITSHMDAEELGDRIGIMANGSLKCCSSIFLKHGYGVTTLVK----- 113
Oy 1139 ISSCRNSSVSYLKKEDSVSSQSSDAGLGSDBESDTLIDVSAISMLRKVSEARLYE 1198
Db 114 -----TSPT-----VSAAHVHRHIPSACVS 136
Oy 1199 DIGHELTYVLPYEAKEGAFVLEHIEDRL-----SDL-GISSGISTETLEELFLAYE 1253
Db 137 EVGNIEISFRLP--LASLPCFEMFRIESCCKNSDSDPGIQSGIVSTLEEVFLRA- 193
Oy 1254 ESGVAETSDGTLFARRRRARAFGRKOSCLRFETEDDADPDNDSDIDPESRETDLSGMDG 1313
Db 194 GGNLDIE-----DKQ-----EDIVSPPTKSLVCISNO 223
Oy 1314 KSTYOK-----GKKLTO-----QGFVALLM----- 1334
Db 224 KSMQPKLLASGNDGAGYIITSVAKAFRLIYAATVLLGFTSIQCCGSIISRMFMRHC 283
Oy 1335 -----KRLIARSRKGFACIVLPAVFCIALVSLVLPFGKYPSELQPMYNEQYT 1389
Db 284 KALFLKRRASRCRDKRYAFQFIIPAVFLFLGLF-----LQKLP----- 323
Oy 1390 FVSNDAPEDTGTLELLNALTKDQPGFTRCMGKNIPDTPCOAGEBWTAPVQTIQDLF 1449
Db 324 --HPQKSTLITTAFAFNLLSGK-----GGGPIPED-----LSVPIAKEVAYI 366
Oy 1450 GNG-----NMNMOPSPACQSSDKIKKMLPVCPGAGGLPPQROKRNADILQDLGR 1503
Db 367 ESGWIQPLRNTSYKFPNP-----KEALDAI--DAAGP 397
Oy 1504 NISDYLVKTYVOIIAKSLKNKIWNEPRYSGFSLGVSNTQALPPSOEVDNAIKOMKKLK 1563
Db 398 TLGPTLLS-----MSEFLMSFD-----QSQSSRE-----G 424
Oy 1564 LAKSSADRLNSGRMTGIDTRNNYKWPENNKGMHAISFLVNNALIRANLQKGEN 1623
Db 425 LSHSDCHHPDGSIG-----YVTLHNGTCQAHGPIYIWMMAALIR--LAIGN- 470
Oy 1624 PSHVGTITFNFHPLNLT-KOLSEVALMTSVLVLSICVIFPAMSEFVAPFVLIQERVS 1682
Db 471 -KNMTIOTRRNHPLEPTKTQRIQRHDLDAFSAIIVNT-----AFSEFIRASVAPVYKREV 525
Oy 1683 KAKHLQFISGVKPYIYMLSNFVDMCNVVPATLVIIIFCFOOKSYVSTINLEVALLL 1742
Db 526 KAKHQQLISGVSIVLSWYMLSTVWDFISPLFPSTPAIILFVAFGEQVIGRFLPVYML 585
Oy 1743 LLYGSIPLMYPASFVEKIPSTF-----YVLTSVNLFT-----GINGS 1782
Db 586 LEYGLAIASSTYCLTFEFTESHMAQANSSYSVLLPISLFVSESSNVILWVHFFSGILM 645
Oy 1783 VATEVLELF--TDNKLNNINDI-----LKSVFILPHFCIGRLIDM--VKNQAMADALE 1833
Db 646 VISFVMGILPATASNSTLKLILIFRYALQNFRLSGFCFSQGLASLALLRQMKKSS 705

```


QY 1834 RFGENREVSPLMDLVGNLFAMAVEGVFELLTVLLIOYREFIRPRPNAKLS----- 1886
 Db 706 H-----GVFENNVYAGSICVLDLEVRLECYRSMILSF-----HGIDTKLSLITTYIGA 755
 QY 1887 -----PL-----NDEDEDVRRERORILLDGGGONDILEIKE 1916
 Db 756 SRLTELYIDRYVSTSFSTEPDLKDTGASTIDMEDDIDVQEDRDRVISGLSDNTMYLXON 815
 QY 1917 LTKIYRRK-----KPADRICVGIIPGECFGLLVNGAGKSTFKMLTGDITTVRGDAFL 1972
 Db 816 LRKYVPGDKHGGPVAAVQSLFFSVQAGCFGLTNGAGKTTLSMLSGEETPTSGTAFI 875
 QY 1973 NKNSTLSIHFEHONMGYCPQFDATITELTGREHVEFFALRGVPEKEVGAVGEMAIKRL 2032
 Db 876 EGDIVASPKAIRQIHIGICFPQDALFEELYKHEHLELTARIKGVDRHIDNVTEKLEVF 935
 QY 2033 GLVYKGEYKAYNSGKNRKLSTAMALIGPPVFLDEPTTGMDPKARFLMN--CALSV 2090
 Db 936 DLKSHKSPFTLSGKNRKLSTVALIAMIGDPIYILDEPSTGMDPVAKRFMDVYSRLST 995
 QY 2091 VKEGSSVYLTSHSMECALCTBRAIMVNGFRCLGSOHLKNRFG----- 2136
 Db 996 RSGKAVILTTTHSMNEAGALCTRIGIMVGRLCIGSPHLLKTRYGMLHELVFPYNGVK 1055
 QY 2137 -----DGYT-----I 2141
 Db 1056 PNEVSNVLENFPCOITQOMLFNVPQPSRLGLDEVCIGVSDSTTPDTASASELSLSPEM 1115
 QY 2142 VVRIA-----GSPN-----DLKPV 2155
 Db 1116 VORIAKFLGNBQVSTVLPPLPEEDVRFDDQLSEQLFRFDGIPLPFPAEWMLTKKESFAL 1175
 QY 2156 QDFELAPGVSYLEKHNMLQYOLPSSL--SLARFISLSQSKRLRHIDYVSQTL 2213
 Db 1176 DSFIQSSFPGATFKNSCNLSIKYLPFGEGGLSLADAGHLERNRNLGIAEYSISOSTL 1235
 QY 2214 DOVEYNFA 2221
 Db 1236 ETIFNHFA 1243

RESULT 14
 t27121
 hypochelical protein Y53C10A.9 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence-revision 15-Oct-1999 #text-change 04-Mar-2000
 C:Accession: t27121
 R:White, S.
 submitted to the EMBL Data Library, November 1998
 A:Reference number: Z20314
 A:Accession: t27121
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1564 <NTL>
 A:Cross-references: EMBL:AL033536; PIDN:CAA22142.1; CESP:Y53C10A.9
 A:Experimental source: clone Y53C10A
 C:Genetics:
 A:Gene: CESP:Y53C10A.9
 A:Introns: 43/3; 92/2; 148/2; 226/3; 354/1; 712/3; 817/1; 875/1; 916/3; 984/3; 1069/2;
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 9.8%; Score 1158.5; DB 2; Length 1564;
 Best Local Similarity 23.0%; Pred. No. 4e-66;
 Matches 433; Conservative 324; Mismatches 673; Indels 451; Gaps 60;

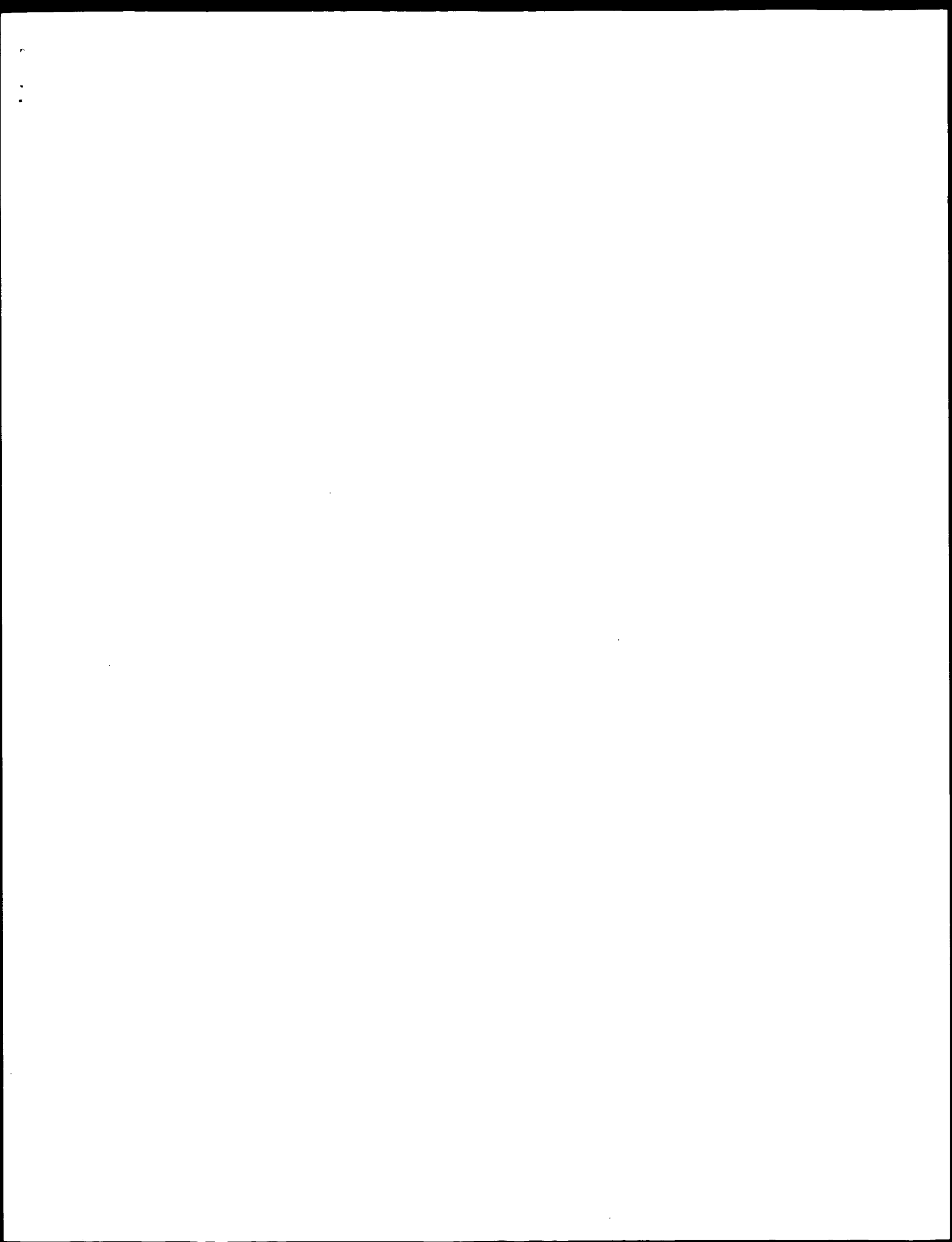
QY 458 WTAODI-----VAFLA-----KHPEDVQSSNGSV--YTWRAPNET-----NQ 493
 Db 22 WTGEVALPLILIAFPAAVMYAKSQAPEDAKSSGSPSIDMLMSTESFHPYVSSCQDPSY 81
 QY 494 AIRTISRMECVNLKLEPIATEWLINKSMELDERKFMAGIYFTGTGTPSISLEPHHY- 552
 Db 82 GVQTVNNVENWVNSPMR-----W-DNTNLSIDLAKNPARKLEIKDVRAACKIIVIVE 133

QY 553 -KTKIRMDIDNVERTNKKIKDGYWDPGRADPFEDMRYVWGCFAY-----LDQVBOA 603
 Db 134 DKTKTMMVLPAT-----GRRSYFNFSYTYANKIMFGISQANNTSITENF 180
 QY 604 IIRVLGTE-KRTGYVMQMPYPCYVDIPLRVMSRSMPLFMTLMIYSVAIYIKIYVE 662
 Db 181 DIKLSITFNEESG-----FGNGFLFVAVCLMIPVISVARALVE 221
 QY 663 KEARLEKTRIMGLDMSIIMFSNFIPLPLVASAGLVIYIKLGLULYSDPSYFVL 722
 Db 222 KSS-VKPYLTITGP--LMMFLEHFLFCVINTFLILTLSTLYIFSDNCPYTVLACI 277
 QY 723 SVAAVYIILCCFLISPLFSRANLAACGGIITYETLPLVYCA-----MODY-----GF 773
 Db 278 FMTHCHCVSILCTSLPLPGKRIYEGMYIITLLIIMHLSLEFEDMLFWVPLLPNT 337
 QY 774 TLKIFASILSPVAFGCEYFALFEEOGIGVQMDNLFESFVEDGPNLTTSIMLFDTF 833
 Db 338 SLKLFVDATFLASGPNQTPSALFSSK-----KTLQSAAYVFGIMISCTYVMLVAALF 391
 QY 834 LYGVMTYITAVPFGQYIDRPWFPCYTSY--FQESDEKS---HPSNQKRMSEIOM 888
 Db 392 MEKLYTFVGHAF-----KRFMRILFSGKGRSKIRERDQVEDRSTILO 436
 QY 889 EEEPTHLK-----LGVSIONLVKYRDMQKAVADVGLALNFEQITSLFCHNGAGKTTMS 944
 Db 437 CKETVEGRGSAIDIELSGLVKYOGEK-AVNGLSRLAIRGOVSLILGNGGKSTFTG 495
 QY 945 ILTGLPPTSGTAYIIGKDIRSEMSTIRONLGVCPQHNVLFDMLYEEHIMFYARLGLS 1004
 Db 496 MITGMQATGKVMIGSIDANANRAEARRELIGYCPQNPYDELTVMEHLRVNALKGRS 555
 QY 1005 -EKHYAKEMQALDVLGPPSKLKSKTSLSGMOKRLSALAFVSGKVVILDEPTAGV 1063
 Db 556 GGSDFKMDAESLLKQLEL-TDKRNTLAKNLSCGMKRLCCAMIGSRVITLIDEPDAGM 614
 QY 1064 DPYSRGIWELLKYRGQFTIITSHHMEADVLGRIATISGKLCVCCSSFLFNQGL 1123
 Db 615 DPSARIDVQNMALVYKADRTILTHMDAEKLGDMIFYMSHGKMAASGSKRYLQKKG 674
 QY 1124 TGYVLTLY-----KKDVESLSGCRNSSSTVSYLKEDSVSOSSDAGLGSDBS 1173
 Db 675 GGMILLTIVFSYHDPMPKRSYFAVDVCTVOSTA--LVKDBR-----GQMIEI 722
 QY 1174 DTLTIDVSAISNLIRKVSFARLVEDIGHELLTVLPLEAKBGAFLRHEIDRLSDIG 1233
 Db 723 SILETEKSRPLPTLTK--ILESVMEDYNNP-----EFQALPBDIOEKRTLE 767
 QY 1234 ISSYGISETLLEIFLKVARE-----SGVDAETSDGTLPARNRRAFGDKOSCLRPPT 1286
 Db 768 LATIGVSMSSLEOVFTIIGECDDIMNGTGYDKT-----ERKEKSTLV 812
 QY 1287 EDDAADPNDSIDIPESRETDLLSGMDGKSGYGVKGMKLTQOQFVALLMKRLLIARRSRG 1346
 Db 813 QYKIQCPK-----QGSFKLMVMVALLQKRAYLYLRNPQV 847
 QY 1347 FFAQIVLPAFVICALVSLIYPPFGKYPSLELQPMKYNQYTFVNDAPEDGTIELLN 1406
 Db 848 ITYQIILP-----LTLWLMFAVFLR--LEKRPKLSIDESFDSQYPHSVTLQLEEN 898
 QY 1407 ALTKDPGFTRCMEGNIPDTPQAGEEWTAPVQTIMDLFQNGNMTQNPSPACOS 1466
 Db 899 E-----N 900
 QY 1467 SDKIKKMLPVCPPGAGLPPPKOKONTADILLQDLTGRNISDYLVKTYVOIIAASLKNTM 1526
 Db 901 DDLRLANLY-----NSFSNF-----EYVFKTL----- 921
 QY 1527 VNEFRYCGFSIGVSNQALPPOSOEVNDATIKOMKHLKLAK--DSADARFLNSLGRFY- 1581
 Db 922 -----GFTVKYVK-----KGSDFKYKISQGRNMAALIMNTIASAMYLND 960

[illegible]

RESULT 15

Query Match	8.68;	Score 1013.5;	DB 2;	Length 373;
Best Local Similarity	65.0%;	Pred. No. 8.2e-58;		
Matches 195;	Conservative 40;	Mismatches 64;	Indels 1;	Gaps 1.



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2002, 12:55:51 : Search time 22.98 Seconds
(without alignments)
3809.613 Million cell updates/sec

Title: US-09-595-526b-2
11797

Perfect score: 11797
Sequence: 1 MACWQQLLLMKNTFRRR.....YDVAVTSTFLDDEKKESTV 2261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11770	99.8	2261	1 ABC1_HUMAN	O95477 homo sapien
2	11256	95.4	2261	1 ABC1_MOUSE	P41233 homo musc
3	5870.5	49.8	2273	1 ABCR_HUMAN	P78363 homo sapien
4	4230.5	35.9	2436	1 ABC2_HUMAN	O9b267 homo sapien
5	4093.5	34.7	2434	1 ABC2_MOUSE	P41234 mus musculu
6	2642.5	22.4	1704	1 ABC3_HUMAN	O99758 homo sapien
7	1537	13.0	1691	1 YLH4_CAEEL	P34358 caenorhabdi
8	411	3.5	330	1 DRRA_STRPE	P32010 streptomyce
9	382.5	3.2	343	1 NOD1_RHISN	P5476 rhizobium s
10	366	3.1	304	1 NOD1_RHIS3	P72335 rhizobium s
11	347	2.9	308	1 YADG_ECOLI	P36879 escherichia
12	344.5	2.9	340	1 NOD1_RHITO	P23703 rhizobium 1
13	343.5	2.9	347	1 NOD1_RHIGA	P50332 rhizobium 9
14	339.5	2.9	1280	1 MDR1_HUMAN	P08183 homo sapien
15	331.5	2.8	355	1 NOD1_RHIME	O52618 rhizobium m
16	329.5	2.8	578	1 YBHE_ECOLI	P75776 escherichia
17	327.5	2.8	1281	1 MDR3_CRIGR	P23174 cricetus
18	327	2.8	894	1 YH1H_ECOLI	P37624 escherichia
19	326	2.8	1276	1 MDR3_MOUSE	P14447 mus musculu
20	325.5	2.8	308	1 NOSF_PSEST	P19844 pseudomonas
21	324.5	2.8	1276	1 MDR2_MOUSE	P14440 mus musculu
22	322.5	2.7	306	1 NOD1_BRAJA	P26050 bradyrhizob
23	321	2.7	1276	1 MDR1_CRIGR	P21448 cricetus
24	317	2.7	1362	1 PMD1_SCHPO	P36619 schistosach
25	316	2.7	1276	1 MDR2_CRIGR	P21449 cricetus
26	315.5	2.7	311	1 NOD1_RHITV	P08720 rhizobium 1
27	315	2.7	1278	1 MDR1_RAT	P08201 rattus norv
28	314.5	2.7	1277	1 MDR1_RAT	P43245 rattus norv
29	313	2.7	354	1 Y415_STNY3	P22040 synechocyst
30	310.5	2.6	1276	1 MDR1_MOUSE	P06795 mus musculu
31	304.5	2.6	1294	1 YOH5_YEAST	O08234 saccharomyc
32	300	2.5	381	1 OPBA_BACSU	O45460 bacillus su
33	298.5	2.5	262	1 YA23_METJA	O58429 methanococc

34	297	2.5	380	1	OPCA_BACSU	O34992 bacillus su
35	296	2.5	335	1	Y719_ANASP	O05067 anabeena sp
36	293.5	2.5	1321	1	AB11_HUMAN	O95342 homo sapien
37	292.5	2.5	305	1	YHCH_BACSU	P54592 bacillus su
38	287.5	2.4	274	1	Y179_MYCPN	O30294 mycoplasma
39	286.5	2.4	274	1	Y179_MYCGE	P47425 mycoplasma
40	285.5	2.4	1279	1	MDR3_HUMAN	P42332 homo sapien
41	284	2.4	306	1	BCRA_BACLI	P42332 bacillus 11
42	284	2.4	1321	1	MDR1_CAEEL	P34712 caenorhabdi
43	284	2.4	1336	1	MAM1_SCHPO	P78966 schistosach
44	281.5	2.4	308	1	YEHX_ECOLI	P33360 escherichia
45	281.5	2.4	343	1	ABC_ECOLI	P30750 escherichia

ALIGNMENTS

RESULT	ID	ABCI_HUMAN	STANDARD:	PRT:	2261 AA.
AC	O95477	Q9UN08: Q9UN07: Q9UN06: Q9UN04: Q9UN09: Q96T85: Q96S56:			
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	01-MAR-2002	(Rel. 41, Last annotation update)			
DE	ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette transporter 1) (ATP-binding cassette 1) (ABC-1) (Cholesterol efflux regulatory protein)				
DE	regulatory protein)				
GN	ABCA1 OR ABC1 OR CERP.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20345099; PubMed=10884428;				
RA	Santamarina-Fojo S., Peterson K.M., Knapper C.L., Qiu Y.,				
RA	Freeman L.A., Cheng J.-F., Osorio J., Remaley A.T., Yang X.-P.,				
RA	Haudenschild C.C., Prades C., Chimini G., Blackmon E.B.,				
RA	Francois T.L., Duveger N., Rubin E.M., Rosier M., Deneffe P.,				
RA	Fredrickson D.S., Brewer H.B. Jr.,				
RT	"Complete genomic sequence of the human ABCA1 gene: analysis of the				
RT	human and mouse ATP-binding cassette A promoter."				
RT	Proc. Natl. Acad. Sci. U.S.A. 97:7987-7992(2000).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TTSUSE-Skin.				
RA	Schwartz K., Lawn R.M., Wade D.P.;				
RT	"ABCA1 gene expression and apoA-I-mediated cholesterol efflux are				
RT	regulated by LXR."				
RL	Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21251004; PubMed=11352567;				
RA	Qiu Y., Cavelier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;				
RT	"Human and mouse ABCA1 comparative sequencing and transgenesis				
RT	studies revealing novel regulatory sequences."				
RL	Genomics 73:66-76(2001).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	Tanaka A.R., Abe-Dohmae S., Arakawa R., Sadanami K., Kidera A.,				
RA	Kloka N., Amachi T., Yokoyama S., Ueda K.;				
RT	"A new topological model of functional human ABCA1-signal peptide				
RT	cleavage and glycosylation of a large extracellular domain."				
RL	Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.				
RN	[5]				
RP	SEQUENCE OF 21-2261 FROM N.A.				
RX	MEDLINE=99194549; PubMed=10092505;				
RA	Langmann T., Klucken J., Reil M., Liebisch G., Luciani M.F.,				
RA	Chimini G., Kaminski W.E., Schmitz G.;				
RT	"Molecular cloning of the human ATP-binding cassette transporter 1				
RT	(ABCA1): evidence for sterol-dependent regulation in macrophages."				
RL	Biochem. Biophys. Res. Commun. 257:29-33(1999).				
RN	[6]				

RP SEQUENCE OF 21-2261 FROM N.A.
 RX MEDLINE=99364413; PubMed=10431238;
 RA Rust S., Rosier M., Funke H., Real J., Amoura Z., Piette J.-C.,
 RT Delzenne J.-F., Brewer H.B., Duverger N., Deneffe P., Assmann G.;
 RA "Tangier disease is caused by mutations in the gene encoding
 RT ATP-binding cassette transporter 1.";
 RL Nat. Genet. 22:352-355(1999).
 RN [17]
 RP VARIANTS FHA THR-1091 AND 1893-GLU-ASP-1894 DEL.
 RX MEDLINE=20001430; PubMed=10533863;
 RA Marcell M., Brooks-Wilson A., Clee S.M., Roomp K., Zhang L.-H., Yu L.,
 RA Collins J.A., van Dam M., Molhuizen H.O.F., Loubser O.,
 RA Ouellette B.F.F., Senses C.W., Fichter K., Mott S., Denis M.,
 RA Boucher B., Pimstone S., Genest J. Jr., Kastelein J.J.P., Hayden M.R.;
 RT "Mutations in the ABC1 gene in familial HDL deficiency with defective
 RT cholesterol efflux.";
 RL Lancet 354:1341-1346(1999).
 RN [18]
 RP VARIANTS TD ARG-597 AND ARG-1477, AND VARIANT FHA LEU-693 DEL.
 RX MEDLINE=99364411; PubMed=10431236;
 RA Brooks-Wilson A., Marcell M., Clee S.M., Zhang L.-H., Roomp K.,
 RA van Dam M., Yu L., Brewer C., Collins J.A., Molhuizen H.O.F.,
 RA Loubser O., Ouellette B.F.F., Fichter K., Ashbourne-Excoffon K.J.D.,
 RA Senses C.W., Scherer S., Mott S., Denis M., Martindale D.,
 RA Frohlich J., Morgan K., Koop B., Pimstone S., Kastelein J.J.P.,
 RA Hayden M.R.;
 RT "Mutations in ABC1 in Tangier disease and familial high-density
 RT lipoprotein deficiency.";
 RL Nat. Genet. 22:336-345(1999).
 RN [19]
 RP VARIANTS TD SER-590; SER-935 AND VAL-937, AND VARIANTS ALA-399 AND
 RP MET-883.
 RX MEDLINE=99364412; PubMed=10431237;
 RA Bodzioch M., Orso E., Klucken J., Langmann T., Boettcher A.,
 RA Diederich W., Drobnik W., Barlage S., Buechler C.,
 RA Porcch-Oezuerne M., Kaminski W.E., Hahmann H.W., Oette K.,
 RA Rothe G., Aslanidis C., Lackner K.J., Schmitz G.;
 RT "The gene encoding ATP-binding cassette transporter 1 is mutated in
 RT Tangier disease.";
 RL Nat. Genet. 22:347-351(1999).
 RN [110]
 RP VARIANTS TD ILE-929; ARG-597 AND ARG-1477, AND VARIANTS FHA LEU-693
 RP DEL; THR-1091; 1893-GLU-ASP-1894 DEL AND LEU-2150.
 RX MEDLINE=20540002; PubMed=11086027;
 RA Clee S.M., Kastelein J.J.P., van Dam M., Marcell M., Roomp K.,
 RA Zwarts K., Collins J.A., Koelant R., Tamasaawa N., Stulc T.,
 RA Suda T., Ceska R., Boucher B., Rondeau C., Desoulh C.,
 RA Brooks-Wilson A., Molhuizen H.O.F., Frohlich J., Genest J. Jr.,
 RA Hayden M.R.;
 RT "Age and residual cholesterol efflux affect HDL cholesterol levels and
 RT coronary artery disease in ABCA1 heterozygotes.";
 RL J. Clin. Invest. 106:1263-1270(2000).
 RN [111]
 RP VARIANTS TD ASN-1289 AND HIS-1800.
 RX MEDLINE=20171564; PubMed=10706591;
 RA Brousseau M.E., Schaefer E.J., Dupuis J., Eustace B.,
 RA Van Berdeghem P., Goldkamp A.L., Thurston L.M., Fitzgerald M.G.,
 RA Yasek-McKenna D., O'Neill G., Eberhart G.P., Weifengach B.,
 RA Ordovas J.M., Freeman M.W., Brown R.H. Jr., Gu J.Z.;
 RT "Novel mutations in the gene encoding ATP-binding cassette 1 in four
 RT Tangier disease kindreds.";
 RL J. Lipid Res. 41:433-441(2000).
 RN [112]
 RP VARIANT TD ASP-1046, VARIANT FHA CYS-230, AND VARIANTS LYS-219;
 RP ILE-825; MET-883 AND LYS-1587.
 RX MEDLINE=20396633; PubMed=10938021;
 RA Wang J., Burnett J.R., Near S., Young K., Zimman B., Hanley A.J.G.,
 RA Connelly P.W., Harris S.B., Hegele R.A.;
 RT "Common and rare ABCA1 variants affecting plasma HDL cholesterol.";
 RL Arterioscler. Thromb. Vasc. Biol. 20:1983-1989(2000).
 RN [113]
 RP VARIANT TD TRP-587, AND VARIANT LEU-2168.
 RX MEDLINE=21157002; PubMed=11257260;
 RA Bertolini S., Pisciotto L., Serl M., Cusano R., Cantafora A.,
 RA Calabresi L., Franceschini G., Ravazzolo R., Calandra S.;
 RT "A point mutation in ABCA1 gene in a patient with severe premature
 RT coronary heart disease and mild clinical phenotype of Tangier
 RT disease.";
 RL Atherosclerosis 154:599-605(2001).
 RN [14]
 RP VARIANTS LYS-219; MET-883 AND ASP-1172.
 RX MEDLINE=21157003; PubMed=11257261;
 RA Brousseau M.E., Bodzioch M., Schaefer E.J., Goldkamp A.L., Kiehl D.,
 RA Probst M., Ordovas J.M., Aslanidis C., Lackner K.J.,
 RA Bloomfield Rudins H., Collins D., Robins S.J., Wilson P.W.F.,
 RA Schmitz G.;
 RT "Common variants in the gene encoding ATP-binding cassette transporter
 RT 1 in men with low HDL cholesterol levels and coronary heart disease.";
 RL Atherosclerosis 154:607-611(2001).
 RN [15]
 RP VARIANT TD LEU-1506.
 RX MEDLINE=21369429; PubMed=11476961;
 RA Lapicka-Bodzioch K., Bodzioch M., Kruehl M., Kiehl D., Probst M.,
 RA Klec B., Andrikovics H., Boettcher A., Hubacek J., Aslanidis C.,
 RA Suttorp N., Schmitz G.;
 RT "Homogeneous assay based on 52 primer sets to scan for mutations of
 RT the ABCA1 gene and its application in genetic analysis of a new
 RT patient with familial high-density lipoprotein deficiency syndrome.";
 RL Biochim. Biophys. Acta 1537:42-48(2001).
 RN [16]
 RP VARIANTS TD ASN-1289 AND TRP-2081, AND VARIANT LYS-219.
 RX MEDLINE=21369433; PubMed=11476965;
 RA Huang W., Moriyama K., Koga T., Hue H., Ageta M., Kawabata S.,
 RA Mawatari K., Yamura T., Eto T., Kawamura M., Teramoto T., Sasaki J.;
 RT "Novel mutations in ABCA1 gene in Japanese patients with Tangier
 RT disease and familial high density lipoprotein deficiency with
 RT coronary heart disease.";
 RL Biochim. Biophys. Acta 1537:71-78(2001).
 RN [17]
 RP VARIANTS LYS-219; ALA-399; MET-771; PRO-774; ASN-776; ILE-825;
 RP MET-883; ASP-1172; LYS-1587 AND CYS-1731.
 RX MEDLINE=21138379; PubMed=11238261;
 RA Clee S.M., Zwiderman A.H., Engert J.C., Zwarts K.Y.,
 RA Molhuizen H.O.F., Roomp K., Jukema J.W., van Wijkand M., van Dam M.,
 RA Hudson T.J., Brooks-Wilson A., Genest J. Jr., Kastelein J.J.P.,
 RA Hayden M.R.;
 RT "Common genetic variation in ABCA1 is associated with altered
 RT lipoprotein levels and a modified risk for coronary artery disease.";
 RL Circulation 103:1198-1205(2001).
 RN [18]
 RP VARIANT TD THR-255, AND VARIANT ATHEROSCLEROSIS ASP-1611.
 RX MEDLINE=21645894; PubMed=11785958;
 RA Nishida Y., Hirano K., Tsukamoto K., Nagano M., Ikegami C., Roomp K.,
 RA Ishihara M., Sakane N., Zhang Z., Tsuji K., Matsuyama A., Ohama T.,
 RA Matsura F., Ishigami M., Sakai N., Hiraoaka H., Hattori H.,
 RA Wellington C., Yoshida Y., Mitsuji S., Hayden M.R., Egashira T.,
 RA Yamashita S., Matsuzawa Y.;
 RT "Expression and functional analyses of novel mutations of ATP-binding
 RT cassette transporter-1 in Japanese patients with high-density
 RT lipoprotein deficiency.";
 RL Biochem. Biophys. Res. Commun. 290:713-721(2002).
 CC -1- FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION
 CC TRANSPORTER. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL
 CC TRANSPORT.
 CC -2- TISSUE SPECIFICITY: WIDELY EXPRESSED, BUT MOST ABUNDANT IN
 CC MACROPHAGES.
 CC -3- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,
 CC EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN
 CC ATP BINDING CASSETTE (ABC) DOMAIN.
 CC -4- DISEASE: DEFECTS IN ABCA1 ARE A CAUSE OF HIGH DENSITY LIPOPROTEIN
 CC DEFICIENCY TYPE I (HDLI), ALSO KNOWN AS TANGIER DISEASE (TD). TD
 CC IS A RECESSIVE DISORDER CHARACTERIZED BY ABSENCE OF HIGH DENSITY
 CC LIPOPROTEIN (HDL) CHOLESTEROL FROM PLASMA, HEPATOSPLENOMEGALY,
 CC PERIPHERAL NEUROPATHY, AND FREQUENTLY PREMATURE CORONARY ARTERY
 CC DISEASE (CAD).
 CC -5- DISEASE: Defects in ABCA1 are a cause of high density lipoprotein

Query Match 99.8%; Score 11770; DB 1; Length 2261;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2255; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MACWQRLRLMLKNTLFRRRQTCOLLLEVAMPFLIFLLISVRLSYPRYEQHECHFPNKA 60
 DB 1 MACWQRLRLMLKNTLFRRRQTCOLLLEVAMPFLIFLLISVRLSYPRYEQHECHFPNKA 60
 QY 61 MSAGLPLPWVQGLICNANPCFRYPFGAPGVGNFNKSIYARLFSDARLLLSQKDT 120
 DB 61 MSAGLPLPWVQGLICNANPCFRYPFGAPGVGNFNKSIYARLFSDARLLLSQKDT 120
 QY 121 SMKDMKRVYRTLOQIKKSSSNLKLODELVDNTEFSGELFHNLSLPKSTYDKMLRADVILH 180
 DB 121 SMKDMKRVYRTLOQIKKSSSNLKLODELVDNTEFSGELFHNLSLPKSTYDKMLRADVILH 180
 QY 181 KVFLOGLHLTSLGNSKSEEMIQDQEVSELCGLPEKELAAERYLRSNMHLKPL 240
 DB 181 KVFLOGLHLTSLGNSKSEEMIQDQEVSELCGLPEKELAAERYLRSNMHLKPL 240
 QY 241 RLINSTRPPSKELAEATYTLHSLGTLAQELFSMRSDMRQEWFLTNVSSSSSTOI 300
 DB 241 RLINSTRPPSKELAEATYTLHSLGTLAQELFSMRSDMRQEWFLTNVSSSSSTOI 300
 QY 301 YQAVSRIVCGHPGGGLTKSLNWEEDNNYKALFGNGTEEDAEFTYDNTSTPYCNDLMLK 360
 DB 301 YQAVSRIVCGHPGGGLTKSLNWEEDNNYKALFGNGTEEDAEFTYDNTSTPYCNDLMLK 360
 QY 361 NLESSPLSRILWKALPRLVGLILYTPDPATROVAEVAEKTFOELAVYHDEGMEELS 420
 DB 361 NLESSPLSRILWKALPRLVGLILYTPDPATROVAEVAEKTFOELAVYHDEGMEELS 420
 QY 421 PKIWTMENSOEMDLVRLMLDSRDNDHFEQOOLGIDMTAODIVAFLAHPEDVOSSNGS 480
 DB 421 PKIWTMENSOEMDLVRLMLDSRDNDHFEQOOLGIDMTAODIVAFLAHPEDVOSSNGS 480
 QY 481 VYTWRAFPNTNOARTISREMECVNLKLEPATEVWMLINKSMELDDRKKMAGIVFVG 540
 DB 481 VYTWRAFPNTNOARTISREMECVNLKLEPATEVWMLINKSMELDDRKKMAGIVFVG 540
 QY 541 ITPGSELPHVHYKIRMDIDNVERTNKIKDGYMDPGPRADPEEDMRKYVWGFAYLQDYY 600
 DB 541 ITPGSELPHVHYKIRMDIDNVERTNKIKDGYMDPGPRADPEEDMRKYVWGFAYLQDYY 600
 QY 601 EQAIIIVLTGETEKKTVYMOQMPYCYVDIIFLRVMSRSMPLFMTLAMIYSAVVIKGIY 660
 DB 601 EQAIIIVLTGETEKKTVYMOQMPYCYVDIIFLRVMSRSMPLFMTLAMIYSAVVIKGIY 660
 QY 661 YEKEARLKEFMRIMGJDNSTIMFSWFISSLIPILVSAGLLVYTKGNLIPYSDPSVAV 720
 DB 661 YEKEARLKEFMRIMGJDNSTIMFSWFISSLIPILVSAGLLVYTKGNLIPYSDPSVAV 720
 QY 721 FLISFVAVVITLQCLISTLFSRANLAAAGGIYFTLYLPYVLCVAMODYVGTLLKTFAS 780
 DB 721 FLISFVAVVITLQCLISTLFSRANLAAAGGIYFTLYLPYVLCVAMODYVGTLLKTFAS 780
 QY 781 LLSVPAFPGCEYFALPEBOGIGVQMDNLRESVEEDGFNLTSISMLPDTFLYGVMTW 840
 DB 781 LLSVPAFPGCEYFALPEBOGIGVQMDNLRESVEEDGFNLTSISMLPDTFLYGVMTW 840
 QY 841 YIAVAPPGGYCIPRPMYFPGCTSYMGESDEKSHPGSNOKRISLCEMEDEPRLHLGVS 900
 DB 841 YIAVAPPGGYCIPRPMYFPGCTSYMGESDEKSHPGSNOKRISLCEMEDEPRLHLGVS 900
 QY 901 IQNLVYVYRDGMKVAVDGALNLFYEGOITSFLGNAGKTTMSITLGTJFPPTSGTAYIL 960
 DB 901 IQNLVYVYRDGMKVAVDGALNLFYEGOITSFLGNAGKTTMSITLGTJFPPTSGTAYIL 960
 QY 961 GKDIRSEMSTIRONLGVCPQHNVLFDMLTYEEHITWYARLKGISEKHVAEEMQALDVG 1020
 DB 961 GKDIRSEMSTIRONLGVCPQHNVLFDMLTYEEHITWYARLKGISEKHVAEEMQALDVG 1020

QY 1021 LPSSKLSKTSQLSGMOQRKLSVALAFVGSKVYILDEPTAGVDPYSRRGIWELLKRYQ 1080
 DB 1021 LPSSKLSKTSQLSGMOQRKLSVALAFVGSKVYILDEPTAGVDPYSRRGIWELLKRYQ 1080
 QY 1081 GRTIILSTHNDHEDADVIGDRITAIISHGKLCVGSGLFKNLQGLGYTLTYKKDVESLS 1140
 DB 1081 GRTIILSTHNDHEDADVIGDRITAIISHGKLCVGSGLFKNLQGLGYTLTYKKDVESLS 1140
 QY 1141 SCRNSSSTVYTLKKEDSVSSSDAGLSGDSHESDTLITDVSAINLIRKHVSEARVEDI 1200
 DB 1141 SCRNSSSTVYTLKKEDSVSSSDAGLSGDSHESDTLITDVSAINLIRKHVSEARVEDI 1200
 QY 1201 GHELTLYVLYPEAKEGAVELEFHEIDRLSDLGISYGISSETTLEELFKVAEESGVDAE 1260
 DB 1201 GHELTLYVLYPEAKEGAVELEFHEIDRLSDLGISYGISSETTLEELFKVAEESGVDAE 1260
 QY 1261 TSDGTLPARRRNRAFGDKQSLRPETDDAADPNDSDIDPESRTDLISGMDGKSYQV 1320
 DB 1261 TSDGTLPARRRNRAFGDKQSLRPETDDAADPNDSDIDPESRTDLISGMDGKSYQV 1320
 QY 1321 GMLTLOQFVALLMKRLLIARRSRKGFPAQVILPAVFYALVSLIVPPGKYPSELO 1380
 DB 1321 GMLTLOQFVALLMKRLLIARRSRKGFPAQVILPAVFYALVSLIVPPGKYPSELO 1380
 QY 1381 PMMYNEQYTFVSNDAPEDTGTLELINALTKDPGFGTRMEGNPIPDTPCQAGEEWTAP 1440
 DB 1381 PMMYNEQYTFVSNDAPEDTGTLELINALTKDPGFGTRMEGNPIPDTPCQAGEEWTAP 1440
 QY 1441 VPQITMDLFQNGNMTQNPSPACOCSSDKIKKMLPVCPCGAGLPPPOKONTADIIQDL 1500
 DB 1441 VPQITMDLFQNGNMTQNPSPACOCSSDKIKKMLPVCPCGAGLPPPOKONTADIIQDL 1500
 QY 1501 TGRNSTDVLTVYQYIITAKSLKNKIWNVEFRYGGSLGVSQTQALPQSOEVDNDAIKOMK 1560
 DB 1501 TGRNSTDVLTVYQYIITAKSLKNKIWNVEFRYGGSLGVSQTQALPQSOEVDNDAIKOMK 1560
 QY 1561 HLKIAKDSADREFLSLGRFMTGLDTRNNVYKWFENKGMHAISSFLYVNNAILRANLOK 1620
 DB 1561 HLKIAKDSADREFLSLGRFMTGLDTRNNVYKWFENKGMHAISSFLYVNNAILRANLOK 1620
 QY 1621 GENPSHYGITAENHPLNLTKOOLSEVALMTTSVDVLSICVIFAMSEVPASVFFLQER 1680
 DB 1621 GENPSHYGITAENHPLNLTKOOLSEVALMTTSVDVLSICVIFAMSEVPASVFFLQER 1680
 QY 1681 VSKAKHLOFISGVKRYIYWLNSFWDMCNVYPATLVIIIFICQOKSYVSTMLPYAL 1740
 DB 1681 VSKAKHLOFISGVKRYIYWLNSFWDMCNVYPATLVIIIFICQOKSYVSTMLPYAL 1740
 QY 1741 LLLLYGMSITPLMYPASVFEKIPSTAYVYVLTYSVNLFIGINGSVATFVLELFTDKLNIN 1800
 DB 1741 LLLLYGMSITPLMYPASVFEKIPSTAYVYVLTYSVNLFIGINGSVATFVLELFTDKLNIN 1800
 QY 1801 DILKSVFLIFPHFLCGRGLIDVKNQAMADALERRGENREYSPLSWDLVGNLFPAMAVEG 1860
 DB 1801 DILKSVFLIFPHFLCGRGLIDVKNQAMADALERRGENREYSPLSWDLVGNLFPAMAVEG 1860
 QY 1861 VYFELLITVLIQYREFIRRPVNAKISPLNDEDEVRERRORRILDOGGONDILLETKELEKI 1920
 DB 1861 VYFELLITVLIQYREFIRRPVNAKISPLNDEDEVRERRORRILDOGGONDILLETKELEKI 1920
 QY 1921 YRRKKRPAYDRICVGIIPGEGCGLLGVNAGKSSFFKMLTODTIVTRDAPLNNKSIISN 1980
 DB 1921 YRRKKRPAYDRICVGIIPGEGCGLLGVNAGKSSFFKMLTODTIVTRDAPLNNKSIISN 1980
 QY 1981 IHEVHONMGYCPQDAILTELLTGREHVEFPALLRGVPEKEVKGVEMAIRKLGLVKYGEK 2040
 DB 1981 IHEVHONMGYCPQDAILTELLTGREHVEFPALLRGVPEKEVKGVEMAIRKLGLVKYGEK 2040
 QY 2041 YAGNTSGGKRLKSTAMALLIGSPVYFLDEPTGMDPARFRFLNNCALSYVKEGSRVLT 2100
 DB 2041 YAGNTSGGKRLKSTAMALLIGSPVYFLDEPTGMDPARFRFLNNCALSYVKEGSRVLT 2100
 QY 2101 SHSMECEALCTRMAIMVNGREFCLGSVOHLKNRFGDGYTIVVRIAGSNPDLKPVODFFG 2160


```

Db 2101 SHSMECEALCTRMALVNGFRFCIGSVOLHKNRFGGTYTVIAGSNPLKFPVQDFG 2160
OY 2161 LAFPGSVLEKEHRNMLQYOLPSSLSLARIPTLSOSKKRIHEDYVSOTLDOVNF 2220
Db 2161 LAFPGSVLEKEHRNMLQYOLPSSLSLARIPTLSOSKKRIHEDYVSOTLDOVNF 2220
OY 2221 AKDQSDDDLKDLSLHKNQTVVDAVLTSLQDEKESYV 2261
Db 2221 AKDQSDDDLKDLSLHKNQTVVDAVLTSLQDEKESYV 2261

RESULT 2
ABCL_MOUSE STANDARD; PRT; 2261 AA.
ID ABCL_MOUSE
AC P41233;
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette transporter 1) (ATP-binding cassette 1) (ABC-1).
GN ABCA1 OR ABC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DRA/2; TISSUE=Macrophage;
RX MEDLINE=94375008; PubMed=8088782;
RA Luciani M.F., Denizot F., Savary S., Mattei M.-G., Chimini G.;
RT "Cloning of two novel ABC transporters mapping on human chromosome 9.";
RL Genomics 21:150-159(1994).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Qiu Y., Gavelier L., Chiu S., Rubin E., Cheng J.-F.;
RT "Human and mouse ABCA1 comparative sequencing and transgenesis studies identify potential regulatory sequences.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CAMP-DEPENDENT AND SITOXYLUREA-SENSITIVE ANION TRANSPORTER. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL TRANSPORT (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT TISSUES. HIGHEST LEVELS ARE FOUND IN PREGNANT UTERUS AND UTERUS.
CC -1- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES, EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN ATP BINDING CASSETTE (ABC) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCA SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC EMBL: X75926; CAA53530.1; ALT_INIT.
DR EMBL: AF287263; AAC39073.1; ALT_INIT.
DR MGD: MGI:99607; Abca1.
DR InterPro: IPR003593; AAA.
DR InterPro: IPR003439; ABC_transport.
DR InterPro: IPR001687; ATP_GTP_A.
DR InterPro: IPR003838; DUF214.
DR InterPro: IPR000897; SRP54.
DR Pfam: PF00005; ABC_tran; 2.
DR Pfam: PF02687; DUF214; 1.
DR Pfam: PF00448; SRP54; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Glycoprotein; Transmembrane; Transport.

```

```

FT TRANSMEM 26 42 POTENTIAL.
FT TRANSMEM 640 656 POTENTIAL.
FT TRANSMEM 690 706 POTENTIAL.
FT TRANSMEM 717 733 POTENTIAL.
FT TRANSMEM 749 765 POTENTIAL.
FT TRANSMEM 771 787 POTENTIAL.
FT TRANSMEM 1041 1057 POTENTIAL.
FT TRANSMEM 1351 1367 POTENTIAL.
FT TRANSMEM 1661 1677 POTENTIAL.
FT TRANSMEM 1708 1724 POTENTIAL.
FT TRANSMEM 1737 1753 POTENTIAL.
FT TRANSMEM 1775 1791 POTENTIAL.
FT TRANSMEM 1854 1870 POTENTIAL.
FT NP_BIND 933 940 ATP (POTENTIAL).
FT NP_BIND 1946 1953 ATP (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 349 349 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 478 478 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 489 489 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 521 521 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 820 820 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1144 1144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1294 1294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1453 1453 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1499 1499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1504 1504 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1637 1637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2044 2044 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2238 2238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 1567 1568 MISSING (IN REF. 2).
FT CONFLICT 2024 2024 MISSING (IN REF. 2).
SQ SEQUENCE 2261 AA; 254011 MW; FA62B21FD1D09F9 CRC64;

Query Match 95.4%; Score 11256; DB 1; Length 2261;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 2149; Conservative 55; Mismatches 57; Indels 0; Gaps 0;

```


- RA Nathans J., Leppert M., Dean M., Lupski J.R.;
 RT "A photoreceptor cell-specific ATP-binding transporter gene (ABCR) is
 RT mutated in recessive Stargardt macular dystrophy.";
 RL *Nat. Genet.* 15:236-246(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97345663; PubMed=9202155;
 RA Azarian S.M., Travis G.H.;
 RT "The photoreceptor rim protein is an ABC transporter encoded by the
 RT gene for recessive Stargardt's disease (ABCR).";
 RL *FEBS Lett.* 409:247-252(1997).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANTS STGD TRP-18 AND CYS-212.
 RX MEDLINE=98163759; PubMed=9503029;
 RA Geber S., Rozet J.-M., van de Pol T.J.R., Hoyng C.B., Munnich A.,
 RA Blankenagel A., Kaplan J., Cremers F.P.M.;
 RT "Complete exon-intron structure of the retina-specific ATP binding
 RT transporter gene (ABCR) allows the identification of novel mutations
 RT underlying Stargardt disease.";
 RL *Genomics* 48:139-142(1998).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS STGD.
 RX MEDLINE=98141123; PubMed=9490294;
 RA Nasonkin I., Illing M., Koehler M.R., Schmid M., Molday R.S.,
 RA Weber B.H.F.;
 RT "Mapping of the rod photoreceptor ABC transporter (ABCR) to 1p21-p22.1
 RT and identification of novel mutations in Stargardt's disease.";
 RL *Hum. Genet.* 102:21-26(1998).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE=99175213; PubMed=10075733;
 RA Sun H., Molday R.S., Nathans J.;
 RT "Retinal stimulates ATP hydrolysis by purified and reconstituted ABCR,
 RT the photoreceptor-specific ATP-binding cassette transporter
 RT responsible for Stargardt disease.";
 RL *J. Biol. Chem.* 274:8265-8281(1999).
 RN [6]
 RP DISEASE.
 RX MEDLINE=98133912; PubMed=9466990;
 RA Cremers F.P.M., van de Pol D.J.R., van Driel M.A., den Hollander A.I.,
 RA van Haren F.J.J., Knoers N.V.A.M., Tijmes N., Bergen A.A.B.,
 RA Rohrschneider K., Blankenagel A., Plinckers A.J.L.G., Deutman A.F.,
 RA Hoyng C.B.;
 RT "Autosomal recessive retinitis pigmentosa and cone-rod dystrophy
 RT caused by splice site mutations in the Stargardt's disease gene
 RT ABCR.";
 RL *Hum. Mol. Genet.* 7:355-362(1998).
 RN [7]
 RP VARIANTS ARMD2, AND VARIANTS
 RX MEDLINE=97442530; PubMed=9295268;
 RA Allikmets R., Shroyer N.F., Singh N., Seddon J.M., Lewis R.A.,
 RA Bernstein P.S., Peiffer A., Zabriskie N.A., Li Y., Hutchinson A.,
 RA Dean M., Lupski J.R., Leppert M.;
 RT "Mutation of the Stargardt disease gene (ABCR) in age-related macular
 RT degeneration.";
 RL *Science* 277:1805-1807(1997).
 RN [8]
 RP VARIANTS STGD W-18; C-212; H-636; M-1019; V-1038; C-1108; W-1640;
 RP S-1977 AND H-2107, AND VARIANTS FFM P-11; P-541; V-1038; E-1091;
 RP C-1508; P-1970 AND R-1971.
 RX MEDLINE=98454319; PubMed=9781034;
 RA Rozet J.-M., Geber S., Souied E., Perrault I., Chatelain S., Ghazi I.,
 RA Leowski C., Dullier J.-L., Munnich A., Kaplan J.;
 RT "Spectrum of ABCR gene mutations in autosomal recessive macular
 RT dystrophies.";
 RL *Eur. J. Hum. Genet.* 6:291-295(1998).
 RN [9]
 RP VARIANTS STGD.
 RX MEDLINE=99138655; PubMed=9972280;
 RA Lewis R.A., Shroyer N.F., Singh N., Allikmets R., Hutchinson A.,
 RA Li Y., Lupski J.R., Leppert M., Dean M.;
 RT "Genotype/phenotype analysis of a photoreceptor-specific ATP-binding
 RT cassette transporter gene, ABCR, in Stargardt disease.";
 RN [10]
 RP VARIANTS STGD, AND VARIANTS.
 RX MEDLINE=99192348; PubMed=10090887;
 RA Maugeri A., van Driel M.A., van de Pol D.J.R., Klevering B.J.,
 RA van Haren F.J.J., Tijmes N., Bergen A.A.B., Rohrschneider K.,
 RA Blankenagel A., Plinckers A.J.L.G., Dahl N., Brunner H.G.,
 RA Deutman A.F., Hoyng C.B., Cremers F.P.M.;
 RT "The 2586G->C mutation in the ABCR gene is a mild frequent founder
 RT mutation in the western European population and allows the
 RT classification of ABCR mutations in patients with Stargardt disease.";
 RL *Am. J. Hum. Genet.* 64:1024-1035(1999).
 RN [11]
 RP VARIANT STGD TYR-54, AND VARIANT ALA-863.
 RX MEDLINE=20077755; PubMed=10612508;
 RA Zhang K., Geribaldi D.C., Kniazeva M., Albini T., Chiang M.F.,
 RA Kerrigan M., Sunness J.S., Han M., Allikmets R.;
 RT "A novel mutation in the ABCR gene in four patients with autosomal
 RT recessive Stargardt disease.";
 RL *Am. J. Ophthalmol.* 128:720-724(1999).
 RN [12]
 RP VARIANTS STGD V-60; R-206; N-300; P-541; A-849; P-974; V-1038; C-1108;
 RP L-1408; R-1488; D-1652; P-1729; E-1961; W-2038; W-2077; H-2107; R-2128
 RP AND Y-2150.
 RX MEDLINE=99221420; PubMed=10206579;
 RA Fishman G.A., Stone E.M., Grover S., Derlacki D.J., Haines H.L.,
 RA Hocky R.R.;
 RT "Variation of clinical expression in patients with Stargardt dystrophy
 RT and sequence variations in the ABCR gene.";
 RL *Arch. Ophthalmol.* 117:504-510(1999).
 RN [13]
 RP VARIANTS GLU-1961 AND ASN-2177.
 RX MEDLINE=20349288; PubMed=10880298;
 RA Allikmets R., Tamur J., Hutchinson A., Lewis R.A., Shroyer N.F.,
 RA Dalakisvili K., Lupski J.R., Steiner K., Paulkroff D., Holz F.G.,
 RA Weber B.H.F., Dean M., Atkinson A., Gail M.H., Bernstein P.S.,
 RA Singh N., Peiffer A., Zabriskie N.A., Leppert M., Seddon J.M.,
 RA Zhang K., Sunness J.S., Udar N.S., Velchits S., Silva-Garcia R.,
 RA Small K.W., Simonelli F., Testa F., D'Urso M., Brancato R.,
 RA Rinaldi E., Ingavst S., Taube A., Wadellius C., Souied E., Ducrocq D.,
 RA Kaplan J., Assink J.M., ten Brink J.B., de Jong P.T.V.M.,
 RA Bergen A.A.B., Maugeri A., van Driel M.A., Hoyng C.B., Cremers F.P.M.,
 RA Paloma E., Coco R., Balcells S., Gonzalez-Duarte R., Kernani S.,
 RA Stanga P., Bhattacharya S.S., Bird A.C.;
 RT "Further evidence for an association of ABCR alleles with age-related
 RT macular degeneration.";
 RL *Am. J. Hum. Genet.* 67:487-491(2000).
 RN [14]
 RP VARIANTS STGD E-60; T-60; E-65; L-68; R-72; C-212; S-230; S-247;
 RP V-328; K-471; P-541; O-572; R-607; K-635; C-653; Y-764; R-765; A-901;
 RP I-959; K-1036; V-1038; P-1063; D-1087; C-1097; C-1108; L-1380; K-1399;
 RP P-1430; V-1440; H-1443; L-1486; Y-1488; M-1537; P-1689; L-1705;
 RP T-1733; R-1748; P-1763; K-1885; H-1898; E-1961; S-1975; S-1977; G-2077
 RP W-2077 AND V-2241, AND VARIANTS O-152; H-212; R-423; I-552; R-914;
 RP O-943; T-1562; T-1868; M-1921; L-1948; F-1970; A-2059; N-2177 AND
 RP V-2216.
 RX MEDLINE=20442027; PubMed=10958763;
 RA Rivera A., White K., Stoehr H., Steiner K., Hemmrich N., Grimm T.,
 RA Jurkies B., Lorenz B., Scholl H.P.N., Apfelstedt-Sylla E.,
 RA Weber B.H.F.;
 RT "A comprehensive survey of sequence variation in the ABCA4 (ABCR) gene
 RT in Stargardt disease and age-related macular degeneration.";
 RL *Am. J. Hum. Genet.* 67:800-813(2000).
 RN [15]
 RP VARIANTS CORD3 GLU-65; CYS-212; PRO-541; ALA-863; GLY-863 DEL;
 RP VAL-1038; LYS-1122; TYR-1480 AND ASP-1598.
 RX MEDLINE=20442040; PubMed=10958761;
 RA Maugeri A., Klevering B.J., Rohrschneider K., Blankenagel A.,
 RA Brunner H.G., Deutman A.F., Hoyng C.B., Cremers F.P.M.;
 RT "Mutations in the ABCA4 (ABCR) gene are the major cause of autosomal
 RT recessive cone-rod dystrophy.";
 RL *Am. J. Hum. Genet.* 67:960-966(2000).
 RN [16]

RP VARIANTS STGD ASP-340; GLN-572; ALA-863; SER-965; VAL-1038; ALA-1780
RP AND HIS-1898, AND VARIANT GLN-943.
RX MEDLINE-20208356; PubMed-10746567;
RA Shroyer N.F., Lewis R.A., Lipski J.R.;
RT "Complex inheritance of ABCR mutations in Stargardt disease: linkage
RT disequilibrium, complex alleles, and pseudodominance.";
RL Hum. Genet. 106:244-248(2000).
RN [17]
RP VARIANTS STGD.
RX MEDLINE-20098082; PubMed-10634594;
RA Papaioannou M., Oaka L., Bessant D., Lois N., Bird A.C., Payne A.,
RA Bhattacharya S.S.;
RT "An analysis of ABCR mutations in British patients with recessive
RT retinal dystrophies.";
RL Invest. Ophthalmol. Vis. Sci. 41:16-19(2000).
RN [18]
RP VARIANTS STGD C-212; D-767; I-897; V-1038; K-1087; K-1399; Q-1640 AND
RP E-1961, AND VARIANT HIS-212.
RX MEDLINE-20174852; PubMed-10711710;
RA Simonelli F., Testa F., de Crecchio G., Rinaldi E., Hutchinson A.,
RA Atkinson A., Dean M., D'Urso M., Allikmets R.;
RT "New ABCR mutations and clinical phenotype in Italian patients with
RT Stargardt disease.";
RL Invest. Ophthalmol. Vis. Sci. 41:892-897(2000).
RN [19]
RP CHARACTERIZATION OF VARIANTS, AND MUTAGENESIS OF GLY-966; LYS-969;
RP GLY-1975 AND LYS-1978.
RX MEDLINE-20472331; PubMed-11017087;
RA Sun H., Smallwood P.M., Nathans J.;
RT "Biochemical defects in ABCR protein variants associated with human
RT retinopathies.";
RL Nat. Genet. 26:242-246(2000).
RN [20]
RP VARIANT STGD ASN-972, AND VARIANTS GLN-943; ILE-1868 AND LEU-1948.
RX MEDLINE-21478761; PubMed-11594993;
RA Eksandh L., Ekstrom U., Abrahamson M., Bauer B., Andreasson S.;
Query Match 49.8%; Score 5870.5; DB 1; Length 2273;
Best Local Similarity 50.0%; Pred. NO. 0;
Matches 1165; Conservative 356; Mismatches 635; Indels 171; Gaps 27;
QY 6 QLRLLMKNTLFFRRQTCQLLEVAWPLFLLISVRLSYRPEYECHEFPNKAAPSAG 65
DB 6 QIQLLLKNTLRRKQIRFVELWPLSLFVLWLRNPNPLSHHECFPNKAMSAG 65
QY 66 TLPRVQGLICNANPCFRPTPGEPVGVGNFKSIVARLFSDARLLLYSQDTSKMD 125
DB 66 MLPMLQGFICVNNPFCOSPTPGESPISVYNSIILARYRDFOELMMAPEQHIGRI 125
QY 126 RKVLRITLQOI-----KSSSNLKLQDFLVNDFEFGFLYHNLSLPRKSTV----DKM 172
DB 126 WTEHLISQFMPTLRTHPERLAGRGIRIROLKDEFTLLEFLKNIGLSVYLLINSQ 185
QY 173 LRADVILAKVFLQGYQLHLTSL-CNGSKSEEMQLQDQEVSE-----LCGLPKEKLAAE 226
DB 186 VRPQPAHGV---PDLAKDIACSEALERFLIFSQGRGAKTVRAVACLSQGTQMWIE 241
QY 227 RVLFSNMDILKPIILKTINLSTSPFSPSKELAEATKTLHSLGLTLAGOELFSMSW---SDM- 281
DB 242 DTLVANDVFEK-----LFRVLPFLIDS---RSQGINLSRWGILSDMS 281
QY 282 -----ROEVMFLTNV-----NSSSSSTOIVQAVSRVIGHCPREGGGLIKLSLWYE 326
DB 282 PRIQEFHRSMDLLWTRPLMONGPEFTTKLMGILSDLCGLYPRGGSGRVLSFMYE 341
QY 327 DNNKALFGNGTEDEAETFYDNSTPYCNDLMKNLESSPLSRITMAKLPVLGKLIYT 386
DB 342 DNNKALFGIDSTKRDPYIDRTTSPCNALIOSLESNPLTKITAMAAKPLDMGKLIYT 401
QY 387 PDTPATROVAEVNKTFOELAVFHDLGAMFELSPTKIWTWENSQEMDLVRLMIDSDND 446
DB 402 PDSPAARILKANSTFEELHVRKLVKAMEVGPQIWTYFEDNSTQNMIMIDLGNPTVK 461

QY 447 HFWEQDGLDLMWTAQDIYAFLLAKHPEDVOSSNGSVYTRREANETNOAIRTIREMECVN 506
DB 462 DFLNROLGEGITAEAILNFIKGPRESQADMANFMDWDFINITDRRLVLMOLECLV 521
QY 507 LKLELEIATEVWLLINKSMELDERKFMAGIYFTGTGSELPHVKKIRKIMIDINVRT 566
DB 522 LKFESEYNDETQIRALSLLEENFMWAGVFPDMYPMYSSLPVKKIKRINDIDVEKT 581
QY 567 NKIKDGYWDPGRADPEFEDRYWCGFAYLQDVBOAILRVLTGTEKTKGYVMQMPYC 626
DB 582 NKIKDYWDGSRADPEDEFERYWCGFAYLQDVBOGIRTSVQAEAVPVLQDMPYC 641
QY 627 YVDDITLRWMSMPLFMTLMTIYSAVITIKIYVEKARKETMRINGLONSLWESMF 686
DB 642 FYDSEFMILNCFLEWLAIVYSMTVKSIYEKELRKLETKNOGVSNAVITWTF 701
QY 687 ISLILVLSAGLVVITLGNLIPYSDSVFVLESAVAVTILQCELISTFSRANLA 746
DB 702 LDFSISMSIFLLTFFIWHGRILNHSDFLFLFLAFSTATIMLCFLSTFFSKASLA 761
QY 747 AACGIIYTYLLPYLVCAWODYVGTILKIPASLSPYAFGCGEYFALFEQSIGYQW 806
DB 762 AACSGVITYTYLLPHILCFAMQDMTAEKRAVSLSPVAFGTEGYLVREEOGLQW 821
QY 807 DNLFESEVEDGFNLTSTSMMLPDTFLGVMTYIEAVFPGOYGPMPWYPTKSYWF 866
DB 822 SNTGNSPTGDEFSFLSNQMLLDAVYGLAWILOYFPDDYGTPLPWYFLDESTWL 881
QY 867 G-----EESDEKSHPGSNQKRSEICMEEPETHLKGISQNLVKV 907
DB 882 GCGCSTREBRALKEPTELEEDPEHP-----EGIHDSFFREHGWPGVCYKLVKI 937
QY 908 YRQGMVAVDGLANTYEQOITSFLHNGAGKTTMSITLGTLPPTSGATYILGDINSE 967
DB 938 FEBCGPRAVDRINTEFENQITAFGLHNGAGKTTLSITGLLPSTGVILGAGDIETS 997
QY 968 MSTIRONLGVQPOHNVLFMLTVEEHIMFYARKLSEKRYVAEKEMOMALDGLSSKLK 1027
DB 998 LNAVRSLSGMCPOHNLFLHLLTYAEHMLFYAQDKGSEADLEHMALEDIGL-HHKRN 1056
QY 1028 SKTSOLSGMQRKLVALAFVGSKYVILDEPTAGVPSRRGIMELLIKYRQRTIILS 1087
DB 1057 EEAQDLSGQMRKLSVAIAFVGDAKVILDEPTSGVPSRRSIRMDLLKYSRGTIIMS 1116
QY 1088 THHMDADVGLGRILAIISHGKLCVSSSLFLKNQGTGYLLTLVKDVESSLSQRNSS 1147
DB 1117 THHMDADLIGDRIALIAOGRLYCSGTPLELKNCFGTGLYTLVLR-MKNIOSQRKSGE 1175
QY 1148 TVSYLKKEDSVQSSSDAGSGHESDGLTIDVSAISNLRKHVSEARLVEDIGHETLV 1207
DB 1176 TCSCSSKGRS---TTPRAVYDOLTPBOYLDGVNELMDVYLHVPRAKVEICGELLIFL 1232
QY 1208 LPEAKKEGAFVELFHEIDRLSDIGISSYGISSETTLEBIFLKVABESGVDAETSDGTL 1267
DB 1233 LPMKNKRRHAYASLFRLEETLADLGLISFGISDTPLEIEFLKVEDSDSGCLFAGG--- 1289
QY 1268 ARNRRAFGDKOSCLRPFEDDAADPNSDI-----DEPSRETLISGM 1311
DB 1290 AQQKRENVNRIHCLDP-REKAGQTPQDSNVCSPGAPAAHPEGQPPPEECGPOINTGT 1348
QY 1312 DGKGSYQVAGMKLTOOQFVALLMKRLLIARRSKKGFPAOIVLPAVFCATLVSLVPPF 1371
DB 1349 -----QVLQHVQALLVKRRQHILRSIKDELADIVLPATPVFLALMLSTIYPPF 1397
QY 1372 GKYPSELOPMWMTNEQYTVSVNDAPEDGTLELLNALTKDPQGTGCMGNPIPDTPCOA 1431
DB 1398 GEYPALTHBWMYQOQYTFEFSMDPEQSFYLDADVLKMPFGNRCLEGMILPEVPC-G 1456
QY 1432 GEEETTAAPVQIIMLFQNGMTMKNPSPACQSSDKKKMLPVCPPRAGGLPPRQKQ 1491
DB 1457 NSTPMKTPSPVSPNITQLFKQKQMTQVNPSPSCRSKRETLKTLPECPREGAGGLPPRQKQ 1516
QY 1492 NTADILLQDLGRNISIDYLVKTYVQIILAKSLKKNIWNERRGGSFSGVNTQALPPSQEV 1551

FT TRANSMEM 706 728 POTENTIAL.
 FT TRANSMEM 749 771 POTENTIAL.
 FT TRANSMEM 766 808 POTENTIAL.
 FT TRANSMEM 813 835 POTENTIAL.
 FT TRANSMEM 850 872 POTENTIAL.
 FT TRANSMEM 892 914 POTENTIAL.
 FT TRANSMEM 1793 1815 POTENTIAL.
 FT TRANSMEM 1846 1865 POTENTIAL.
 FT TRANSMEM 1875 1897 POTENTIAL.
 FT TRANSMEM 1904 1926 POTENTIAL.
 FT TRANSMEM 1988 2010 POTENTIAL.
 FT NP_BIND 1025 1032 APP (POTENTIAL).
 FT NP_BIND 2088 2095 APP (POTENTIAL).
 FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 369 369 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 477 477 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 485 485 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 531 531 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 545 545 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1409 1409 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1497 1497 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1550 1550 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1558 1558 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1613 1613 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1678 1678 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1776 1776 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2055 2055 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 2436 AA; 269971 MW; 9E6688D615DE06D CRC64;

Query Match 35.9%; Score 4230.5; DB 1; Length 2436;
 Best Local Similarity 39.8%; Pred. No. 2.4e-259;
 Matches 998; Conservative 347; Mismatches 730; Indels 435; Gaps 61;

QY 6 QRLILMLKNTFRKRCOTQLLLEVAMPFLFLLISVRLSPYEQHECHFPKA-MPSA 64
 DB 6 QLOLLMLKNTLKRSPFWLAFELIFPLVLFLLGLRKPRTISYKEVFFYTAAPL TSA 65
 QY 65 GTLPWVGICNANNPCFRYPTEGEAGVGNFNKSTIVARLFS DARRLL---LYSQKDT 120
 DB 66 GILPVMOSLCPDQORDEFGFL-----QYANSTVYOLLERLDRLRYVEEGLFPDARP 115
 QY 121 SMKDMKRVLTLOIKKSSNKLKLODFVNDNETFSG-----FLYHNLSTP 165
 DB 116 SLSELEALR--QHLEALISGPGTSGHLDSTVSSPDSVARNPQELMRFLTQNLSTP 173
 QY 166 KSTYDKMLRADY---ILKRVPLQGYOHLTS--LCNGS-----KSEBMT--- 204
 DB 174 NSTQALLAARVDPPEVYHLLFGPSSALDSQGLHKQEPWRSRUGNPLRMEELLAPA 233
 QY 205 ---Q---GDOEYSELGCLPKKEKLAEE-----RVLRSMMDI 235
 DB 234 LLEOLJCTPGSGELGRILTYPESOKGALQGYRDVAVCSGQAARARREFSGLSAELRNDLV 293
 QY 236 LKPLRTINSTSPSPKELAE--TKTLHSLGLTQDELSSMRSWSDMRQEVMLTNVNS 293
 DB 294 AK-VSQQLGIDAPRGSSSPQAAPPRLQALLGDLD-----AKKVLQDQDVLS 341
 QY 294 SSSSTQIYQAVSRIVCGHPRGGLIKITSLMWYEDNNKALFGNGTEDEDAFTYDNTTP 353
 DB 342 ALALLLPQACTGRTGPPRPAAGAGGAN-----GTGAGAVMGPMATAEBCAPSAALATP 396

QY 354 YCNILMKNLSSPLSLIMKALKPLLVG----- 381
 DB 397 ---DLQOCGSAFY--LMAGLQPLCGNNRTIEREALRGNMSSLGFTSGEQNLGLV 451
 QY 382 -----KILYPTDPATROYMAEVNKTFOELAVPHDEGMEELSPKIMTFMENSEMD 434
 DB 452 HLMSTNPKILVAPAGEVDVRLKANETFAFGVNTHYAQVWLISAEIRSFLOGRLQ 511
 QY 435 LVRLMLDSRDNHFMEOQLDGLDWTADIVAFIAKHPEDVOSSNGSVYTMTEAENETN-- 492
 DB 512 HLRLV-----QOYVAELRLHPE---ALNLSDELPRALRQDFFS 547
 QY 493 -----QALRTIS-----REMECVNLKLELATEWLINKSMKME--LLDERKFWAG 535
 DB 548 LPSGALLQQLDITDMAACGRTQFMKSKYVDLFKQFPBESIVNTLQAOQDQVNTYFAS 607
 QY 536 IYFTGTPGSEILPHNVKIKIMDIDNVERTNIKIDGYWDPGRADPRADPRADPRADPRAD 595
 DB 608 VIFQTRKDG--LRPHVHYKIKRONSSFTKTEINELRAVWRGPNNG--GRFYLYGFVW 662
 QY 596 LODVVEQAIIRVLTGTE--KKGCVYVQOMPRQYVDIFLRYMSRMLPMTLANTYSAV 654
 DB 663 IODMMERATIDTFVGHVDVPESTYOMFPYPCYTRDDLFVIEHMMPLCMVTSVYAM 722
 QY 655 IIKGIVYEKEARKLKTMRIMGIDNSILMFSEISSILPLVYAGLIVLTKLGNLPRYS 714
 DB 723 TIQHIYAEHRLKEMVTMTGMLNANVHWAMPTIGVQLSISVYALTAIILKYGVLMHSH 782
 QY 715 PSVVEFVSVAENVTLLOCELSTLFSRANLAAACGGIITFLYLYVLC-----VAMQD 769
 DB 783 VVILMFLAVYAVATIMCFELSVLSYKAKLASACGGIIFYSVPMYVAIIRREVADK 842
 QY 770 YVGFILTKFASLISVAFGCEYFALPEDEGIGVOMNLPSPVEEFGNLTISML 829
 DB 843 ITAFK-KCLASLMTSTTAGLSKRYALTEVAGVGIQMTTFQSPSPYEGDPNILLAVTLM 901
 QY 830 FDTFLYGVMTYVTEAVFPQYVIGPRPWPYFCTKSYWGE--ESDEKSHPSGNOKMS-- 884
 DB 902 VDAVYGLITWITVIAVHPQMYGLPRPWPYFQDKSVWLSGRTAEWEMPMARFRLSLV 961
 QY 885 ---ETC-----MEEPRLKLGVSIONLVKYYRQGMKAUVDGLINFTEGQIT 929
 DB 962 EBDQACAMSRPFEETRGMEERTHPLVYVCYDKLTKYKDKDKLALMLKLSINTENOV 1021
 QY 930 SFLGNHAGKTTMTSLNGLPPTSGTAYILGKDIRSESTIRONLGVCPQHNVLFDLT 989
 DB 1022 SFLGNHAGKTTMTSLNGLPPTSGTAYILGKDIRSESTIRONLGVCPQHNVLFDLT 1081
 QY 990 VEEHIMFYARLKGLEKHNKAEEMQALDVLPSKSLKSKTSQLSGQMKLSVALAFV 1049
 DB 1082 VEEHIMFYARLKGLEKHNKAEEMQALDVLPSKSLKSKTSQLSGQMKLSVALAFV 1140
 QY 1050 GSKRVVILDEPTAGVDPYSRGIWELLKTRGRTIILSTHMDVADYLDGRALISBKL 1109
 DB 1141 GSRALILDEPTAGVDPYARRAIDMLIKKPGRTIILSTHMDVADYLDGRALISBKL 1200
 QY 1110 CCYGSLELAKNQLGCTGYTLTKKDYESSLSCRRSSSVYSLKKEDSVSSSSDAGGS 1169
 DB 1201 KCCGSPFLKGYGGDYRTLLVKRPAEPG-----GPOEPGLAS 1238
 QY 1170 DHESDFLTLIDVS--ATSNLRKHVSPEARLVEDIGHETLYVLPYEAKEGAFELRHEID 1227
 DB 1239 SPGRAPLSSCGSELOYSOTIRKHVASCILVSDTSELSTILPSEAKKAGAFRLQOHLR 1298
 QY 1228 RSLDGLISSYGETTLEIFLVAEE-----SGVDA-ETSDGFLP----- 1267
 DB 1299 SDALHLSFGLMDTTLTEVFLKVESEDLSENSADYKESRKDVLPQAEQASGEHAG 1358
 QY 1268 -----ARRNRA--RGDQOSCLRPTEEDDADPNDSIDIPESR 1303
 DB 1359 NLARCELTQOSASLQASASSVSGARBEGATYDGYRPLP--DNPQDP--NVSIDEV 1415
 QY 1304 ETDLLSGMDKGSYGVKWKLTQOQFVALLMRRLIARRSRKGFPAQIVLPAVFICIALV 1363


```

DB 1750 AILRLNPKSKGNPAAYGLTVNHNPNKTSASLS-IDYLLQGTDDVIAIFIIYAMSFVA 1808
QY 1671 SFVPELLOEVSNAKHLQFISGVKPIYVMISNVMMCNVVPATLVIIIFIOQOKSVY 1730
DB 1809 SFVPELLOEVSNAKHLQFISGVKPIYVMISNVMMCNVVPATLVIIIFIOQOKSVY 1868
QY 1731 SSTNPLVALLLLLYSGITPLMPYASFVKIPSTAYVYVLTYSNLEIGINGSVATFVLEL 1790
DB 1869 SPINFPAYLSLFLYGSTIPYIPYASFEVSSAYVFLIVINLEIGITATVATFVLEL 1928
QY 1791 FT-DNKLNINILKSVLELFPFCRGILDMVKQAMADALERGE-NRFPSPISMDL 1848
DB 1929 FEHDKLVNASTYKSCFLFPNINLGHLMEMAYNEYIAKIGQKMSKSPMDI 1988
QY 1849 VGRNLFMAVEGVVFLITVLIQREFIRPVPYNAKLSPLNDEDEDVRRERQRLDGGQ 1908
DB 1989 VTRGLVAMTEGVFGLITIMCQNFRLQPLPVSTKPYED-DVDVASERQVRLGDAD 2047
QY 1909 NDLEIKELTKITRRK---KKPAVDRCVGIPEGECHGLGVNAGAKSSFFKMLTGDITY 1965
DB 2048 NDWKIKINLTKYVKSRIKIGILAVDRCLGVRGECEGGLGVNAGAKSTFFKMLTGDIST 2107
QY 1966 TRGAPFLNKSIIISNIEHVQNMGCYQCPDITELLTGREHVEFFALRGVEKGVK 2025
DB 2108 TGGFAFNGHSVYLKDLQVOOSIGYCFQFALDELTAHRLQYRLRKIPKDEAQY 2167
QY 2026 EMALIRKILGVKYGKYGAGNTSGGKRRKLTAMALLIGSPVYVLEDEPTGMDPKARRPLWN 2085
DB 2168 KWALEKLEIKRYADKPAGTYSGGKRRKLTALIALIGYPAIFIDEPTGMDPKARRPLWN 2227
QY 2086 CALSVVEGVSYLTSMSMECEALCTRNAIMVNGRPRCIGSOHLKNRGDDYTIYVRL 2145
DB 2228 LILDLITGSSVYLTSSMECEALCTRLIMVNGRLCIGSIOLHKNRGDDYTIYVRL 2286
QY 2146 AGSNPDLKPYODEFGLAPGSPVLEKHKRNMLQYOLPSSLSLARIPSSLSQSKRLHIED 2205
DB 2287 TKSQONKADVRFENRNPPEAMLEKRRHRTKVQYOLKSEHISLAQVFEKMGVGVGIGIED 2346
QY 2206 YVSQOTLDOYFVFAKQSD 2227
DB 2347 YVSQOTLDOYFVFAKQSDN 2368

```

```

RESULT 6
ABC3_HUMAN STANDARD; PRT; 1704 AA.
ID ABC3_HUMAN Q92473;
AC Q92473;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE ATP-binding cassette, sub-family A, member 3 (ATP-binding cassette transporter 3) (ATP-binding cassette 3) (ABC-C transporter).
GN ABC3 OR ABC3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thyroid carcinoma;
RX MEDLINE=9632608; PubMed=8706931;
RA Klugbauer N., Hofmann F.;
RT "Primary structure of a novel ABC transporter with a chromosomal localization on the band encoding the multidrug resistance-associated protein.";
RT FEBS Lett. 391:61-65(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97179225; PubMed=9027511;
RA Connors T.D., van Raay T.J., Petry L.R., Klinger K.W., Landes G.M., Burn T.C.;
RT "The cloning of a human ABC gene (ABC3) mapping to chromosome

```

```

RT 16p13.3.
RL Genomics 39:231-234(1997).
CC -1- FUNCTION: MAY BE A TRANSPORTER, ITS NATURAL SUBSTRATE HAS NOT BEEN
CC FOUND YET (BY SIMILARITY). MAY ACT AS AN EFFLUX PUMP FOR
CC CHEMOTHERAPEUTICS DRUGS.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, FOLLOWED BY BRAIN,
CC PANCREAS, SKELETAL MUSCLE AND HEART. WEAKLY EXPRESSED IN PLACENTA,
CC KIDNEY AND LIVER. ALSO EXPRESSED IN MEDULLARY THYROID CARCINOMA
CC CELLS (MTC) AND IN C-CELL CARCINOMA.
CC -1- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,
CC EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN
CC ATP BINDING CASSETTE (ABC) DOMAIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCA SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL: U78735; AAC50967.1; -.
CC EMBL: X97187; CAA65825.1; -.
CC MIM: 601615; -.
CC
CC InterPro: IPR003593; AAA.
CC InterPro: IPR003439; ABC_transportr.
CC InterPro: IPR001687; ATP_GTP_A.
CC Pfam: PF00005; ABC_tran. 2.
CC SMART: SM00382; AAA; 1.
CC PROSITE: PS00211; ABC_TRANSPORTER; 1.
CC KW ATP-binding; Transport; Transmembrane.
CC
CC FT TRANSMEM 22 42 POTENTIAL.
CC FT TRANSMEM 249 269 POTENTIAL.
CC FT TRANSMEM 307 327 POTENTIAL.
CC FT TRANSMEM 344 364 POTENTIAL.
CC FT TRANSMEM 373 393 POTENTIAL.
CC FT TRANSMEM 405 425 POTENTIAL.
CC FT TRANSMEM 447 467 POTENTIAL.
CC FT TRANSMEM 925 945 POTENTIAL.
CC FT TRANSMEM 1100 1120 POTENTIAL.
CC FT TRANSMEM 1144 1164 POTENTIAL.
CC FT TRANSMEM 1183 1203 POTENTIAL.
CC FT TRANSMEM 1213 1233 POTENTIAL.
CC FT TRANSMEM 1245 1265 POTENTIAL.
CC FT TRANSMEM 1306 1326 POTENTIAL.
CC FT NP_BIND 566 573 ATP (POTENTIAL).
CC FT NP_BIND 1416 1423 P -> S (IN REF. 2).
CC FT NP_BIND 36 36 L -> P (IN REF. 2).
CC FT CONFLICT 196 196
CC FT CONFLICT 1704 AA; 191387 MW; AF0098DAF7A04F5F CRC64;
SQ SEQUENCE

```

```

Query Match 22.4%; Score 2642.5; DB 1; Length 1704;
Best Local Similarity 35.7%; Pred. No. 6.3e-159;
Matches 639; Conservative 300; Mismatches 523; Indels 327; Gaps 48;

```

```

QY 534 AGIVFTGIRPGSLD-LPHVKKYKIRMDIDNVERTN-----KIKDGYW----- 574
DB 131 AAVFEPHPNHSKEPLPLAVKYLHFR-----SYTRKNYMTQIGSPFLKEGHTTSLRPL 187
QY 575 --DPGRADPFED--MRYVWGFAVLDVYBOAIIIVLTGTE-----KKGIVMQMPY 624
DB 188 FPNPGRRELTPDGGPGYIRGFLAVQAVDAIMEYHADATROLQRLVITTKRPY 247
QY 625 PCYVDIETFRWRSRSLPPLMTLAMIYSVAVITIKGIYEEKALKTMTIMGDSIIMFS 684
DB 248 PPFIADPFLVAIOYOYLPLLLLSFTYTLTARAVAOEKRLKYMRRMGSLSLWHWSA 307
QY 685 WFTSSILPLVSGAGLVVLKLG-----NLDPSPSVVFLSVFAVVTILOCFLISTL 739
DB 308 WFLIFPLFLIIAASFMTLLFCYKVRPNVAVLSRSDPSLVLAFLCFAISTISFSRMSTF 367

```

QY 740 FSRANLAACGGIYFTLLPYVLCVAMODYGFTLKIPASLLSPVAFGCEYAFEE 799
 DB 368 FSKANAAAFGGFLYFTYIYFVAPRYNMWTLISOKLCSLLSVNAAAGQILGKEBA 427
 QY 800 OGIGVOMDMLFESPVE-EDGFMILTSISMEDTEFLYGMVYIBAVEPGOYGIKPRPWY 858
 DB 428 KMGIGOMRDL-SPVAVDDDFCGOVLGMLLDSVLYGLVYMEAVPFGOGVQPMWF 486
 QY 859 PCKTSYFGE-----ESDEKSHPGSNOKRMEICMEEPYHLKIGVSLQNLVKKYRDM 912
 DB 487 FTMSYWCCKPRAVAVGKEEDSDP---EKALRNEYFEAPEDLVAGIKIKHSKVFYRGN 543
 QY 913 K--VAADGALNPFSGOITSLFNGHAGKTTMTSLTGFPPTSGATYLGDISSEMT 970
 DB 544 KDBAAARDNLNLYBSOITVLLGHNGAGKTTLSMLTGLPPTSGATYLSGTEISODMVO 603
 QY 971 IRONLGVCPQHNVLFDMLVVEEHIWEYARLKLSEKHVAEMEQMALDVGSSKLKSKT 1030
 DB 604 IRRSLGICQHDILPDNLVVAEHLVYQAOLKLSRQCKCEYKQMLHIGL-EDKWNRS 662
 QY 1031 SOLSGMOKKSLVALAFVGSKVYIIDEPTAGVDSRRCIGVIBLLKTKRGCTTILSTH 1090
 DB 663 RFLSGMRRLSIGIALINGSKVLIIDEPTSGMDAISRAIWDLQROKSDRTIYVLTTHF 722
 QY 1091 MDEADVLGRIALISHGKLCVSSSLFKNOLGTGYLLVKKDVSSLSGCRNSSTVS 1150
 DB 723 MDADLGRIRALMAKGLQCCSSLEFKOKYAGTHMLVE-----P 766
 QY 1151 YLKEDSVSQQSSDAGLSDHSDTLIDVSAISMLIRKHSBARLVEDIGHETVYLPY 1210
 DB 767 HCNPED-----ISQLVHHVNPATLSSAGALSFILPR 800
 QY 1211 EAKGCAFEVLEHREIDRLSDGISYISSETTLEIFLKVAB--ESGVDAETSDGTLPA 1268
 DB 801 ESTHR--FEGLEPAKLEKKEGELGASIFGASITTEVEFLVRLKLVDSMDIAIO--LPA 856
 QY 1269 ---RRRRRAFG--DKOSCLRPTEEDADPNPND---SDIDPESRETDLSGMDGKGSYQV 1319
 DB 857 LOYQHRRSADNAVSNLC-----GAMPDSGICALIEERTAVKMLTGL----- 901
 QY 1320 KGMKLTQOQFVALLMKRLLIARRSRKGFPAQIYLPVAFVCIALVLSLIVPFGKYPSELE 1379
 DB 902 ---ALHCQGFMAFLKKAAYSREMKVAAQVYLPVLTCTALL----- 942
 QY 1380 QPMYVQOTTFVSNDAPEDTGTELLNALTDPGEGTRCMEGNIPIDTQOAGEHEWTTA 1439
 DB 943 -----ALNYSSELEFDPML--RLTLG-----EYGR 966
 QY 1440 PVPQITMDLFQNGNMTQNPSPACQSSDKIKMLPVCPPGAGGLPPQKONTADILQD 1499
 DB 967 VVFSVPGISQLOQLSEHLKALQABG-----QEPREVLOD 1003
 QY 1500 LTRGNISDYLKTYVOIILAKSLKNKIWNEFRY---GFSLSGVSTQALPPSQEVNDAL 1555
 DB 1004 L-----EEFLI-----FRASVEGGGFN----- 1020
 QY 1556 KMKKHLKAKLAKOSSADRLNLSGRFMTGIDTRNNVAVVNNNGKMAHISSEFLVYNNALIR 1615
 DB 1021 -----ECL--VAASFRDGERVVALNLRNNOYHSPALALVNDMLLKR 1063
 QY 1616 ANLQKGENSHYGITAFNHP-----LNLTKOQLSEVALMTSDVAVSICVIFAMSFVA 1670
 DB 1064 ---LLCG---PHASIVVSNFPQPSALQAAKADQENE---GKGPDIALLN--LEFAMFLAS 1113
 QY 1671 SEVVFLOEVRSAKHLQFISGVKPYIYMLSNVDMCMTVPATVLIIFICFOOKSYV 1730
 DB 1114 TFSILAVSEKAVQAKHVOFSGVHVASFWLSALLMDLISFLPSLLLVFKAFVDRAPT 1173
 QY 1731 SSTNLPLVALTLLLGSTPLPYPASVFKISTAYVYVNLGTINGSVATFVLEL 1790
 DB 1174 RDGHMADTLLLLLYGMAITPLMTLMANFFLGAATATYTRLTITNLSGT---ATLWMT 1229
 QY 1791 ---FTDKLNNINDILKSVFLIPHFCLGRLIDWKN-----QAMADALERFG- 1836

DB 1230 IMRIPAVKLEELSKTLDHVLVLPNHLGMAVSSFEYENYERRYCTSSVAAHCKYNI 1289
 QY 1837 ---ENRFVSLSMWL--VGRNLFMAAVEGVFFELITVLIQTRFTRPPNAKL----- 1885
 DB 1290 QYOENFY---AWSAPGGRFVASMAASGCAYLLLEFLLEITNLLQRLGICALRRRTL 1345
 QY 1886 -----SPLNEDDDVRERRORILLDGGGQNDI---LEIKELTKYRRKRRP--AVDRICV 1934
 DB 1346 TELYTRMVLPEDDVDADERIRILLAPSPDSILHPLIKELSKYV--BORPPLAVDRSL 1404
 QY 1935 GIPGECFGLGVAGVAGKSTFKMLTGDTYTRGDAFLNKNSILSNIHEYHOMNGYCPQF 1994
 DB 1405 AVQKGECEGLGFGAGAGTTFKMLTGESLTSQDADFVGHRRISDVQKVRQIRGCPQF 1464
 QY 1995 DATTELLTGRHVEPFRALLRGVPERKEVKGEMAIRKLGLVYKEKAGNYSGNKRLS 2054
 DB 1465 DALLDHMTGRMLVYARLGRIPERHIGACVENTLRGLLEPHANKLVRYSGNKRRLS 1524
 QY 2055 TAMALIGRPVPLDEPTGMDPKARPRFLMNCALSVYKEGRSVLTSMSCEALCTRM 2114
 DB 1525 TGIATIGRPVAVFLDEPSTGMDPVARRLMDTVARARESGAIIITSHSMECEALCTRL 1584
 QY 2115 AIMVGRFRCLSYVQHLNKRFGDGTIVRI--AGSNPDLKPYODPFGLAAPGSVLEKH 2172
 DB 1585 AIMVGGCFKCLGSPQHLKSKRGSGVSLAKYQSGQGEALEEFAFADLPFGSVLEDEH 1644
 QY 2173 RNMLOYLPSSLSLARIPLSLSQSKRLIEDYVSQTTIDQYFVNA 2221
 DB 1645 QGMVYHILPGRDLISWAKVGLERAKERYGVDDYSVQISLEOVFLSPA 1693

RESULT 7
 YLH4 CAEEL STANDARD; PRT; 1691 AA.
 AC P34358; P34359;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Putative ABC transporter C48B4.4 in chromosome III.
 GN C48B4.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditiodea;
 OC Rhabditiidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL NZ;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
 Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
 Latreille P., Lighting J., Lloyd C., Mortimore B., O'Callaghan M.,
 Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shomkeen R.,
 Sims M., Smaildon N., Smith A., Smith M., Southam E., Staden R.,
 Sultson J., Thierry-Mieg J., Thomas K., Vaughan K.,
 Waterston J., Watson A., Weinstock L., Wilkinson-Sproat J.,
 Woldman P.;
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RT Nature 368:32-38(1994).
 RN [2]
 RP REVISIONS.
 RA Dudin R.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS: C48B4.4A AND C48B4.4B
 CC (SHOWN HERE); MAY BE PRODUCED BY ALTERNATIVE SPLICING.
 CC -I- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; 229117; CA82384.2; -
 DR EMBL; 229117; CA82383.2; -
 DR PIR; S40724; S40724.
 DR PIR; S40725; S40725.
 DR Wormpep; C48B4.4A; CE24856.
 DR Wormpep; C48B4.4B; CE24857.
 DR Interpro; IPR003593; AAA.
 DR Interpro; IPR003439; ABC_transport.
 DR Pfam; PF00005; ABC_tran; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 2.
 DR Hypothetical protein; ATP-binding; Transport; Alternative splicing.
 NP_BIND 567 574 ATP (POTENTIAL).
 NP_BIND 1398 1405 ATP (POTENTIAL).
 FT VARSPIC 979 980 MISSING (IN ISOFORM C48B4.4A).
 FT SEQUENCE 1691 AA; 189770 MW; AA89734EC8F669E6 CRC64;

Query Match 13.0%; Score 1537; DB 1; Length 1691;
 Best Local Similarity 24.9%; Pred. No. 7, 8e-69;
 Matches 482; Conservative 345; Mismatches 679; Indels 428; Gaps 58;

QY 458 WTADIV-----AFLAHPEDEVSSNGSV-----TWREAFENETN-----492
 DB 24 WTELELLPCLLGLPLVLYVKNADHTSPENIDNFQVGTVEDVPLESFIKPIYKRW 83
 QY 493 -----QAIRTI-----SRMECVNLNKL-----EPATEWMLINKS 523
 DB 84 CLRSDDVVGITSKDAAKRIVYDLMKKFAERFOSAKLKSVKNSSEQLTL--VLRND 140
 QY 524 MELIDE-----RKFWAGIVFTGTPGSIELPHVYKIRMDIDVERTNKIKDGYWDPG 578
 DB 141 LPMLEPFCAINSYAAGVFEVDVYTNKL-----NYRILGKPEEYWHLETSYNYPG 196
 QY 579 RADPEEDM-----RYWGGFAYLDVQVQAIIRVLGTGEEKTGYVMQMPYCYVD-----629
 DB 197 SSGYRSRIPSSPPYWTSAFLTFQHAIESPSSVOSGAPDPLITLRGLPBPRTYSSVA 256
 QY 630 --DIEFLRMHSMPLMTLAMIYSVAIIIGIYKEARELKEPMRINGLDNIIMPSMFI 667
 DB 257 FIDF-----PFMAFVTFIVHITRELAENHA--VKPYLTAGLSTFMYAAHV 307
 QY 688 SSLIPLLVAGLIVLILKGLNLPYSDSVFVFLSVFAVVTLLQCLISTFLSRANLAA 747
 DB 308 MAFLKPFVI--FLCSIIFLFVMEFVSPALIVLVMLGAVIFGAFVASFNNNTSAI 365
 QY 748 ACGGIIIFTLXPLVLCVAVQADYVGLTKIFASL--LSPV-----AFGCGCEFFAL 796
 DB 366 K-----ALLVAGAMIGISYKLRPELDQISSCFELGLNINGAFALAVASID 412
 QY 797 FEEGIGVQMDNLF--ESPVEDGENTLTSSIMLFTFELGVMTWYIEAV--FPGGYGIPR 854
 DB 413 YMRERELNLTNNNDSSLH---FSLGVALVMMIVDILMMSIGALVYDHTRTADSLSRT 469
 QY 855 PWYFPCIKSWFGESSEKSHPG--SNOKRMEICMEEPETH-----895
 DB 470 LFDE-----APEDENDQTDVTAQNTIRINQMPNMASTSLNPNMADSDSLEGSTEA 522
 QY 896 -----KLGVSIONLVKVVARDKQVAVDGLALNFEGQITSPFLGNGNAGKTTMGLNG 948
 DB 523 DGAADTRADIIYVKNLKVSTIGERAVDGLSLRAVAGQCSILLGHGAKSTFFSSIAG 582
 QY 949 LFPPTSGTAVILKDKINSEMTIRONLGVCPQHNVLFDMTLVEEHIMFAARLKGLEKHY 1008
 DB 583 IIRTNGRITITGVDYQENEPGETRHHIGMCPQYNPLIDQLTVEHKLIVYGLKGAENKE 642
 QY 1009 KAEKEMALDVGLPSSKIKSKTSQLSGGMORKLSVALAFVGGSKVVILDEPTAGVDPSR 1068

DB 643 KQMKRLSDVKL--DEKENEKAVNISGMRKRLCYCMALIGSEVYLLDEPTAGDPCAR 701
 QY 1069 RGIWEILLKRGQRTITLTSTHMEADVDLGRDAITASHGLCCVSGSLPLKNOGTGYLL 1128
 DB 702 QDVQKLVKRNKARTILTLTHYWEAEIRGDMWYFLMSHOKLVAAGNOLKOKPFTGYLL 761
 QY 1129 TLVKKVESLSSCRNSSSTVYLKEDSVSSSDAGLSGHESDTLTIDVSAISNLTIR 1188
 DB 762 TVV-----LDHNGDKRKMAV--ILTDVCT 783
 QY 1189 KHYSEARIVEDIGHETLVVLYPEAKGAFVLEPHID-----DR 1228
 DB 784 HYKKEERGMHQOILEITLPEARKKE--FVPLFQALEIQRNRYNSVFNMPMTLSQ 841
 QY 1229 LSDGISYSYGISETTELEILFLVKAESGYDAETSDGTLPARRNRARFGQSCLRPTED 1288
 DB 842 LATLEMRSPGLSLNTELEQFITIGK-----VXKALSRQNSRSHNSRNASPSILKP 894
 QY 1289 DAADPRDSDIDPESRETDLISGMDKGSYQVQGWKLTQQOFALLMKRLIARSRKGF 1348
 DB 895 AGYDTQSTKSDSYOK--LMDSOARGP--EKSQVAKMAVAFISIRKKFLYSRRMAQDLF 951
 QY 1349 AOLVPAVFCIALVPSLIVPEFGKYPSELQPMWYNEQYTFVSDADPDGTLELMAAL 1408
 DB 952 TOYLIP--IILGLVGSIL-----TLKSNNTDQ-----977
 QY 1409 TKDPGFGTCMEGNIPIPTPCQAGEEWTTAPVQPTINDLPONGWMTQNPSPACOCSSD 1468
 DB 978 -----FSVRSLS-----TP--SGIE-----PSKVYRPFENG--1001
 QY 1469 KIKKMLPVCPPAGGLPPQQRKQNTADTIQDITGRNISYLVKTYVQIIAASLAKKIWN 1528
 DB 1002 -----IPEANFEKILRKSGGEVLYNNTKNDLPNTLSL-----IG 1039
 QY 1529 EFRYGGFSLGVSNTQALPSPQSEVNDAIKOMKHLKLAQSSADRFNSIGRMTGLDTRN 1588
 DB 1040 E-----MPRA-----ITIGMTMNS--D 1053
 QY 1589 NKVWFNNKGMAHAISSFLNVLNAILRANLQGENPSHYGITAFAHPLNLTAKOOLEVAL 1648
 DB 1054 NEALFENMRYHYHLPTLISMIRARLTGVDAISSGVFLSKYSNSNLPLSQL-----1108
 QY 1649 MTSVDVLISGVIFAMSVPPASFVFLIOEVRSAKHLQFISGVKPYIYMLSNVWMC 1708
 DB 1109 ----IDVLAPMLILFAVNTSTFWFLIEKTCQFAHQDFLTGSPITFEYSASLITYGI 1164
 QY 1709 NYVPATVLIIFICFOOKSYVSTNLPVLAALLLGLMSITPLMPYPAFFKIPSTAYV 1768
 DB 1165 LVSILCLIFLPMFLAF-----HMYDHLAIVLFWFLYFFSSVPFIYAVSPLFQSPSKANY 1220
 QY 1769 VLTSNVLFINGSVATFVLELTQNKLNINDILKSFL-----IPHFCLRGGLDMV 1823
 DB 1221 LLIWQVYISGAALLAVELIFW-----IFNIDEMKSLIVNIFMFLPVSFAFGSAII--1272
 QY 1824 KQAMADALERGENRFPSP-----LSMDLVGRNLPAMAVEGFVFLTVLVLOYRFR--1877
 DB 1273 -----TINTYG--MLPSEELMNMDCGNAMLMGTBFVCSFALVLLQFQFVRRFL 1322
 QY 1878 -----PREVNKSLPLNDE--DEVARERORILLDGGQNDILEIKELTKYRRKKRPA 1928
 DB 1323 SOVMTVRRSSHNNOVPMAGDLPRVCSEYSEERBRVHRVNSQSAIYIKDLFTF--GRETA 1380
 QY 1929 VDRICVGPFGRCFGLLVNAGAKSSTFKMLTGGDTTYRGDAFLNKSILSNHIEVQNM 1968
 DB 1381 VNEICLAVQKRCFGLLVNAGAKTTPNTNITLQGSFASGAMIGGRVYELI-----SI 1435
 QY 1989 GYCPQFADATTELLTGREHVEFFALLRGVPEKEVGVGEMARLKGIVYGEKYGANTSGG 2048
 DB 1436 GYCPFDALMDLTRELELEIAQMHGRENKA--KALLIECYGMATAHADKLVYRFSSG 1493
 QY 2049 NKRKLSTMALIGPVPVLEDEPTTGMDPKARRLMLNALSIVKEGNS--VVLTSMSNEC 2107
 DB 1435 -----SI 1435

```

Db 1494 OKRKISVGVALLAPTOMITLDEPTAGIDPKAREVWELLMLCRHSNSALMLTSHSMEC 1553
Qy 2108 EALCIRMAIIVNGRRRCISGVOLHKNRGDGTIVYRIRAGSNPDLPKPYODFFGLAPGSSV 2167
Db 1554 EALCSRIAVLNGSLIAGISOELKSLYGNNTMTLSLEPEQNRDMVVO-LVOTRLPMSV 1612
Qy 2168 LKEKHNNM---LOYOLPSSL--ARFISLSQSKKRRLHIEDYSVSOTTLDOVFVNF-- 2221
Db 1613 LTTTSTNKLNLKWDLPKEDCSAKFEMVQALAKDLGVKDFPILAQSSLLETFRLAGL 1672
Qy 2222 -KDQSDDDLKDLIS 2234
Db 1673 DEDQDLTFHSTVEIS 1686

RESULT 8
DRRA_STRPE STANDARD; PRT: 330 AA.
AC P32010:
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Daunorubicin resistance ATP-binding protein drra.
GN DRRA.
OS Streptomyces peucetius.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1950;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 29050;
RX MEDLINE=92020891; PubMed=1924314;
RA Guilfoile P.G., Hutchinson C.R.;
RT "A bacterial analog of the mdr gene of mammalian tumor cells is
RT present in Streptomyces peucetius, the producer of daunorubicin and
RT doxorubicin."
RL Proc. Natl. Acad. Sci. U.S.A. 88:8553-8557(1991).
CC -1- FUNCTION: DRRA AND DRB MAY ACT JOINTLY TO CONFER DAUNORUBICIN AND
CC DOXORUBICIN RESISTANCE BY AN EXPORT MECHANISM.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).

```

```

Qy 1008 VKAEMEQMALDVGLPSK---LKSQTSLQSGMORKISVALAFVGSKVYILDEPTAGVD 1064
Db 116 ARERAEALIDEGFGLDADRILKT---YSGGMRRRLDIASIVYTPDLLFLDEPTGLD 171
Qy 1065 PYSRGRIWELL-LKRYOGRTIILSTHMDADVIGDRITAIISHGKLCVSSFLKNQLG 1123
Db 172 PRSRNQWMDIYRALVDAGTYLTLTYLTDADQADNIAIVIDGRVIAEGTTEGLKSSLG 231
Qy 1124 TGYVLTLLVKDVESLSLSCRRSSSTVSYLKKEDSVQS-----SDPAGLSCHESDTLT 1177
Db 232 -----SNVLRRLRHLDQSRAREERLISAEIGVTIHRDSDPTA 268
Qy 1178 ID-----VSAISNLIRKHVSEARLVEDIGHLELTYVLPYEAKRGAVELFHEIDR 1228
Db 269 LSARIDDPQGMRLAEISRTH----- 290
Qy 1229 LSDGISGYSSETTLEIFLKVAEESGVDATSD 1263
Db 291 ---LEVRSFISGSSIDEVFLALGHPADDRSTEE 322

RESULT 9
MOD1_RHISN STANDARD; PRT: 343 AA.
ID MOD1_RHISN
AC P55476:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Modulation ATP-binding protein I.
GN MOD1 OR Y4HF.
OS Rhizobium sp. (strain NGR234).
OC plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes."
RL Nature 387:394-401(1997).
CC -1- FUNCTION: FORMS, WITH NODJ, A MEMBRANE TRANSPORT COMPLEX INVOLVED
CC IN THE NODULATION PROCESS. IT PROBABLY EXPORT A MODIFIED BETA-1,4-
CC LINKED N-ACETYLGLUCOSAMINE OLIGOSACCHARIDE.
CC -1- SUBCELLULAR LOCATION: Membrane-associated.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).

```


QY 2137 DGYTIVRIAGS 2148
 Db 1266 IYFSMVSVOAGT 1277

RESULT 15

NCBI_RHIME STANDARD: PRT; 355 AA.

AC 052618;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Modulation ATP-binding protein I.
 GN NODI OR RA0472 OR SWA0864.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OG Plasmid pSymba (megaplasmid 1).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396509; PubMed=11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
 RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
 RA Kallman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire
 RT Sinorhizobium meliloti pSymba megaplasmid."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 RN [2]
 RP SEQUENCE OF 143-355 FROM N.A.
 RC STRAIN=1021;
 RA Barnett M.J., Long S.R.;
 RT "Nucleotide sequence of nodJ' region of Rhizobium meliloti pSymba."
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: FORMS, WITH NODD, A MEMBRANE TRANSPORT COMPLEX INVOLVED
 CC IN THE NODULATION PROCESS. IT PROBABLY EXPORT A MODIFIED BETA-1,4-
 CC LINKED N-ACETYLGLUCOSAMINE OLIGOSACCHARIDE.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated.
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

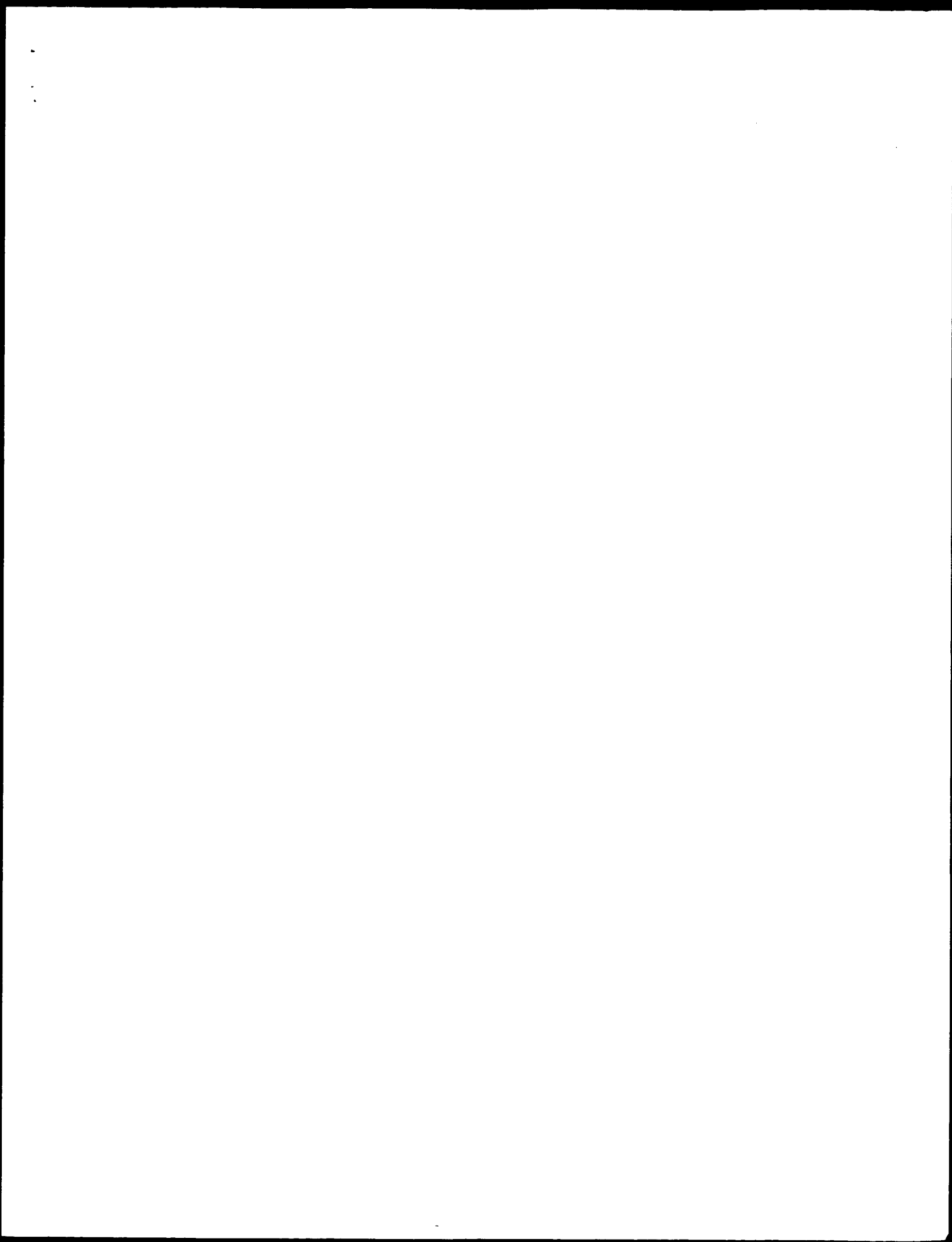
CC -----
 DR EMBL: AE007237; AAK65130.1; -
 DR EMBL: AF043118; AAB97762.1; -
 DR InterPro: IPR003593; AAA.
 DR InterPro: IPR003439; ABC_transportr.
 DR InterPro: IPR001687; ATP_GTP_A.
 DR Pfam: PF00005; ABC_tran.1.
 DR PROSITE: PS00211; ABC_TRANSPORTER.1.
 KM Modulation: Membrane; ATP-binding; Transport; Plasmid;
 KW Complete proteome.
 FT NP_BIND 89 96 ATP (POTENTIAL).
 SQ SEQUENCE 355 AA; 39268 MM; 4DC8696D98C335DC CRC64;

Query Match 2.8%; Score 331.5; DB:1; Length 355;
 Best Local Similarity 33.9%; Pred. No. 1.5e-13;
 Matches 74; Conservative 52; Mismatches 85; Indels 7; Gaps 4;

QY 891 EPTHLKLGSIQNLVKKVYDGMKVAVDGLALNFYEGQITSFGLHNGACKTTTMSILITGLF 950
 Db 52 KPT---VALDVASVTKSYD--KPYINGLSTFVAAGCEGFLGPNAGACKSTITRRIILGMT 106

QY 951 PPTSGTAYIIIGKDIRSEMSTIRONLGYCPQHNVLFPMLVYEEHIMFYARLKGLSEKHVKA 1010
 Db 107 TPGTGEITVIGVPYPSRARLARIRIGVPOQDMIDEFTYRENLVFGFRFRSTREIEA 166
 QY 1011 EMEQMALDVGLPSSKLSKTSQSLGMRKLSVALAFVGGSKVVIIDEPTAGVDPSRRG 1070
 Db 167 VIPSL-LEFARLENKADARVSDLSGGMKRLTLARALINDPOLLIIDEPTGLDPRARL 225
 QY 1071 IWEILLK-VYQGRITILSTHMDADVDLGRVIAIISHG 1107
 Db 226 IWERLRSILARGKTIILTHIMEAEERLCDCVLEAG 263

Search completed: September 15, 2002, 13:02:25
 Job time: 394 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2002, 12:58:01 ; Search time 71.36 Seconds

(without alignments)
5481.243 Million cell updates/sec

Title: US-09-595-526B-2

Perfect score: 11797

Sequence: 1 MACWPQLRLMLKNTLFRRR.....VDVAULTSFLDEKYEKSTV 2261

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:.*
2: SP bacteria:.*
3: SP fungi:.*
4: SP human:.*
5: SP_invertebrate:.*
6: SP_mammal:.*
7: SP_mhc:.*
8: SP_organelle:.*
9: SP_phage:.*
10: SP_plant:.*
11: SP_rodent:.*
12: SP_virus:.*
13: SP_vertebrate:.*
14: SP_unclassified:.*
15: SP_virus:.*
16: SP_bacteriap:.*
17: SP_archaeap:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11786	99.9	2261	4	Q96S56
2	11774	99.8	2261	4	Q96T85
3	5888	49.9	2310	11	Q03600
4	5864.5	49.7	2281	6	002698
5	5775.5	49.0	2146	4	Q9BZC4
6	5763.5	48.9	2146	4	Q9NR73
7	5732	48.6	2159	11	Q91V24
8	5376	45.6	2008	4	Q96S58
9	4249.5	36.0	2434	11	Q9ESR9
10	4240.5	35.9	2436	4	Q9HC28
11	3345.5	28.4	1529	4	Q9HPU0
12	3229.5	27.4	2277	4	Q96UT3
13	2485.5	21.1	1713	5	Q9VRG4
14	2060	17.5	1802	5	Q9FXV8
15	2041.5	17.3	1660	5	Q9VUJ9
16	2012.5	17.1	867	4	Q96HC2

17	2012	17.1	1843	5	Q9GOS2	Q9GOS2	leishmania
18	1984	16.8	1816	10	Q9SDB1	Q9SDB1	arabidopsis
19	1863.5	15.8	1447	5	Q01790	Q01790	caenorhabd
20	1794.5	15.2	1750	5	Q9BKL1	Q9BKL1	lypposoma
21	1538.5	13.0	1704	5	Q76287	Q76287	caenorhabd
22	1534.5	13.0	1463	5	Q9VVK6	Q9VVK6	caenorhabd
23	1534.5	13.0	1981	5	Q9VVK7	Q9VVK7	caenorhabd
24	1342	11.4	1581	4	Q94911	Q94911	caenorhabd
25	1271.5	10.8	1544	5	Q9NKF0	Q9NKF0	caenorhabd
26	1257	10.7	1363	4	Q9H7T8	Q9H7T8	caenorhabd
27	1219.5	10.3	1382	5	Q9V912	Q9V912	caenorhabd
28	1158.5	9.8	1564	5	Q9XW49	Q9XW49	caenorhabd
29	1152	9.8	1500	5	Q9VRE4	Q9VRE4	caenorhabd
30	1028	8.7	1602	6	Q95JZ4	Q95JZ4	caenorhabd
31	1013.5	8.6	1431	5	Q9NSL2	Q9NSL2	caenorhabd
32	1010.5	8.6	1431	5	Q9XUD4	Q9XUD4	caenorhabd
33	929.5	7.9	581	6	Q95JL1	Q95JL1	caenorhabd
34	846	7.2	269	4	Q9NTR0	Q9NTR0	caenorhabd
35	826	7.0	953	10	Q9FKF2	Q9FKF2	caenorhabd
36	819.5	6.9	856	4	Q96MD8	Q96MD8	caenorhabd
37	805	6.8	950	10	Q9FLT5	Q9FLT5	caenorhabd
38	800	6.8	1197	5	Q9VRG3	Q9VRG3	caenorhabd
39	788.5	6.7	1011	10	Q9STU0	Q9STU0	caenorhabd
40	748	6.3	1384	12	Q9EMR9	Q9EMR9	caenorhabd
41	693	5.9	900	10	Q9STT5	Q9STT5	caenorhabd
42	691.5	5.9	917	10	Q9FLT8	Q9FLT8	caenorhabd
43	679	5.8	865	4	Q96MS4	Q96MS4	caenorhabd
44	671	5.7	737	4	Q96PZ9	Q96PZ9	caenorhabd
45	670.5	5.7	592	5	Q96OV4	Q96OV4	caenorhabd

ALIGNMENTS

RESULT 1
Q96S56 PRELIMINARY; PRT; 2261 AA.
ID Q96S56
AC Q96S56:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ABCAL.
DE ABCAL.
DE ABCAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanaka A.R., Abe-Dohmae S., Arakawa R., Sadanami K., Kidera A.,
RA Kioka N., Amachi T., Yokoyama S., Ueda K.:
RT "A new topological model of functional human ABCAL-signal peptide
cleavage and glycosylation of a large extracellular domain.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB055982; BAB63210.1; -;
DR EMBL: 2261 AA; 254300 MW; 21A2CF8F3F518D6D C6C64;

Query Match	99.9%	Score 11786;	DB 4;	Length 2261;
Best Local Similarity	99.8%	Pred. No. 0;		
Matches 2257;	Conservative 4;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MACWPQLRLMLKNTLFRRRQTCLLEVAMPFLFILISVRSYPRYQHECHFPNKA	60	
DB	1	MACWPQLRLMLKNTLFRRRQTCLLEVAMPFLFILISVRSYPRYQHECHFPNKA	60	
QY	61	MPASGTLFWOGIICNANNPCFRYPTEGAPGVGNFNKSIVARLFSDARLLYSQKDT	120	
DB	61	MPASGTLFWOGIICNANNPCFRYPTEGAPGVGNFNKSIVARLFSDARLLYSQKDT	120	
QY	121	SMKDMRKVRLTLOQIKRSSNMLKLDLVDNETFSGFLYHNLSPKSTVDKMLRADVILH	180	
DB	121	SMKDMRKVRLTLOQIKRSSNMLKLDLVDNETFSGFLYHNLSPKSTVDKMLRADVILH	180	

```
QY 181 KVLQGYQLHLTSLCNGSKSEEMTOLGDOEYSELGCLPKREKLAAREVLRSMNDILKPL 240
Db 181 KVLQGYQLHLTSLCNGSKSEEMTOLGDOEYSELGCLPKREKLAAREVLRSMNDILKPL 240
QY 241 RTLNSTSPFSKELAEKTLHLSLGLTAELEFSMSMSMROEVMFLTNVSSSSSTQI 300
Db 241 RTLNSTSPFSKELAEKTLHLSLGLTAELEFSMSMSMROEVMFLTNVSSSSSTQI 300
QY 301 YQAVSRIVCGHPREGGKATKSLMWYEDNNYKALFGCGNGTDEDAETEPFNDSTTYPCNDLWK 360
Db 301 YQAVSRIVCGHPREGGKATKSLMWYEDNNYKALFGCGNGTDEDAETEPFNDSTTYPCNDLWK 360
QY 361 NLESSPLRIIWKALPDLVGLKLLYTPDPTRQVMAEVNKTFOELAVFHOLEGMMEEELS 420
Db 361 NLESSPLRIIWKALPDLVGLKLLYTPDPTRQVMAEVNKTFOELAVFHOLEGMMEEELS 420
QY 421 PKITWEMENGOEMDLVYMLLDSRDNHFWEOQLDWTADODIVAFIAKHPEDVOSSNGS 480
Db 421 PKITWEMENGOEMDLVYMLLDSRDNHFWEOQLDWTADODIVAFIAKHPEDVOSSNGS 480
QY 481 VYTWREAFNETNOAIRTISRMECVNLKLEPIATEVWMLINKSMELDERKFWAGIVFTG 540
Db 481 VYTWREAFNETNOAIRTISRMECVNLKLEPIATEVWMLINKSMELDERKFWAGIVFTG 540
QY 541 ITTGSIELPHHVYKTRMDIDNERTNKIKDGYWDPGRADPRDEDMRYWGGAYIQDYV 600
Db 541 ITTGSIELPHHVYKTRMDIDNERTNKIKDGYWDPGRADPRDEDMRYWGGAYIQDYV 600
QY 601 EOAIIIRVLTGTERKGTGYMOOMPYPGYVDIFLRVMSRSMPLFMTLAMIYSVAVIIGKIV 660
Db 601 EOAIIIRVLTGTERKGTGYMOOMPYPGYVDIFLRVMSRSMPLFMTLAMIYSVAVIIGKIV 660
QY 661 YEKEARLKEPMRIMGDNLILMFWSITSLIPLVASAGLLVILKIGNLIPYSDPSVVEY 720
Db 661 YEKEARLKEPMRIMGDNLILMFWSITSLIPLVASAGLLVILKIGNLIPYSDPSVVEY 720
QY 721 FLVSFAVVTLLQCFILSTLSSRANLAAAGGIYFTLYLPYVLCVAMODYVGTGLTKFPS 780
Db 721 FLVSFAVVTLLQCFILSTLSSRANLAAAGGIYFTLYLPYVLCVAMODYVGTGLTKFPS 780
QY 781 LLSVPAFGCEYFALFEEOGIGVOMDNLFESEVEDGENLTLSISMLFEDTFLYCVMTW 840
Db 781 LLSVPAFGCEYFALFEEOGIGVOMDNLFESEVEDGENLTLSISMLFEDTFLYCVMTW 840
QY 841 YIAVAFPGGYGIRPMYFPCTKSYWFGESDEKSHPSGSMOKRISLTCMEEBEPHKLGV 900
Db 841 YIAVAFPGGYGIRPMYFPCTKSYWFGESDEKSHPSGSMOKRISLTCMEEBEPHKLGV 900
QY 901 IONLVKVRDGMKVAVDGALANFEYEGOITSFLGNAGAKTTTMSILTGLFPPTSGTAYIL 960
Db 901 IONLVKVRDGMKVAVDGALANFEYEGOITSFLGNAGAKTTTMSILTGLFPPTSGTAYIL 960
QY 961 GKDIRSEMSTIRONLGVCPQHNLFDMLTVEEHIWYARLKGISEKHVAEMEOMALDVG 1020
Db 961 GKDIRSEMSTIRONLGVCPQHNLFDMLTVEEHIWYARLKGISEKHVAEMEOMALDVG 1020
QY 1021 LPSKSLKSKTSLGSMOKRSLVALAFVGSKVYILDEPTAGVDPYSRSGIEMELLKYRQ 1080
Db 1021 LPSKSLKSKTSLGSMOKRSLVALAFVGSKVYILDEPTAGVDPYSRSGIEMELLKYRQ 1080
QY 1081 GRITIIISHHMDADVGLGRILAIISHGKLCVSSSLFLKNOLGTGYLLLVKKDVSSLS 1140
Db 1081 GRITIIISHHMDADVGLGRILAIISHGKLCVSSSLFLKNOLGTGYLLLVKKDVSSLS 1140
QY 1141 SCNNSSSYLYLKKEDSVSSSDAGIGSDHSDTLTIDVSAISNIRKHVSEARIVEDI 1200
Db 1141 SCNNSSSYLYLKKEDSVSSSDAGIGSDHSDTLTIDVSAISNIRKHVSEARIVEDI 1200
QY 1201 GHELTVVLPEAAKEGAFELFHEIDRLSDIGISSYGISETTLBEBFLKVAEESGVDAE 1260
Db 1201 GHELTVVLPEAAKEGAFELFHEIDRLSDIGISSYGISETTLBEBFLKVAEESGVDAE 1260

QY 1261 TSDGTLPARNRRAFGDKOSCLRPFTEDDAADPNDSDIDPESRETDLISGMDGKSYGVK 1320
Db 1261 TSDGTLPARNRRAFGDKOSCLRPFTEDDAADPNDSDIDPESRETDLISGMDGKSYGVK 1320
QY 1321 GKKLTOOQFVALIKRRLIARSRKGFPAQIYLVAVFYCALVSLYVPPGKIPSELO 1380
Db 1321 GKKLTOOQFVALIKRRLIARSRKGFPAQIYLVAVFYCALVSLYVPPGKIPSELO 1380
QY 1381 PMWYNEOQTFVNDAPEDTGTLELINALTKDPGFCRMBEKNPIPDPPCOAGEEMWTAP 1440
Db 1381 PMWYNEOQTFVNDAPEDTGTLELINALTKDPGFCRMBEKNPIPDPPCOAGEEMWTAP 1440
QY 1441 VPQITMDLFPONGNWTQNPSPACQSSDKIKKMLPVCPPGAGLEPPPOKONTADIILODL 1500
Db 1441 VPQITMDLFPONGNWTQNPSPACQSSDKIKKMLPVCPPGAGLEPPPOKONTADIILODL 1500
QY 1501 TGRNISDYLVTYVOIITAKSLKNKIWNEFPYGGSGLSGVSTQALPPOEYVNDAIKOKKK 1560
Db 1501 TGRNISDYLVTYVOIITAKSLKNKIWNEFPYGGSGLSGVSTQALPPOEYVNDAIKOKKK 1560
QY 1561 HLKIAKDSADREFLNSLGRFMTGDTNRNNVYVFNKNGMAISSFLVYNNAILRANLOK 1620
Db 1561 HLKIAKDSADREFLNSLGRFMTGDTNRNNVYVFNKNGMAISSFLVYNNAILRANLOK 1620
QY 1621 GENPSHYGITAPNHPNLNTKQOLSEVALMTTSVDYLVSTCYIFPMSFVPASFVFLIOER 1680
Db 1621 GENPSHYGITAPNHPNLNTKQOLSEVALMTTSVDYLVSTCYIFPMSFVPASFVFLIOER 1680
QY 1681 VSKAKHLOFISGVKPVITWLSNFWDMCNVYVPAVLVITIFICPOOKSYVSTMIPIJAL 1740
Db 1681 VSKAKHLOFISGVKPVITWLSNFWDMCNVYVPAVLVITIFICPOOKSYVSTMIPIJAL 1740
QY 1741 LLLLYGMSITPLMPASFVFKIPSTAYVVLTSVNLFFJGINSVATVELEFTDKNLNNIN 1800
Db 1741 LLLLYGMSITPLMPASFVFKIPSTAYVVLTSVNLFFJGINSVATVELEFTDKNLNNIN 1800
QY 1801 DILKSVFLIFPHFCGRGLIDMWKNQAMADALBERGRENREYSPISMDLYGRNLEPAMAVEG 1860
Db 1801 DILKSVFLIFPHFCGRGLIDMWKNQAMADALBERGRENREYSPISMDLYGRNLEPAMAVEG 1860
QY 1861 VVFLITVLIOYREFIRRPVNAKLSPLNDEDEDVRRERORILIDGGQNDILEIKELTKI 1920
Db 1861 VVFLITVLIOYREFIRRPVNAKLSPLNDEDEDVRRERORILIDGGQNDILEIKELTKI 1920
QY 1921 YRRKKRPADVRLCYGIRPGECFGLGVNGAKSSTFKMLTGDITVTYKDAEFLANKNSTLSN 1980
Db 1921 YRRKKRPADVRLCYGIRPGECFGLGVNGAKSSTFKMLTGDITVTYKDAEFLANKNSTLSN 1980
QY 1981 IHEVHQNNGYCPQPDALITELLTGREHVEFFALLRGVPEKEVGKVGEMAIRKLGIVKGEK 2040
Db 1981 IHEVHQNNGYCPQPDALITELLTGREHVEFFALLRGVPEKEVGKVGEMAIRKLGIVKGEK 2040
QY 2041 YAGNMSGNKRKRLSTAMALIGGPVYVLEDEPTTGMDRKARFLMNCALSVYKBEGRSVLT 2100
Db 2041 YAGNMSGNKRKRLSTAMALIGGPVYVLEDEPTTGMDRKARFLMNCALSVYKBEGRSVLT 2100
QY 2101 SHSMEECALCTRMAIWMNGRFRCLGSVOHLKNRFGGTYITVARIASNDIKKVPQDFFG 2160
Db 2101 SHSMEECALCTRMAIWMNGRFRCLGSVOHLKNRFGGTYITVARIASNDIKKVPQDFFG 2160
QY 2161 LAFPGSVLYKEKHNMLQYOLPSSLSLARJFSIISOKRKLHIEDYSVSOTTLDOYVNF 2220
Db 2161 LAFPGSVLYKEKHNMLQYOLPSSLSLARJFSIISOKRKLHIEDYSVSOTTLDOYVNF 2220
QY 2221 AKDOSDDHLDKLSLHKNOTVVDVAVLTSPLQDDEKVESEY 2261
Db 2221 AKDOSDDHLDKLSLHKNOTVVDVAVLTSPLQDDEKVESEY 2261

RESULT 2
Q96T85 PRELIMINARY; PRT; 2261 AA.
AC Q96T85;
```


DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ATP-BINDING CASSETTE 1 SUB-FAMILY A MEMBER 1.
 GN ABCA1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21251004; PubMed=11352567;
 RA Qiu Y., Cavelier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;
 RT "Human and Mouse ABCA1 Comparative Sequencing and Transgenesis Studies
 RT Revealing Novel Regulatory Sequences.";
 RL Genomics 73:66-76(2001).
 DR EMBL; AF287262; AAA43526.1; -.
 KW ATP-binding.
 SQ SEQUENCE 2261 AA; 254238 MW; 248DF04C8FF041A5 CRC64;

Query Match 99.8%; Score 11774; DB 4; Length 2261;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2256; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MACWQRLRLMKNLFFRRROTCLLFFVAMPFLIFLILISVLSYPPEOHECHPKA 60
 DB 1 MACWQRLRLMKNLFFRRROTCLLFFVAMPFLIFLILISVLSYPPEOHECHPKA 60
 QY 61 MSAGLIPVVGIGICNANPCFRYPGPBAPGVGNFNKSIYARLFSDARRLLYSOKDT 120
 DB 61 MSAGLIPVVGIGICNANPCFRYPGPBAPGVGNFNKSIYARLFSDARRLLYSOKDT 120
 QY 121 SKDMKRVLRITQQIKKSSSNLKLODFLVNFTFSGFLYHNLSEPKSYDKMLRADVILH 180
 DB 121 SKDMKRVLRITQQIKKSSSNLKLODFLVNFTFSGFLYHNLSEPKSYDKMLRADVILH 180
 QY 121 SKDMKRVLRITQQIKKSSSNLKLODFLVNFTFSGFLYHNLSEPKSYDKMLRADVILH 180
 DB 121 SKDMKRVLRITQQIKKSSSNLKLODFLVNFTFSGFLYHNLSEPKSYDKMLRADVILH 180
 QY 181 KVFLOGYOLHTSLICNGSSEEMIOIGDOVESLGLPEKLAARVLRSMNDILKPTL 240
 DB 181 KVFLOGYOLHTSLICNGSSEEMIOIGDOVESLGLPEKLAARVLRSMNDILKPTL 240
 QY 181 KVFLOGYOLHTSLICNGSSEEMIOIGDOVESLGLPEKLAARVLRSMNDILKPTL 240
 DB 181 KVFLOGYOLHTSLICNGSSEEMIOIGDOVESLGLPEKLAARVLRSMNDILKPTL 240
 QY 241 RLINSTSPPSKELAEATKTLHLSLGTLLAQELFSMRSMDRQEWFLTNVSSSSSTOI 300
 DB 241 RLINSTSPPSKELAEATKTLHLSLGTLLAQELFSMRSMDRQEWFLTNVSSSSSTOI 300
 QY 241 RLINSTSPPSKELAEATKTLHLSLGTLLAQELFSMRSMDRQEWFLTNVSSSSSTOI 300
 DB 241 RLINSTSPPSKELAEATKTLHLSLGTLLAQELFSMRSMDRQEWFLTNVSSSSSTOI 300
 QY 301 YQAVSRIVCGHPEGGLKIKSLNWTEDNNYKALFGNGTEDEAETFYDNSTPYCNDLMK 360
 DB 301 YQAVSRIVCGHPEGGLKIKSLNWTEDNNYKALFGNGTEDEAETFYDNSTPYCNDLMK 360
 QY 301 YQAVSRIVCGHPEGGLKIKSLNWTEDNNYKALFGNGTEDEAETFYDNSTPYCNDLMK 360
 DB 301 YQAVSRIVCGHPEGGLKIKSLNWTEDNNYKALFGNGTEDEAETFYDNSTPYCNDLMK 360
 QY 361 NLESSPLSRITKALKPILVGLKILYTPDPATROVMAEVNKTFOELAVFHDLBGMWEELS 420
 DB 361 NLESSPLSRITKALKPILVGLKILYTPDPATROVMAEVNKTFOELAVFHDLBGMWEELS 420
 QY 361 NLESSPLSRITKALKPILVGLKILYTPDPATROVMAEVNKTFOELAVFHDLBGMWEELS 420
 DB 361 NLESSPLSRITKALKPILVGLKILYTPDPATROVMAEVNKTFOELAVFHDLBGMWEELS 420
 QY 421 PKIWTMENSOEMDLVRMLDSRDNDHFWEQOLDGIDMTAODIVAFIAKHPEVOSSSNGS 480
 DB 421 PKIWTMENSOEMDLVRMLDSRDNDHFWEQOLDGIDMTAODIVAFIAKHPEVOSSSNGS 480
 QY 421 PKIWTMENSOEMDLVRMLDSRDNDHFWEQOLDGIDMTAODIVAFIAKHPEVOSSSNGS 480
 DB 421 PKIWTMENSOEMDLVRMLDSRDNDHFWEQOLDGIDMTAODIVAFIAKHPEVOSSSNGS 480
 QY 481 VYTWREAFNETNOAIRTISRMECVNLKLEPIATVWMLINKSMELDERKFMAGIVFTG 540
 DB 481 VYTWREAFNETNOAIRTISRMECVNLKLEPIATVWMLINKSMELDERKFMAGIVFTG 540
 QY 481 VYTWREAFNETNOAIRTISRMECVNLKLEPIATVWMLINKSMELDERKFMAGIVFTG 540
 DB 481 VYTWREAFNETNOAIRTISRMECVNLKLEPIATVWMLINKSMELDERKFMAGIVFTG 540
 QY 541 ITPGSEIPLPHVYKTRIMQIDNVERTNKKIKDGYWDPGPADPEDEMRARYWGGAYLQDYY 600
 DB 541 ITPGSEIPLPHVYKTRIMQIDNVERTNKKIKDGYWDPGPADPEDEMRARYWGGAYLQDYY 600
 QY 541 ITPGSEIPLPHVYKTRIMQIDNVERTNKKIKDGYWDPGPADPEDEMRARYWGGAYLQDYY 600
 DB 541 ITPGSEIPLPHVYKTRIMQIDNVERTNKKIKDGYWDPGPADPEDEMRARYWGGAYLQDYY 600
 QY 601 EQAIIIRVLGTEKKTKGVYMOQMPYPCYVDIDFLRVASRSMPLFMTLAWIVSAVAILKGIIV 660
 DB 601 EQAIIIRVLGTEKKTKGVYMOQMPYPCYVDIDFLRVASRSMPLFMTLAWIVSAVAILKGIIV 660
 QY 601 EQAIIIRVLGTEKKTKGVYMOQMPYPCYVDIDFLRVASRSMPLFMTLAWIVSAVAILKGIIV 660
 DB 601 EQAIIIRVLGTEKKTKGVYMOQMPYPCYVDIDFLRVASRSMPLFMTLAWIVSAVAILKGIIV 660
 QY 661 YEEEARLKEKTRIMGIDNSILMFSSITSLIPLVSNAGLLVYLKIGNLLPSYSDPSVAVY 720
 DB 661 YEEEARLKEKTRIMGIDNSILMFSSITSLIPLVSNAGLLVYLKIGNLLPSYSDPSVAVY 720
 QY 661 YEEEARLKEKTRIMGIDNSILMFSSITSLIPLVSNAGLLVYLKIGNLLPSYSDPSVAVY 720
 DB 661 YEEEARLKEKTRIMGIDNSILMFSSITSLIPLVSNAGLLVYLKIGNLLPSYSDPSVAVY 720

QY 721 FLSEFAVVTLLQCLISTLFSRANLAAACGIIYFTLLPYVLCVAMQDVGFTLKIFAS 780
 DB 721 FLSEFAVVTLLQCLISTLFSRANLAAACGIIYFTLLPYVLCVAMQDVGFTLKIFAS 780
 QY 781 LLSPVAFGCEGFALFEEOGIGVOMDNLFESPVEEDGFNLITTSISMALFDTFLYGVMTW 840
 DB 781 LLSPVAFGCEGFALFEEOGIGVOMDNLFESPVEEDGFNLITTSISMALFDTFLYGVMTW 840
 QY 841 YIEAVFPGQYIGIPRPWPFPCTKSYWESEDESHPSNOKRMSSEICMEEPHILKIGVS 900
 DB 841 YIEAVFPGQYIGIPRPWPFPCTKSYWESEDESHPSNOKRMSSEICMEEPHILKIGVS 900
 QY 901 IONLVKYYRDMKAVVAGLALNFEGOITFSLGHNKAGKTTMSILTGLPPTSGTAYIL 960
 DB 901 IONLVKYYRDMKAVVAGLALNFEGOITFSLGHNKAGKTTMSILTGLPPTSGTAYIL 960
 QY 901 IONLVKYYRDMKAVVAGLALNFEGOITFSLGHNKAGKTTMSILTGLPPTSGTAYIL 960
 DB 901 IONLVKYYRDMKAVVAGLALNFEGOITFSLGHNKAGKTTMSILTGLPPTSGTAYIL 960
 QY 961 GKDIRSEKSTIRONLIGVCPHNVLFDMILVEEHIMFYARLKLKSHVKAEMEQMALDVG 1020
 DB 961 GKDIRSEKSTIRONLIGVCPHNVLFDMILVEEHIMFYARLKLKSHVKAEMEQMALDVG 1020
 QY 1021 LPSSKLSKTSQLSGGMQKLSVALAFVGGSKVYIIDEPTAGVDYSRKGIWELLKRYQ 1080
 DB 1021 LPSSKLSKTSQLSGGMQKLSVALAFVGGSKVYIIDEPTAGVDYSRKGIWELLKRYQ 1080
 QY 1081 GRITILSTHMDADVLDRIALISHGKLCVSSFLKMQLGTYLTLVKKDVESSL 1140
 DB 1081 GRITILSTHMDADVLDRIALISHGKLCVSSFLKMQLGTYLTLVKKDVESSL 1140
 QY 1141 SCRNSSTVSYLKKEDSVSSSDAGLGSDESPTLIDVSAISNLRKHVSEARLYEDI 1200
 DB 1141 SCRNSSTVSYLKKEDSVSSSDAGLGSDESPTLIDVSAISNLRKHVSEARLYEDI 1200
 QY 1201 GHELTLYVLYPAKREGAVELFHEIDRLSDGISSTTLEETLEFLVAEBSGVDAE 1260
 DB 1201 GHELTLYVLYPAKREGAVELFHEIDRLSDGISSTTLEETLEFLVAEBSGVDAE 1260
 QY 1201 GHELTLYVLYPAKREGAVELFHEIDRLSDGISSTTLEETLEFLVAEBSGVDAE 1260
 DB 1201 GHELTLYVLYPAKREGAVELFHEIDRLSDGISSTTLEETLEFLVAEBSGVDAE 1260
 QY 1261 TSDGTLFARNRRAFGDKOSCLRPTEDDAADPNDSDIDPESRTDLLSGMDGKGSYQV 1320
 DB 1261 TSDGTLFARNRRAFGDKOSCLRPTEDDAADPNDSDIDPESRTDLLSGMDGKGSYQV 1320
 QY 1321 GSKLTOGOVALLMKRLILARSRKGFPAQIVLAVYCTALVSLVYPPRGKPSLEIQ 1380
 DB 1321 GSKLTOGOVALLMKRLILARSRKGFPAQIVLAVYCTALVSLVYPPRGKPSLEIQ 1380
 QY 1321 GSKLTOGOVALLMKRLILARSRKGFPAQIVLAVYCTALVSLVYPPRGKPSLEIQ 1380
 DB 1321 GSKLTOGOVALLMKRLILARSRKGFPAQIVLAVYCTALVSLVYPPRGKPSLEIQ 1380
 QY 1381 PMWNEYOTFEVSNDAPEDTGILELNLALTDPGFGTRCMENPILPDPICQAGEEMTAP 1440
 DB 1381 PMWNEYOTFEVSNDAPEDTGILELNLALTDPGFGTRCMENPILPDPICQAGEEMTAP 1440
 QY 1381 PMWNEYOTFEVSNDAPEDTGILELNLALTDPGFGTRCMENPILPDPICQAGEEMTAP 1440
 DB 1381 PMWNEYOTFEVSNDAPEDTGILELNLALTDPGFGTRCMENPILPDPICQAGEEMTAP 1440
 QY 1441 VPOTIMDLFONGNMTQNPSPACQSSDKIKKMLPYCPGAGLPPQKQNTADILQDL 1500
 DB 1441 VPOTIMDLFONGNMTQNPSPACQSSDKIKKMLPYCPGAGLPPQKQNTADILQDL 1500
 QY 1441 VPOTIMDLFONGNMTQNPSPACQSSDKIKKMLPYCPGAGLPPQKQNTADILQDL 1500
 DB 1441 VPOTIMDLFONGNMTQNPSPACQSSDKIKKMLPYCPGAGLPPQKQNTADILQDL 1500
 QY 1501 TGRNISDYLVKTYVOI IAKSLKNKIWNEFRYGGESLGSVSTQALPSPQEVNDAIKQMK 1560
 DB 1501 TGRNISDYLVKTYVOI IAKSLKNKIWNEFRYGGESLGSVSTQALPSPQEVNDAIKQMK 1560
 QY 1501 TGRNISDYLVKTYVOI IAKSLKNKIWNEFRYGGESLGSVSTQALPSPQEVNDAIKQMK 1560
 DB 1501 TGRNISDYLVKTYVOI IAKSLKNKIWNEFRYGGESLGSVSTQALPSPQEVNDAIKQMK 1560
 QY 1561 HIKLAKDSSADBEFLSLDRFMTGIDTRNNVAVWENKMKMHAISFLYINNAIIRANLQK 1620
 DB 1561 HIKLAKDSSADBEFLSLDRFMTGIDTRNNVAVWENKMKMHAISFLYINNAIIRANLQK 1620
 QY 1561 HIKLAKDSSADBEFLSLDRFMTGIDTRNNVAVWENKMKMHAISFLYINNAIIRANLQK 1620
 DB 1561 HIKLAKDSSADBEFLSLDRFMTGIDTRNNVAVWENKMKMHAISFLYINNAIIRANLQK 1620
 QY 1621 GENPSHYGITAFNHPNLNTKQOLSEVALMTTSDVLSICVIFAMSFVPASVFFLQER 1680
 DB 1621 GENPSHYGITAFNHPNLNTKQOLSEVALMTTSDVLSICVIFAMSFVPASVFFLQER 1680
 QY 1621 GENPSHYGITAFNHPNLNTKQOLSEVALMTTSDVLSICVIFAMSFVPASVFFLQER 1680
 DB 1621 GENPSHYGITAFNHPNLNTKQOLSEVALMTTSDVLSICVIFAMSFVPASVFFLQER 1680
 QY 1681 VSKAKHLOFISGVKPYIWLNSFWDMKCNYYVPALVLIIFICQOQSYSVSTMLPYAL 1740
 DB 1681 VSKAKHLOFISGVKPYIWLNSFWDMKCNYYVPALVLIIFICQOQSYSVSTMLPYAL 1740
 QY 1741 LLLLGWSTITPLMYPASVFPKIPSTAYVVLTVSNLFGINGSVATFVLELTTDKLNNIN 1800
 DB 1741 LLLLGWSTITPLMYPASVFPKIPSTAYVVLTVSNLFGINGSVATFVLELTTDKLNNIN 1800
 QY 1741 LLLLGWSTITPLMYPASVFPKIPSTAYVVLTVSNLFGINGSVATFVLELTTDKLNNIN 1800
 DB 1741 LLLLGWSTITPLMYPASVFPKIPSTAYVVLTVSNLFGINGSVATFVLELTTDKLNNIN 1800
 QY 1801 DILKSVFLIPFHCIGRLIDMKVKNQAMADALEREGENREYVPSLWDLVGRNLFAMAVEG 1860

Db 1801 DILKSVLIPHPFLGKGLIDMVNQAMADALEFGENREVSPLSMVLGRNLFAMAVEG 1860
QY 1861 VVFLITVLIOYRFFIRPRPVNAKLSPLNDEDEVDREBORIILDGGOQNDILEIKELTKI 1920
Db 1861 VVFLITVLIOYRFFIRPRPVNAKLSPLNDEDEVDREBORIILDGGOQNDILEIKELTKI 1920
QY 1921 YRRRKRAVDRIKVGIRPGECFGLGVNGAGKSSTFMMLTGDPTTVTKGDAFLKNKSLSN 1980
Db 1921 YRRRKRAVDRIKVGIRPGECFGLGVNGAGKSSTFMMLTGDPTTVTKGDAFLKNKSLSN 1980
QY 1981 IHEHOMMGYCPDPDATTETLTGHEHEFFALLRGVPEKRVGVGEMATIKLGLVYKGEK 2040
Db 1981 IHEHOMMGYCPDPDATTETLTGHEHEFFALLRGVPEKRVGVGEMATIKLGLVYKGEK 2040
QY 2041 YAGNYSGNKRKLTAMALIGPPVYFLDEPTTGMDPKARRFLMNCALSYVKEGSRVLT 2100
Db 2041 YAGNYSGNKRKLTAMALIGPPVYFLDEPTTGMDPKARRFLMNCALSYVKEGSRVLT 2100
QY 2101 SHSMECEALCTRAIMVNRFRCLGVOHLKRRFGDGTIVVRIAGSNPDLKPVODFCG 2160
Db 2101 SHSMECEALCTRAIMVNRFRCLGVOHLKRRFGDGTIVVRIAGSNPDLKPVODFCG 2160
QY 2161 LAEPGSYLAKERHNMLOYOPLSSLSLARIETLSOSKKRLHIEDYSVQTTLDQYFVNF 2220
Db 2161 LAEPGSYLAKERHNMLOYOPLSSLSLARIETLSOSKKRLHIEDYSVQTTLDQYFVNF 2220
QY 2221 AKQOSDDHLKOLSIHKNQTVVDAVLTSLQDEKKEKSYV 2261
Db 2221 AKQOSDDHLKOLSIHKNQTVVDAVLTSLQDEKKEKSYV 2261
RESULT 3
ID 035600 PRELIMINARY: PRT: 2310 AA.
AC 035600;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ATP-BINDING CASSETTE TRANSPORTER.
GN ABCA4 OR ABCR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=97345663; PubMed=9202155;
RA Azarian S.M., Travis G.H.;
RT "The photoreceptor rim protein is an ABC transporter encoded by the
RT gene for recessive Stargardt's disease (ABCR).";
RL FEBS Lett. 409:247-252(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Azarian S.M., Travis G.H.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF000149; AAC23916.1; .
DR MGI: 109424; Abca4.
DR InterPro: IPR003593; AAA.
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR001687; ATP_GTP_A.
DR Pfam: PF00005; ABC_tran. 2.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW ATP-binding. 2310 AA; 260207 MW; 8370068A62EF294 CRC64;
SQ SEQUENCE 2310 AA; 260207 MW; 8370068A62EF294 CRC64;

Query Match 49.9%; Score 5888; DB 11; Length 2310;
Best Local Similarity 50.1%; Pred No. 0;
Matches 1168; Conservative 362; Mismatches 624; Indels 178; Gaps 27;

QY 6 QRLRLMKNLTERRRQTCOLLLEVAMPLEFIILLISVRLSPYRPOHCPNPKAMP5AG 65
Db 6 QYOLLKMKWTLRKQKIRFVELVWPLSLFVLLWLNANPLSQHCHFPNPKAMP5AG 65
QY 66 TLRWGCIICNANPCFRYPTRPEAPGVGVGNFKSIVARLFSADARRLLYSOKDTSMKM 125
Db 66 LRPWLQGIIECNMNNPCQNPPTGESPTGSYNNSILARVRDFQELFMDPREVOHLQGY 125
QY 126 KVLRTLOI-----KSSNLKLODPLVDNETSGFLYHNLSLPKSTVDKMLRAD 176
Db 126 KVLRTLOI-----KSSNLKLODPLVDNETSGFLYHNLSLPKSTVDKMLRAD 176
QY 177 VILHKVFLQYOLHLTSL-CNGSKSEEMI---QLGDOEVE-LGGLPKERKLAARVLR 230
Db 177 VILHKVFLQYOLHLTSL-CNGSKSEEMI---QLGDOEVE-LGGLPKERKLAARVLR 230
QY 186 VAEQGFAYGVPLDELTLDIACSEALLQRFIFPSQRGAQTVBDALCPISQVYTLQMIEDTLY 245
Db 186 VAEQGFAYGVPLDELTLDIACSEALLQRFIFPSQRGAQTVBDALCPISQVYTLQMIEDTLY 245
QY 231 SMMDLIKPLRTLNSTSPPKELAEATKTLHSIGTL---AQELFSMRSM---SDMR- 282
Db 231 SMMDLIKPLRTLNSTSPPKELAEATKTLHSIGTL---AQELFSMRSM---SDMR- 282
QY 246 ADVDEFK-----LHVLPRTLDSSSQGINLRFVGGILSDLSIP 282
Db 246 ADVDEFK-----LHVLPRTLDSSSQGINLRFVGGILSDLSIP 282
QY 283 -----QEVNF-----LTNVSSSSSTQIYQAVSRIYCGHPGGGLKIKSLMWYED 327
Db 283 RMQKFIHRPSVQDILLWGRPLQNGRPETFTQWMSILSDLCGYRPEGGSRVFSFMYED 342
QY 328 NNYKALFGNGTEEDAEFTFDNSTTPPYCNDLMKNLESSPLRIITWALKPLVGLKIITYP 387
Db 328 NNYKALFGNGTEEDAEFTFDNSTTPPYCNDLMKNLESSPLRIITWALKPLVGLKIITYP 387
QY 343 NNYKAFGLGIDSTRKDPAYSIDKRTTSPCNLSIOSLESNPRTKIMWRAKPLLMKILFTTP 402
Db 343 NNYKAFGLGIDSTRKDPAYSIDKRTTSPCNLSIOSLESNPRTKIMWRAKPLLMKILFTTP 402
QY 388 DPAARYQVAEYKRFQELAEVHDEGMMELSPRTFMENSOEMDLYRMLLDSRONDH 447
Db 388 DPAARYQVAEYKRFQELAEVHDEGMMELSPRTFMENSOEMDLYRMLLDSRONDH 447
QY 403 DSPAARRIKMKNANSTFEELDVRKILYKAMEVGVQIYWFEEKSTQMYIYRTLDHPYKD 462
Db 403 DSPAARRIKMKNANSTFEELDVRKILYKAMEVGVQIYWFEEKSTQMYIYRTLDHPYKD 462
QY 448 FWEQOLDGLDWTADITVAFLAKHPEDVOSSNGSVYTWREAFNETNOAIRTISREMECVNL 507
Db 448 FWEQOLDGLDWTADITVAFLAKHPEDVOSSNGSVYTWREAFNETNOAIRTISREMECVNL 507
QY 463 FNRQLGEEGITTEAVLNFEFSNGPOEKQADMTSPDMHIDINIRFLRANQVLECIYL 522
Db 463 FNRQLGEEGITTEAVLNFEFSNGPOEKQADMTSPDMHIDINIRFLRANQVLECIYL 522
QY 508 NKLEFIAREVWMLINKSMELDERKFMAGIVFTGTPGSELPHVYKKIRMDIDNVERTIN 567
Db 508 NKLEFIAREVWMLINKSMELDERKFMAGIVFTGTPGSELPHVYKKIRMDIDNVERTIN 567
QY 523 DFEFSTDEVOITQORALSLLEENRFMAGVGPMTAPMASSLPPIVKKIRKIDVDIVERTN 582
Db 523 DFEFSTDEVOITQORALSLLEENRFMAGVGPMTAPMASSLPPIVKKIRKIDVDIVERTN 582
QY 568 KIKDGYWDPGRADPFEDDMRYMGGFAYLQDVQRAIIRVLTGTEKRTGVYMQMPYCY 627
Db 568 KIKDGYWDPGRADPFEDDMRYMGGFAYLQDVQRAIIRVLTGTEKRTGVYMQMPYCY 627
QY 583 KIKDRYWDGSPRADPVEDFRYIWGFAVLQDMVQGIYKSGMQAEPLIGVYLQDMPCF 642
Db 583 KIKDRYWDGSPRADPVEDFRYIWGFAVLQDMVQGIYKSGMQAEPLIGVYLQDMPCF 642
QY 628 VDDIFLRWMSMPLFMTLAWIYSVAIYIKGIYVEKEKRLKETKRNGLDNLIMESWFI 687
Db 628 VDDIFLRWMSMPLFMTLAWIYSVAIYIKGIYVEKEKRLKETKRNGLDNLIMESWFI 687
QY 643 VDDSMIILNRCFLEFVLAWIYSVSMTVKGIYLEKELRLKETLKNQGVSAVATWCTMFL 702
Db 643 VDDSMIILNRCFLEFVLAWIYSVSMTVKGIYLEKELRLKETLKNQGVSAVATWCTMFL 702
QY 688 SLLPLVLSAGLLVYLKGLNMLLPYSDPSVYFVLSFAVYTLIQCLISTLFSRANLAA 747
Db 688 SLLPLVLSAGLLVYLKGLNMLLPYSDPSVYFVLSFAVYTLIQCLISTLFSRANLAA 747
QY 703 DFSFIMALSTILLTLFIMHGRILHYSDFILFLPLNAFATIMQSLTLSTPSKASLAA 762
Db 703 DFSFIMALSTILLTLFIMHGRILHYSDFILFLPLNAFATIMQSLTLSTPSKASLAA 762
QY 748 ACGGITYFTLYPLVYLCVAMODYVGFILKIPASLLSPVAFGCEYFALFEBOGIYQMD 807
Db 748 ACGGITYFTLYPLVYLCVAMODYVGFILKIPASLLSPVAFGCEYFALFEBOGIYQMD 807
QY 808 NLFESPVEDEGFNTTSSIMKLPDTPLYGVMTVTIYEAVFQGVGVIIPRWPFPCPKSWFG 867
Db 808 NLFESPVEDEGFNTTSSIMKLPDTPLYGVMTVTIYEAVFQGVGVIIPRWPFPCPKSWFG 867
QY 823 NIGKSPLEBGEFSLSKMKMLDLAALXGLAMLDVYFEDGVTPLPWKFLLOESTYWLG 882
Db 823 NIGKSPLEBGEFSLSKMKMLDLAALXGLAMLDVYFEDGVTPLPWKFLLOESTYWLG 882
QY 868 -----EESDEKSHPGSNOKRMSIECEBEFTHLKLGSIQNTLVKY 908
Db 868 -----EESDEKSHPGSNOKRMSIECEBEFTHLKLGSIQNTLVKY 908
QY 883 GEGCSTREERALEKTEPLETEMEDEPHR-----EGMNSPFERELPGLVPCVKANLVKVF 938
Db 883 GEGCSTREERALEKTEPLETEMEDEPHR-----EGMNSPFERELPGLVPCVKANLVKVF 938
QY 909 RDGKAVAVDGLALNFYBQITSLGHNGAGKTTMSITLGLPPTSGTAVYILAKDIRSEM 968
Db 909 RDGKAVAVDGLALNFYBQITSLGHNGAGKTTMSITLGLPPTSGTAVYILAKDIRSEM 968
QY 939 EPSGRPAVDRLNITFYENQITAFIGHNAGKTTTSLTGLPPTSGTAVYILAKDIRSEM 998
Db 939 EPSGRPAVDRLNITFYENQITAFIGHNAGKTTTSLTGLPPTSGTAVYILAKDIRSEM 998
QY 969 STIRONLGVCPQOHNVLDMLTVEEHVFWYARIKGLSKHAKAMEOMALDVGPSKILKS 1028
Db 969 STIRONLGVCPQOHNVLDMLTVEEHVFWYARIKGLSKHAKAMEOMALDVGPSKILKS 1028
QY 999 DVVRQSLGMCPCQNHILHLLVLAHLLFVLAQLKGRSWEAEQLEMEALIEDTGL-HHKRME 1057
Db 999 DVVRQSLGMCPCQNHILHLLVLAHLLFVLAQLKGRSWEAEQLEMEALIEDTGL-HHKRME 1057

Db 345 YKAFGLIDSTRKDEIYSYDERTTFCNALIQSLESNPLKIANRAKPLIMGLIFTPDS 404
 QY 390 PATROVAEYKKTFOELAVFHDLEGMELSPKIMTFEMNSEMDLYRMLDSRDNHFW 449
 Db 405 PATRILKLNANSFTEELERAKLVKWEVEGPOQWYFEDSTQSMKROLLENPIYAKAF 464
 QY 450 EOODLDQMTAODIVAFKAPHEDVOSSNGSVYTWREAFNEIOALITISREMECVNLK 509
 Db 465 NROIGEGJIAEAVLNLNGPREGQADVDNFMWDIFNITDRAILANQYLECLIDK 524
 QY 510 LEPIATEWMLINKSMELDERKEMAGIVFTGIPGSIELPHHYKRYKMDIDVERTNKI 569
 Db 525 FESYDDEFOQLORSLILEENRFAGVYFPDMHWTSSLPYHKYKIRMDIDVEYKTKI 584
 QY 570 KDWGPRPADPEEDKRYWGFAYLQDVVEQALIKVLITGEKTKGVYQOMPRCYVD 629
 Db 585 KDRWDSGPRADEVEDRYIMGFAFYLODMVEHCITRSQAOEEVPGVYIQMPYPCFVD 644
 QY 630 DIFLRVSRMPLFMTLAMIYSAVITIKGIVYEKARKETKMLMGDINSILMFWSISS 689
 Db 645 DSFMTILNKCPLEPMVLAMIVSMTVKSTVLEKELKTKETLNQGNHNYIMCTWFLDS 704
 QY 690 LIPPLASAGLIVLLKGNLIPYSDPSVEVFLSVFAVITILQCFILSTFBRANLAAC 749
 Db 705 FSIKMSICLLTIFIMGRILHYSNPFILFLPLAFSIATIMOCFILSTFBRASILAAC 764
 QY 750 GGIYFLLYLYCYAMQDYVGTIKIFASLSPAVAFGCEYFALFEBOGIGVQMDNL 809
 Db 765 SGVYFLYLYPHLICFMQORITADMKMAVSLSPVAFGTEFLAXFEBOGIGLOMSNI 824
 QY 810 FESVEEDGNLTJTSIMMLFDTFLYGMVITEAVPQOYGIIPRYFPCSTSYMPG-- 867
 Db 825 GNSMDEDEFSFLMSKMMMLDALIYGLLWYIDQVFPBGYGRPLRYFLQESYIMLGE 884
 QY 868 -----BESDEKSHPGSNQ-----KRMSEICMEEPHLKLGVSIONLVKYRDMKV 914
 Db 885 GCSTRERARALEKTEPIEEMEDDEYREGINDCEFERELPGLVPGCVKNLVIFEPYGR 944
 QY 915 AYDGLALNFEGOTSTFLNGAGKTTMSILGLPPTSGTAYILGKDIRSMSTTRON 974
 Db 945 AYDRLNTFESQITLALGNAGKTTLSIMGLDLPYISGVYAGGKDEITMLDITROS 1004
 QY 975 LGVCPQHNVLFDMLYBEHIMFYARLKGLSEKHYKAKEMEQMALDVLGPPSSKLSKTSOLS 1034
 Db 1005 LGMCPQHNILFHLVLAENHILFYAOLKGRSMDQAOLEMAMLEDITGI-HHKRNEERADLS 1063
 QY 1035 GGMQRKLSVALAFYGGKVYIDEPYAGVYRSRGITWELLKRYOGRITILSTHMDXA 1094
 Db 1064 GGVOYKRLSVAFYAGKAVYVLDPTSGVDPYRSRSTIMDLLEKYSRGTITIMSTHMDXA 1123
 QY 1095 DVLGDRITAITSHGKLCVGSFLKNQDGTGYLLTVKKDVESSLSCRSSSTVSYLAK 1154
 Db 1124 DILGDRITAITSHGKLCVGSFLKNQDGTGYLLTVKKDVESSLSCRSSSTVSYLAK 1182
 QY 1155 EDVYSSSSDAGISDGHESDTLITDVSALSMLIRKHVSEARLEVEDIGHETLYLPEYAK 1214
 Db 1183 GFSYRCACAEALTPREGVLDG--DYNELTDMVHNHVRPAKIVECIGQELIFELPKNNK 1239
 QY 1215 EGAFLVFLHETIDRLSLGISGISETTELEFLKVAESGVDAETSDGTLEPARNRRA 1274
 Db 1240 QRAVASLFRLEETLADLSSFGISDPTLEIFLKYTEDLDSGHLFAGTOOKREN-- 1296
 QY 1275 FGDKOSCLRP-----FTJEDAADPNDSIDIPESRFTDLISGMDGSGYQVWKRLTQOO 1328
 Db 1297 INLRHPSGSEKAGOTPOSSSHRGEPAHNRGQPPREVEGHSKRN-----CARLIVOH 1352
 QY 1329 FVALLMKRLLIARRSRKGFPAQITLPAVFCIALVLSLIVPRGKYPSELQPMWYNEQY 1388
 Db 1353 VOALLVYRFQHTIRSHKDLAQIVLDPATFVFLALMLSLIIPRGEVPALEIHWMYGQY 1412
 QY 1389 TTVSNAPREDTGTLELLNATKDPGFGTRCMENGPIDTPPCQAGEEMWTAPVQITML 1448
 Db 1413 TFFSMQOPDSEWMLALADVLVYKPGFGRCLKEWLEPEPC-GNSSPMKTPSPSPDVTHL 1471

QY 1449 FONGMNTMONPSPACOCSSDKIKKMLPYCPGAGGLPPOROKONTADILQDITGNISDY 1508
 Db 1472 LQOQKWTADQPSRCSCSTREKLTMLPBCPBAGGLPPORQRTSTELQDITGRNVSDF 1531
 QY 1509 LVKTYQIITAKSLANKIWNFEYRGFSLGVSNTOALPPSOEVDNAIKOMKHLKLAKDS 1568
 Db 1532 LVKTYPALIRSLSKSKFWNEQRYGISVG-----GKLPAPEFTGEALV----- 1575
 QY 1569 SADRPLNSLGR-----FMTGIDTNNYKVMFNNGKGMHAISFLNVI 1609
 Db 1576 -----GFLSDLGOLMNVSGGPMTRKAKEMPAFLKQLETEDNKIWMFNNGKGMHAISFLNVA 1632
 QY 1610 NNAILRANLOKGENPSHYGITAENHPLNLTKQOLSEVALMTTSVDVLSICVIFAMSFP 1669
 Db 1633 HNAILRASLHKRKNBEEGYITVISOPLMLTKRQLESEITVLTTSVDAVAALVIFIRAMSEVP 1692
 QY 1670 ASFVFLIOERYSKAKHLOFISGVKPVYIMLSNFVMDCNVVPATVITIIIFIGQOKSY 1729
 Db 1693 ASFVFLYLOERYKAKHLOFISGVSPVYTYWLTNFMIDIMNTVSALVVGIFIGQOKAY 1752
 QY 1730 VSTNLPVYALALLLGYNSITPLMYPASFEVKIPSTAVVLTSVLFTIGINGSVATVLE 1789
 Db 1753 TSEMLPVALMLMIXMAVYPMYPAFLDIPSTAVALSANLFTIGINSATVPLE 1812
 QY 1790 LFTDNK-LNNINDIILKSVFLIFPHFCLOGLIDMYKQAMADALERGENRVPPLSMDL 1848
 Db 1813 LFEENRKLIRIAMRKLIIFPHFCLOGLIDLISQAVTDVYAQOFEARSSNPFOWDL 1872
 QY 1849 VGRNLPAMAVEGVFELLTVLLOYRFFLRPRVYNAKLSPLNDEDEDVYRERORITLDDGGQ 1908
 Db 1873 ICKNLAAVAEYVFLTLILQYOFFFSRKTTPERAKERTIDEDDDVAEEOQRIISGKN 1932
 QY 1909 NDILEIKELTKIYRRKRRPAVDRIQVIGIPGECFGLLVGNAGKSSFFKMLTGTDTYTRG 1968
 Db 1933 TDILRLNELTKYSGTSSPAVDRLCVGVRPGEFGLLVGNAGKTTPKMLTGTDTYTRG 1992
 QY 1969 DAFLNKSTLSIHVHONMGCPQFDATITELGHEHVEFFALLRCVPEKEVOKYGEWA 2028
 Db 1993 DATVAGKSTLNIISDVHOSMGCPQFDATIDILGHEHLYIYARIRGVPAREIERVTWMS 2052
 QY 2029 IRLKGLVYGEKYAGNYSGNKRRKLTAMALIGBPVFLDEPTTGMOPKARFLMNCAL 2088
 Db 2053 IOSTGLSYADRLATYSGGNKRRKLTALIGCPRYLDELDEPTTGMOPKARFLMNCAL 2112
 QY 2089 SYVKGSRVYLTSHSMECEBALCTRMALMVNGRRRCVSGVLOHLKRRGDTIYVIRLAGS 2148
 Db 2113 GIIRERAVVLTSHSMECEBALCTRLAMVNGAFQCLQTIOLHLSKSPGDTYVIMKIRSP 2172
 QY 2149 N-----PDLKPYODFFGLAFPGSVLKEKRNMLQYOLPSSLSLARIFSILSQSKRLIE 2204
 Db 2173 KDDLPLDLPQVQFQGNFPGSVQREHRYNTILOVOVS--SSLARIFRLVSHKDSLIE 2230
 QY 2205 DYSVQSTLDQVYVFNPAQDSDDDLKDLSLH 2236
 Db 2231 EYSVTQTLTDQVYVFNFAQONE--TYDLPLH 2259
 RESULT 5
 Q9BZC4 PRELIMINARY; PRT; 2146 AA.
 AC Q9BZC4;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE ABC TRANSPORTER MEMBER 7.
 GN ABCA7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=21328888; PubMed=11435699;
 RA Broccardo C., Osorio J., Luciani M.-F., Schriml L.M., Prades C.,
 RA Shulem S., Arnould I., Naudin L., Lafargue C., Koster M., Jordan B.,
 RA Mathe M.G., Dean M., Denelle P., Chimini G.,
 RT "Comparative analysis of the promoter structure and genomic
 RT organization of the human and mouse ABCA7 gene encoding a novel ABCA
 RT transporter.";
 RT Cytogenet. Cell Genet. 92:264-270(2001).
 RL EMBL; AF328787; AK00959.1; -.
 DR InterPro: IPR003593; AAA.
 DR InterPro: IPR003439; ABC_transporter.
 DR InterPro: IPR01687; ATP_GTP_A.
 DR InterPro: IPR01899; Gram_pos_anchor.
 DR Pfam: PF00005; ABC_tran; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
 DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
 DR ATP-binding.
 KW SEQUENCE 2146 AA; 234306 MW; 239172805AD97E75 CRC64;

Query Match 49.0%; Score 5775.5; DB 4; Length 2146;
 Best Local Similarity 50.3%; Pred. No. 0;
 Matches 1148; Conservative 368; Mismatches 605; Indels 161; Gaps 26;

QY 1 MACWPOLRLILMKNTLFFRRRCOTCOLLEAVAMPFLIFLILSVLSVPPYEOHECHPNKA 60
 DB 1 MAFWTOLMLLKNMFKRROPVOLLVLELMLPFLFLIYAAVHSHPLLEHHECHPNKP 60
 QY 61 MSAGTLPWVGIGICNANPCERYPTPGAPGVGNFNKSIYARLFSDARLLYLSQKDT 120
 DB 61 LPSAGIVPMLOGLICVNMTCFQPLTGPBEPGLSNFNDSVRLADARTVILGASAH 120
 QY 121 SKMDKRVLTQOLIKSSSNLKLDFLVNDFSGFLYHNLSLKSTYDKMLRADYIIL 180
 DB 121 TLAGLKLTLATLRAKSTQO-----PQPTQSPLEPPML-- 154
 QY 181 KYFLQGYOHLTSLGNSKSEMIQLGDOVSEFLGCPREKLAARVLRSMNDILKPL 240
 DB 155 -----DVAEL-----LTSLL 164
 QY 241 RLINSTSPPEKELAEATYTLHLSIGTLAQLAEFSMSMSMDQEVNLTNNSSSSSTQI 300
 DB 165 RT--ESLGLALGOAQLSLLEAAGDLAQLAELATLSVELR--ALLQRPKTSGLPL 219
 QY 301 YQAVSTVCGHPBGGLTKLSLNMVEDNNYKALFGSNGIEEADAEFTYDSTPYCNDL 360
 DB 220 ---LSALCSVGRPSSTVGPSSLNMYEASDLMELVG---QEPESALPDSLSLSPACSELIG 272
 QY 361 NLESSPLSRIIMKALPRLVGLILYTPDPATROVAEYVKTFOELAVFHDELSGMEELS 420
 DB 273 ALDSHPLSLRLMRRLPLILGKLLFAPDTPFTKLAQVNRFEELTLRDVREVMELG 332
 QY 421 PKTWTWENSQEMDLYRMLDSRDNDHFWEQDLGIDMTAODIVATLALHPELVOS---- 476
 DB 333 PRIFTMNDSSNVMLQRLLOMDQEGR-RQPRGGRD-----HMEALRFLDLP 379
 QY 477 -SNGSVYTRAEAFNETNOAIRTISRFMECVNLKLEPIATEVYLINSMELDERFMAG 535
 DB 380 GSGG--YSMDADADYGLVLTIGRTYECISLKLKLEAPSEALYBRALQLLAEHFMAG 437
 QY 536 IFTGTIPGSELPH-----HVKYKIRMDIDNVERTNKIKDGYWDQPRADPEDMK 587
 DB 438 VVFLGEDSDSDPEHPTPDLPGLPGHVRIRIKIMDIDVYTRTNKIRDRFWDPCPADPLTLDR 497
 QY 588 YVNGGFYLODVYOAIIIRLTGTEKKTGYVMOOMPVCVVDIIFLRVMSRSLPMTLA 647
 DB 498 YVNGGFYLODVYOAIIIRLTGTEKKTGYVMOOMPVCVVDIIFLRVMSRSLPMTLA 557
 QY 648 WTSVAVIINGIYKEARLKETMRINGLDSNLTMSFSLSLPLVYAGLLVILKLG 707
 DB 558 WTSVAVIINGIYKEARLKETMRINGLDSNLTMSFSLSLPLVYAGLLVILKLG 617

QY 708 NLTPSDPSVVEFLSEYFAVNTILQCFILSTLSEFRANILAAACGIIYFTLYLPVLCVW 767
 DB 618 DILPYSHGVLFLFLAFAVATVQSFLSFFERANILAAACGIIAFSLYLPVLCVW 677
 QY 768 QDYVGFLLKIFASLLSPVAFGECEYFALFEEOGIVQWMDNLFESPYEEDGFNLITIS 827
 DB 678 RDRLPAGGRVAAISLLSPVAFGCESEALLLEEGEGQWIMHVGTRPT-ADVFSLAQVSL 736
 QY 828 MLFTFLYGVMTWILEAVFPQGYIIPRPWYPRCKISWYFEESESEKHPGSONKRMSEIC 887
 DB 737 LLLAALYGLATWYLEAACPQGYIPEPWNPFFRRSYWCGRPPKSPAPCPPLD-PKVL 795
 QY 888 MEEDPHTLKLVSIONLYKYVRDGMKYAVDGLANFEGQITSEFGHNGAGKTTMSILT 947
 DB 796 VEEAPRGISPVSVRSLEKRPFGSPQALRGLSLDFQGHNTATLGHNGAGKTTTSLIS 855
 QY 948 GLPPTSTFAYILKDIRSEKSTIRONLCVCPQHNVLFDMLTVEHIMFARLKLSEKH 1007
 DB 856 GLFPSCGSAFTLGHVYRSSMAIRPHLYCPOYVNLFDMLTVEHIMFARLKLSEKH 915
 QY 1008 VKAEMQALDVGLPSSKLKSKTSQLSGQMKRLSVLALFVGSKVYILDEPTAGVDPYS 1067
 DB 916 VGEEDRLQDVGL-VSKQSVQTRHLISGQMKRLSVLALFVGSQVYILDEPTAGVDPAS 974
 QY 1068 RGLIMELLKRYRQRTIILSTHNDVADVLGDRITAIISHGKLCVGSGLFLKNQLTGY 1127
 DB 975 RGLIMELLKRYRQRTIILSTHNDVADVLGDRITAIISHGKLCVGSGLFLKNQLTGY 1034
 QY 1128 LTLVKKDVESSLSCRSNSSVSYLKKEDSVSQSSSDAGLSDBESDTLTIDVAISNLI 1187
 DB 1035 LTLVKKDVESSLSCRSNSSVSYLKKEDSVSQSSSDAGLSDBESDTLTIDVAISNLI 1082
 QY 1188 RKHYSEARLVEDIGHLELYVLYPEAKEGAVVELFHEIDDLSDIGISSYSETTELEI 1247
 DB 1083 QHWVGARLVLELPHLELVLYPYGAHDSGATLFPREDTLALRLTGYISDTLSLEI 1142
 QY 1248 FLKVAESGVDAETSDGTLPPARRNRARG-DKQSLRPFTEDDAADPNDSDIDESSETD 1306
 DB 1143 FLKVAESGVDAETSDGTLPPARRNRARG-DKQSLRPFTEDDAADPNDSDIDESSETD 1200
 QY 1307 LLSGMDKGSQYVGNKLTQOQFVALLMKRLILARRSKGFAQIVLPAYVVCALVPSL 1366
 DB 1201 QGSGPDVAG--RVQGMALTRQQLALRLKRLARRSRGLFAQIVLPALVGLALVPSL 1258
 QY 1367 IYPPGKXPSLEQWMTNEQYTFEVSNDAPEDTGLLELNLATFDPGFGTRCMEGNIPD 1426
 DB 1259 IYPPGKXPSLEQWMTNEQYTFEVSNDAPEDTGLLELNLATFDPGFGTRCMEGNIPD 1308
 QY 1427 TPCQAGEEBWTTAPVPTIMDFONGNTWONPSPACCCSSDKIKMLPVCPPAGGLIP 1486
 DB 1309 PVOQSSHRFSAPPEYAPAVAKVLASGNMTPESSPACCCSSDPGARRLPDCPAAAGGPP 1368
 QY 1487 POKKQNTADLIODLGRNIDSVLYVYTOITAKSLKNKIWNEFPYGFSGVSGVNTQALP 1546
 DB 1369 POAVNGSEVYONLGRNIDSVLYVYTOITAKSLKNKIWNEFPYGFSGVSGVNTQALP 1427
 QY 1547 PSQAEVDAIKQKKHILAKLAKOSSADRFNLSLGRFMTGLDTRNNYKWNENKGMHAISFL 1606
 DB 1428 SCQELGRSVEELMALISPLPGALDRVLRNLTAHSHSDIADDSLIKWNENKGMHMAFV 1487
 QY 1607 NVINNAILRANLOKGENSHYGTAFNPNLITKQOLEVALMTSYVULVLSICVIFAMS 1666
 DB 1488 NNASNAIILRANLPGRPARHASTITLNLPLNTKQOLEVALMTSYVULVLSICVIFAMS 1547
 QY 1667 FVPASFVFLIOERYSKAKHLOFISGVPRVLYWLSNFWDMCMNVVPAATLVYIIFICPOQ 1726
 DB 1548 FVPASFVFLIOERYSKAKHLOFISGVPRVLYWLSNFWDMCMNVVPAATLVYIIFICPOQ 1607
 QY 1727 KSYVSTNLPVALLLLYGSITPLMPASGVKRTIPSTAYVYLVSVNLFINGINSVATF 1786
 DB 1608 RAYVAPANLPALLLLLYGWSITPLMPASGVKRTIPSTAYVYLVSVNLFINGINSVATF 1667
 QY 1787 VLELFTDNKLNINILKSVFLIFPHFCLGRGLDMVYVNOAMADALEBFGENRFPVPSLW 1846

```

Db 1668 VLEFSPDKLOEVRSLKOVFLIPHPOLGGLDMVRNOMADAFRLDROQSPRLW 1727
QY 1847 DLVGRNLFAMAVEGVFELLTVLQYRFFIRPRPVNAKLSPDLNDEDEVDREORILDDG 1906
Db 1728 EVGKNLLAMVIOGRLPFLFTLLQHSRLPLPQPRVRSIPLGGEEDVDARERERVQGA 1787
QY 1907 GQNDILEKELTKYRKRRAVDRICVGPFGCEFGLLGVNGAGKSTKMLTGTDTV 1966
Db 1788 TQGGVVLVRLNLTQVYKQGRMPADRLDGLPFGCEFGLLGVNGAGKSTRTMVGDTIAS 1847
QY 1967 RGDALFNKSLTSLNHEHONMGYCPQFDATITELLTGREHEHFPALLRGYRPEKGVKVE 2026
Db 1848 RGEAVLNGHSHVAREPSAHLMSGCPQSDAFELLTGREHLLARLGRVPEAOVQTAG 1907
QY 2027 WAIKRLGLVYKGYEAGYSGNKRKLSTAMALLGPPVVELDEPTTGMDPKARFLMNC 2086
Db 1908 SGLARLGLSWYADRPAGTYSGNKRKLATATLALVGDPAVVELDEPTTGMDPSARFLMNS 1967
QY 2087 ALSVYKGRSVYLLSHMEDEEALCTMALMNVNGRFGCLSVQHLKRRFGDGTIYVRIA 2146
Db 1968 LLAVVREGSRVYLLSHMEDEEALCSRLALMVNGRFGCLSPDHLKGRFAAGHTLRLVP 2027
QY 2147 GSNPDLKPVDFGLAPPGSVYKKEHNNMLQYOL-PSLSLARIFSTLSQSKRLHIED 2205
Db 2028 AARS--QPAALFAVAFEPFSGSELRAHGRRLRFQLPFGRCALARVFEELAVHGAHEVED 2085
QY 2206 YSVSQTLTLDVYFVFAKQSDDDHLKDLISLKNQTV-VDAVAV-----LTSELDQEKV 2257
Db 2086 FSVSQTLMEVFLYFSKQDKDE---DTERQKAGVGVDEAPGLQHPKRVSQGLDEPSTA 2142
QY 2258 ES 2259
Db 2143 FT 2144

RESULT 6
Q9NR73 PRELIMINARY; PRT: 2146 AA.
ID Q9NR73:
AC Q9NR73:
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE MACROPHAGE ABC TRANSPORTER.
GN ABCA7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE-20334305; PubMed-10873640;
RA Kaminski W.E., Orso E., Diederich W., Klucken J., Drobnik W.,
RA Schmitz G.,
RT "Identification of a Novel Human Sterol-Sensitive ATP-Binding Cassette
RT Transporter (ABCA7).";
RL Biochem. Biophys. Res. Commun. 273:532-538(2000).
DR EMBL: AF250238; AAF85794.1; -.
DR InterPro: IPR003439; AAA.
DR InterPro: IPR003439; ABC_transport.
DR InterPro: IPR001687; ATP_GTP_A.
DR Pfam: PF00005; ABC_tran; 2.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
KW ATP-binding.
SQ
SEQUENCE 2146 AA: 234469 MW: 67916EB2D75FFOD CRC64;

```

```

Query Match 48.9%; Score 5763.5; DB 4; Length 2146;
Best local similarity 50.2%; Pred. No. 0;
Matches 1146; Conservative 308; Mismatches 607; Indels 161; Gaps 26;

```

```

QY 1 MACQWRLRLKLNKLTFRRRQTCOLLLEVAWPLFTLLISVRLSYPRYEQHECHFPNKA 60
Db 1 MAFWTQPLMMLKNNFMYRRRQPVQLLELLMPLFLFTLLVAVRHSHPLLEHHECHFPNKP 60
QY 61 MSPAGLTVMOGICIANNPFRPTPGAPGVGNFNKSIYARLPSDARRLLYSQDVT 120
Db 61 LPSAGTVPMLOGLICVNNVTCPPQLTPGEBPRLNPNFNDISVRLDAKRYVLGASASAR 120
QY 121 SMKMRKVYRTLOQIKKSSNNKLQDLVDNTEFSGFVHNLKSTYDVKMLRADVITIA 180
Db 121 TLAGLGLATILAAARSTQ-----PQPKQSTLEPRL-- 154
QY 181 KVFLOGYQLHTSLGSKSSEMIQDGOVSELGLPKEKILAAAEVRLSRNMILKPI 240
Db 155 -----DVAEL-----LTSIL 164
QY 241 RLINSTPPSKELAEATITLHSLGTLAQELFSRMSMDMQEVMFLTNSSSSSTQI 300
Db 165 RL--ESLGLAQOAPLHSLLEAEDLAQELALRSLVEL--ALLQRPRTSGPLEL 219
QY 301 YQAVSRIVCGHPEGGLKIKSLNMYEDNNYKALFPGNGTEDEDAETFYDNTTPYCNDLMK 360
Db 220 ---LSBALCSVGRSPSTVGPLNMYEASDLMELV---QPEESALPPSSLSPPACSELIG 272
QY 361 NLESSPLSRIKALKPLVGLKILYTPPTPATROYMAEVNKTPOELAVFHDLQGMWELLS 420
Db 273 ALDSHPLSLRLMRRLKPLTGKILFLAPDTPFRKLAQVNRFEETLRLRYREVEMIG 332
QY 421 PKIWTFMESQMDVYRMLDSDRDNDHFWEQDLQDLMDTADIVAFLLKHPEDVOS---- 476
Db 333 PRIFTFMDSSNVAMIQRLQMDQDCR--RQPPGGRD-----HMBALSTLDP 379
QY 477 -SNGSVYTWREAFNETNOAIRTISRMECVNLKLEPATEVWLINKSMELDERKFWAG 535
Db 380 GSGG--YSWQDAHADYGHVLTGVTBCLSLDKLEAPSEALVSRALQLEAHERFVAG 437
QY 536 IYFTGTGTSIELPH-----HKYKIRMDIDNVERTNKIKQYMPGGRADPEEMR 587
Db 438 VVFLQPEDSSDPTHEPTPDGLGPHVRIKIRMDIDVTPTNKRIRDEFMGPGAAPLDPDL 497
QY 588 YWGGFAVYLDVDEQAIIKRLVLTGTEKTVGYWQMPYCYVDLFLRVMSMPLFMTLA 647
Db 498 YWGGFVYIQLDLYERAARVLSGANPRAGVILQCMHYCYVDVFLRLVLSLPLFLTLA 557
QY 648 WLYSAVVIKGLIVYKKEARKLKTMRIMGLDMSIIMFSNFISLLPLVLSAGLLVILKLG 707
Db 558 WLYSVTLVYKAVVREKETRLRDMRAGLSRAVIMLGMFLSLGPFLLSALVILVILKLG 617
QY 708 NLLPYSDPSVYVFLSVFAVYVITLQCFILSTFSEFANLAAACGGITVTLVPLVLCVAV 767
Db 618 DILPISHQGVYFLAAARAVATVOSFLLSAFSRAANLAAACGGIATFSLVPLVLCVAV 677
QY 768 QDYVFTLKIFASLLSPVAFGCEYFALFBEQIGVQWMDLFPSPVEDEDFNLTTISM 827
Db 678 RDLRLPAGGRVAAASLLPVAFGGCESTLALBDEQGAQMHVNGVRPT ADVESLAQVSG 736
QY 828 MLFDPLFLGVMWYLEAVFPQOYIGIPRWYTPCKTSYFGESEDSKSPGNSQKRMSEIC 887
Db 737 LLLDALYGLAMWYLEAVCPQOYIGIPRWYTPCKTSYFGESEDSKSPGNSQKRMSEIC 887
QY 888 MEEPTTHLKIGSIONLVKYVRDGMKVAVDGLALNFEQGTITSLGHNGAGKTTMSILT 947
Db 796 VBEAPRGLSPGVSVSLKRRPGSQPRLRLSLDFQGHITLALGHNGAGKTTTSLIS 855
QY 948 GLPPTSGTAVYILGKDIRESEKSTIRQNVGCPQHNVLFDMLTVBEHITFYARLKLSEKH 1007
Db 856 GLFPSSGSAFILLGHVYSSMAAIRPHIGVCPQYNNVLFMLTVDEHWFYGRLLGSLAAV 915
QY 1008 VKAEMQMALDVGLPSSKSLKSTQSOLSGQMOKRISVLAFAVGSQVYVILDEPTAGVDPYS 1067
Db 916 VGPEDDRLLQDVGL-VSKQSVQTRHLSGQMOKRISVLAFAVGSQVYVILDEPTAGVDPAS 974

```

1068 RGIETELLKTRQGTITLLSHHDEADYLDRIAIIISHGLCCVSSSLFLKNOLGTGY 1127
 1128 LTLVKKDVESSLSQSRNSSSTFVSYLTKEDSVSSQSSDAGLSHDSHPLTIDVSAISMII 1187
 1035 LTLVAKRLPLTTN-----EKADTMEGSDVTRQKKNKSSQSRGTPOLLALV 1082
 1168 RKHVSEARLVEDIGHETLYVPEYAKGAFVLFHEIDRLSDIGISSYGISETTEEEI 1247
 1083 QHVVPGARLVEPLPHELVLPYTGADHGSFATLRELDTRLAEIURLTGYSIGDSTLEEI 1142
 1248 FLKVAEESVDAEISDGTLPARRNRAG-DKOSCLRFTEEDADPMDSDIDPESRETD 1306
 1143 FLKVAEESVDAEISDGTLPARRNRAG-DKOSCLRFTEEDADPMDSDIDPESRETD 1200
 1307 LLSGMDGKSYOVKGMKLTQOQFVALLKRLILARRSRKGFQVLPVAVFCALVPSL 1366
 1201 QGSGPDVAG--RVQGMALTRQQLALLKRLFLARRSRKGFQVLPVAVFCALVPSL 1258
 1367 IYPPFGKPSLELOPMWYNEQYTFVSNDAPEDTGTELLNALTTRPGGTGCMENRIPD 1426
 1259 IYPPFGKPSLELOPMWYNEQYTFVSNDAPEDTGTELLNALTTRPGGTGCMENRIPD 1308
 1427 TPCQAGEEEMTAPVOTIMDLFONGNMTMOPSPACOCSSDKIKMLPVCPPGAGLPP 1486
 1309 PVPQSSSHFSAPEYPAEYAKVLAGSNMTPESSPACOCSSDKIKMLPVCPPGAGLPP 1368
 1487 PORKONTADIIODLTGRNISDYLVKTYOIIAKSLKNITWNEFRYGGFSLGVSNTQALP 1546
 1369 PAVNTSGSEVYONLGRNISDYLVKTYOIIAKSLKNITWNEFRYGGFSLGVSNTQALP 1427
 1547 PGEVNDATKOKKXKHLAKDSSADREFLNSLGRFMTGIDTRNNVYVFNKMKWHMIISSL 1606
 1428 SCQELGRSEVEELMALISPLPGALDVLKNTLMAHSDLAQDSLKIKWENKMHSHSAVAV 1487
 1607 NVYNNAILRANLQKGENPESHGITAFAFNHPLNTKQOLSEVALMTTSVDVLSICVIFAMS 1666
 1488 NNASNAILRAHLRPGARARAHSTITLNLHPLNTKQOLSEVALMTTSVDVLSICVIFAMS 1547
 1667 FVPASFTVLIEREYVRAHQLQMGSLPTLYWLNFMIDMCNLYLPACIIVLILFAFOQ 1607
 1727 KSVVSTNLPVATLILLYGWSITPLMYPASFEKIPSTAYAVLVSFNLTGINSVATF 1786
 1608 RAYVAANRPALELLLELGLWSITPLMYPASFEKIPSTAYAVLVSFNLTGINSVATF 1667
 1787 VLELFTDNKLNINILKSVFLIFPHFCGLRGLIDMVKQAMADALEREGENREVSPLSM 1846
 1668 VLELFTDNKLNINILKSVFLIFPHFCGLRGLIDMVKQAMADALEREGENREVSPLSM 1727
 1847 DLYGRNLFMAAVGCVFELITVLIQYRFFIRPRPVAKISPLNDEBEDVRRERQRLDGG 1906
 1728 EYVGNKMLAMVIOGPLEFTLLQHSRLPQPRVRSPLGEEBEDVAREKEREVVOGA 1787
 1907 GOMDILEIKELFTKIRRRKPAVDRIQVLPCEPCGLICVNGAGKSTFEKMTGDTYT 1966
 1788 TQGDVILVRLUTYVYGGQRPAVDRIQVLPCEPCGLICVNGAGKSTFEKMTGDTYT 1847
 1967 RGDAPFNKNSIISNIHEVHONMGYCPQFDATTELLTGREHVEFALLRGVKEKVGKE 2026
 1848 RGEVILAGHVSAREPFAHLSMGYCPQSDAIFELLTGREHVEFALLRGVKEKVGKE 1907
 2027 WAIKRLGLVYGEKYAGNAGSGKRLSTAMALIGRPVYFLEDEPTTGMDPKRRRLMNC 2086
 1908 SGLARLGLSMYADRPAGYSGGNKRLATALALVADPAVYFLEDEPTTGMDPKRRRLMNC 1967
 2087 ALSVAGRSVNLTSMSMECEALCYRMAIMVNGRRCGLSVOHILNKRDCGDIIVVIRA 2146
 1968 LLAIVRGRSVNLTSMSMECEALCYRMAIMVNGRRCGLSVOHILNKRDCGDIIVVIRA 2027
 2147 GSNPDLKPVODFFGLAPGGSVLEKEHRLMLQYOL-PSLSLSLARIFSLSQSKRLHIED 2205

2028 AARS--QPAAPFAAEEPPSELRHAGGRRLRFQLEPGRCALARVGEALVHGAHEVED 2085
 2206 YVSQTLIDQVFNFAKQSDDDLKDLKSLKNOTV-VDAV-----LTSFLQDEKKA 2257
 2086 FSVSQTLMEVFLYFSKQCKDE---DTEBQKEAGVGVDPAFGLQHPKRVSOFLDDPSTA 2142
 2258 ES 2259
 2143 ET 2144

RESULT 7
 ID 091V24 PRELIMINARY; PRT: 2159 AA.
 AC 091V24;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ATP-BINDING CASSETTE TRANSPORTER SUB-FAMILY A MEMBER 7.
 OS ABCA7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SMPAIN-OL129, AND DBA/2;
 RX MEDLINE-2132888; PubMed-11435699;
 RA Brocardo C., Osorio J., Luciani M.-F., Schrieml L.M., Prades C.,
 RA Shulen S., Arroul I., Naudin L., Latareque C., Rosier M., Jordan B.,
 RA Maitel M.G., Dean M., Denefle P., Chimi G.
 RT "Comparative analysis of the promoter structure and genomic
 RT organization of the human and mouse ABCA7 gene encoding a novel ABCA
 RT transporter.";
 RL Cytogenet. Cell Genet. 92:264-270(2001).
 DR EMBL: AF287142; AAK56863.1;
 DR EMBL: AF287141; AAK56862.1;
 KW ATP-binding.
 SO SEQUENCE 2159 AA; 236882 MW; CD2B3FE0D88822B CRC64;

Query Match 48.6%; Score 5732; DB 11; Length 2159;
 Best Local Similarity 50.6%; Pred. No. 0;
 Matches 1144; Conservative 362; Mismatches 581; Indels 176; Gaps 31;

QY 1 MACPOLMLLMKNTERRROTCOLLEVAMPDLFFILISVRLSYPRYEOHECFPKA 60
 DB 1 MALGTOLMLLMKNTYRRROPQLVLELWPLFFLIVAVRSHRPLEHNECHFRKP 60
 QY 61 MSACTLPWVOGIIICNANNPCFRYPTPEAGVYGNFNKSIIVARLFSRARLLYSOKDT 120
 DB 61 LPSACTVWIGLGVNANNVNSCFQHPPTPEKPGVLSNFKDSLISRLADTRVL---GGH 116
 QY 121 SKDKRKVLRLTQIKKSSNLKODFLVDNETSGFLYHNLSPKSYVDMKLADYLH 180
 DB 117 STODMIDALGKILPV----- 131
 QY 181 KYFLQYQLHLTSLNGSKSEEMIQLOEVESELGLPKKELAAEYVL-RSNMDILKPI 239
 DB 132 -----LRAVGGARPOE---SQPTSQ--GSTYKLL---EKLQASASD---PV 169
 QY 240 LKTLNSTSPFSKELAEATKTLHSLAGTLAGLQELFSMRSMUSDROEWMFLVYNNSSSTQ 299
 DB 170 L-----GQAGDSMRKPSDAIRDLAQELTLPISLMELR--ALLRPRGSAGSL 215
 QY 300 IYQAVSRIVC---GHPGEGGLIKSLNMYEDNNKALFGGNGTEDEATTFDNTTPYCN 356
 DB 216 L---VSEALCSTKGPSSPGCL---SLNMYEANOQLEMG---DEVAPALDNTSPACS 265
 QY 357 DLMKNLESSPSIRIIMKLLPLLVGKILYTPPTPAVROVAEYVNTFOELVHDLBGM 416
 DB 266 EFGVGLDHPVSRILMLRKLPLITLCKIIFAPDNTTRKLMQVNOVOTFEELALLRDLHLM 325

QY 417 EELSPKMTWENSOEDMLVRLDSDNDHFWEQQLDGLDWTADIVAFIAHNPEDVOS 476
 Db 326 GVLSPQIFNFMNDSTNVAMLORLLDVGTGO--RQOTPRRQKLEALDKDL-----DP 376
 QY 477 SNGSVNWRFAFNFTNOAIFRTISRFMCVNLKLEPIATVWMLINKSMELDERKKTWAGI 536
 Db 377 SRGG-YSMREAHADMGRLAGITLCOOMECSVDKLEAVSSEALVSRALTEGRRKIMAGI 435
 QY 537 VFTG-----ITPGSIE-----LPHHKKYKIRMDINVERTNKIDGYMDPGRRPDEMDRY 588
 Db 436 VFLSPREHLPDSELSPALSPGHLEKIRMDIDVTRKTKIRKFPNDPGSADPMDLRK 495
 QY 589 VMGSAFLDQVBOAIIIRVLTGEKTYVMQMPYPCYVDIIFLVMSSMDLFWTLAW 648
 Db 496 VMGSAFLDQVBOAIIIRVLTGEKTYVMQMPYPCYVDIIFLVMSSMDLFWTLAW 555
 QY 649 IYSAVAIIKIGIYEKEARLEKTRIMRIMGDINSILFMSWTSLLPLVSAGLLVIIKLG 708
 Db 556 IYSAVAIIKIGIYEKEARLEKTRIMRIMGDINSILFMSWTSLLPLVSAGLLVIIKLG 615
 QY 709 LLDPSDVSVEFLSVFAVVTIIQCELIISTLFSRANLAAAGGIYFTLYLPVLCVANO 768
 Db 616 ILPSHVPVIFLFLAFAVATVQSFLLSAFGRANLAAAGGLAVFALYLPVLCVANO 675
 QY 769 DYGFITLIKIFASLSPAFGEFGEFALPEOGIGVOMNLFSPVEDGCFNLTISIM 828
 Db 676 ERLHGLGLASLSPAFGEFGEFALPEOGIGVOMNLFSPVEDGCFNLTISIM 734
 QY 829 LDFPLVGVMTWYIEAVFPQGYIPRPVYFCTKSYWFGESDEKHPGNSOKRMSEICM 888
 Db 735 LLDVAVIIGLAWYIEAVFPQGYIPRPVYFCTKSYWFGESDEKHPGNSOKRMSEICM 793
 QY 889 EEPETHLKGIVSTIONLVKYVRDGMKAVVGLALNFEQGITSLFGLNGAGKTTMSILFG 948
 Db 794 EEPETHLKGIVSTIONLVKYVRDGMKAVVGLALNFEQGITSLFGLNGAGKTTMSILFG 853
 QY 949 LPPPTGATVILIKDIRSEMSTIRONMGVCPQHNVLFDMITVEEHTMFARLKISEKIV 1008
 Db 854 LPPSSGASITLGHVQYTMMAIRPHLIGICPOYNVLFDMITVEEHTMFARLKISEKIV 913
 QY 1009 KALMEDMALDVGLPSSKLSKTSQLSGMOQKLSVALAFVSGSKVYLIDEPAVDPPYSR 1068
 Db 914 GPERELIRHVG-LTKRQYTRHLSGMOQKLSVALAFVSGSKVYLIDEPAVDPPYSR 972
 QY 1069 RGIMELLKYRGRTITLSTHMDADVLDGDRITAIISHGKLCOCVSSPLRKLKNOIGGYTL 1128
 Db 973 RGIMELLKYRGRTITLSTHMDADVLDGDRITAIISHGKLCOCVSSPLRKLKNOIGGYTL 1032
 QY 1129 TLVKVYESSLSGCRNSSSTVYLKEDSVSSQSSDAGLSDHESDT----- 1175
 Db 1033 TLVKVYESSLSGCRNSSSTVYLKEDSVSSQSSDAGLSDHESDT----- 1081
 QY 1176 -----LTIIVSALSNLIRKHVSEARLVEDIGHEITVYLPYEAKEGAFVLLFHEIDR 1228
 Db 1082 PARGANPIPTPARILIEVQOHPCQAOVEDLPHELLVLPYAGALDGSFAVFELODQ 1141
 QY 1229 LSDLGISYGISSETLEELIFLVAEESVDAETSDGTLPARNRRAFGKOSCL-RPFE 1287
 Db 1142 LELIGITGIGISDTNLEIFLKVVEDAHREGDSRQHLR-----TCTQPTPG 1191
 QY 1288 DDAADPNDDIDPESEHEDULLSGMCKGSYQKGMKLTQOQVALLMKRLIARSKRGF 1347
 Db 1192 PHSVLEHNEMLAQ-----GL-APNAAOVQGMVLTQOQVALLMKRLIARSKRGF 1242
 QY 1348 FAQIVLPAFVAGIALVFLPVPFGKYSLELOPMVYNEQVYFVNSDAPEDTGTLELNA 1407
 Db 1243 FAQIVLPAFVAGIALVFLPVPFGKYSLELOPMVYNEQVYFVNSDAPEDTGTLELNA 1302
 QY 1408 LKRDGEGFRCEKGNIPPTPOAGEEKTAP-VQGITMDFONGNNTMONPSPACCS 1466
 Db 1303 LKRDGEGFRCEKGNIPPTPOAGEEKTAP-VQGITMDFONGNNTMONPSPACCS 1362

QY 1467 SDKIKKMLPVCPPGAGLPPPOKONFADLILODLTGRNISDLYKTYOIIAKSLKNIK 1526
 Db 1363 QGARRILPDCPAGAGGPPPPAVAGLEAVQNLGRNVSDPIYKTYSLVRGLKTKWK 1422
 QY 1527 VNEFRGFSLSGVSTQALPSPQEVNDALIKONKHKLAKDSSADRFNLSGRPTGLDT 1586
 Db 1423 VDEVRGFSLSG-GRDPLPTEGHEVVRTLAEIRALSPQGNALDRILNLTQWALGIDA 1481
 QY 1587 RNNVWVFNKKNHAISSFLVNTNAILRANLOKENSNGITAFNPLVLTQOQSEV 1646
 Db 1482 RNSLWVFNKKNHAISSFLVNTNAILRANLOKENSNGITAFNPLVLTQOQSEV 1541
 QY 1647 ALMTSSVDVLSICVIFAMSPVASEVVELIOERYSKAKHLOPISGVKPVYIWLSPFVMD 1706
 Db 1542 TLIASVDVLSICVIFAMSPVASEVVELIOERYSKAKHLOPISGVKPVYIWLSPFVMD 1601
 QY 1707 MGNVVPATVITVIFTCQOQSYSTVTLPVYALALLLYGMSITPLMPASPFVKIDSTA 1766
 Db 1602 MGNVVPATVITVIFTCQOQSYSTVTLPVYALALLLYGMSITPLMPASPFVKIDSTA 1661
 QY 1767 YVLTSMVLTGINGSVATFVLETFEDNKLNNINDILKSVPFLPHPCGLGLDMVKNQ 1826
 Db 1662 YVLTSMVLTGINGSVATFVLETFEDNKLNNINDILKSVPFLPHPCGLGLDMVKNQ 1721
 QY 1827 AMADALEPGENREVSPLSMDIVGRNLEFAMAVEGVFELITVLIQYREFIRPREVNAKS 1886
 Db 1722 AMADALEPGENREVSPLSMDIVGRNLEFAMAVEGVFELITVLIQYREFIRPREVNAKS 1781
 QY 1887 PLNDEDEVRRERKORILLEGONDIETELKELTKYRRKRPAVARICVDPGCGFLIG 1946
 Db 1782 PLNDEDEVRRERKORILLEGONDIETELKELTKYRRKRPAVARICVDPGCGFLIG 1841
 QY 1947 VNGACKSTFPMVLTGDTVTYRGDAFLNKSILSNIEHVONMGYPOFDAITELLTGREH 2006
 Db 1842 VNGACKSTFPMVLTGDTVTYRGDAFLNKSILSNIEHVONMGYPOFDAITELLTGREH 1901
 QY 2007 VEEFALLGPEKEVKGKGAEMAIRKLGVYKGEYAGYSGGNRKISTMALIGRPVY 2066
 Db 1902 LELPARLGVBEAOVAGTALSGLVRLGPSTADRPAGTSGGNRKISTMALIGRPVY 1961
 QY 2067 FLDEPTTGMDEKARFLMNCALSVKKGSRVYLTSHSMECEALCTPMALMVNGRFLC 2126
 Db 1962 FLDEPTTGMDEKARFLMNCALSVKKGSRVYLTSHSMECEALCTPMALMVNGRFLC 2021
 QY 2127 SVOHLKNGRGGTYIVRIAGSNPDLKPVODFCLAPPGVSLKKNHMTQYL-PSLS 2185
 Db 2022 SVOHLKNGRGGTYIVRIAGSNPDLKPVODFCLAPPGVSLKKNHMTQYL-PSLS 2079
 QY 2186 SIARIFSLISQSKRRHLIEDSVSQTLIDQVVFARQSDDD 2228
 Db 2080 TLTFRVRELAAGRAHVEDPSVQTLLEVLYLFSKQGE 2122

RESULT 8
 ID Q96S58 PRELIMINARY; PRT; 2008 AA.
 AC Q96S58;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE ABCA-SSN.
 GN ABCA/ABCA-SSN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21255283; PubMed=11355874;
 RA Tanaka A., Ikeda Y., Abe-Dohmae S., Atrakawa R., Sadanami K.,
 RA Kidera A., Nakagawa S., Nagase T., Aoki R., Kioka N., Amachi T.,
 RA Yokoyama S., Ueda K.,
 RT "Human ABCA1 Contains a Large Amino-Terminal Extracellular Domain


```

QY 2259 S 2259
Db 2006 T 2006

RESULT 9
Q9ESR9 PRELIMINARY; PRT; 2434 AA.
ID Q9ESR9
AC Q9ESR9;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ABC2.
GN ABC2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=20427713; PubMed=10970803;
RA Zhao L., Zhou C., Tanaka A., Nakata M., Hirabayashi T., Amachi T.,
RA Shioda S., Ueda K., Inagaki N.;
RT "Cloning, characterization and tissue distribution of the rat ATP-
RT binding cassette (ABC) transporter ABC2/ABCA2."
RL Biochem. J. 350:865-872(2000).
DR EMBL; AB037937; BAB16596.1; -.
DR InterPro; IPR003593; AAA.
DR InterPro; IPR003439; ABC_Transport.
DR Pfam; PF00005; ABC_tran; 2.
DR SMART; SM00382; AAA; 2.
DR ATP-binding.
KW SEQUENCE
SQ 2434 AA; 270925 MW; CD424A9C4F63513F CRC64;

Query Match 36.0%; Score 4249.5; DB 11; Length 2434;
Best Local Similarity 39.1%; Pred. No. 9.4e-272;
Matches 992; Conservative 346; Mismatches 713; Indels 483; Gaps 60;

QY 6 QLRLLKNTLERRQTCQLLEVAWPLFTLLISVRLSYPRYEHCHRPKNKAMPAG 65
Db 6 QLRLLKNTLERRQTCQLLEVAWPLFTLLISVRLSYPRYEHCHRPKNKAMPAG 65
QY 125 MRKVLRTLQ-----IKSSSNLKLQDFIVNETFSGFLYHNLSLPKST 168
Db 125 MRKVLRTLQ-----IKSSSNLKLQDFIVNETFSGFLYHNLSLPKST 168
QY 116 LGSLEALHQLRALSSGPGWESHARPAVSSPLSDVARDKRELMLFMONLSLPNST 175
Db 116 LGSLEALHQLRALSSGPGWESHARPAVSSPLSDVARDKRELMLFMONLSLPNST 175
QY 169 VDKMLRADY----- 177
Db 169 VDKMLRADY----- 177
QY 176 AQAALLARVPSEYRLLFGLPLDGLKFLKQEPWHLGNSPLFQMEELLAPALLE 235
Db 176 AQAALLARVPSEYRLLFGLPLDGLKFLKQEPWHLGNSPLFQMEELLAPALLE 235
QY 178 -----IL-----HKVFLQGYOLHLTSLGSKSEEMIQGLDQVESELGLPK 219
Db 178 -----IL-----HKVFLQGYOLHLTSLGSKSEEMIQGLDQVESELGLPK 219
QY 220 EKLAARVLRNSMDLKLRLTL-----NSTSPFSKLEAEATKLLHSLGLTIAOELFS 274
Db 220 EKLAARVLRNSMDLKLRLTL-----NSTSPFSKLEAEATKLLHSLGLTIAOELFS 274
QY 283 -----ATE-----LRNOLDIAK-IAOQLGFNVPGSDPQAPSPQSLALIGDLLVQVLIQD 335
Db 283 -----ATE-----LRNOLDIAK-IAOQLGFNVPGSDPQAPSPQSLALIGDLLVQVLIQD 335
QY 275 MRKSDMRQVEMFLTNSSSSSTQIQAIVSYVCGHPEGGGLKIKSLNMYEDNNKALF 334
Db 275 MRKSDMRQVEMFLTNSSSSSTQIQAIVSYVCGHPEGGGLKIKSLNMYEDNNKALF 334
QY 336 V-----DVLALALLLPQACAGRAPAPQ-----GSPSGPA-----NSTGVA 373
Db 336 V-----DVLALALLLPQACAGRAPAPQ-----GSPSGPA-----NSTGVA 373
QY 335 GGNTEEDAEFTFYDNTTPPCNDLMLKTLSSPLRIIWKALKPLVG----- 381
Db 335 GGNTEEDAEFTFYDNTTPPCNDLMLKTLSSPLRIIWKALKPLVG----- 381
QY 374 ANGPNTTVEEGTOSPTVTPASPTLQOGCSAFVQ-ILWAGLOPILCGNNNTTEPEALRNG 431
Db 374 ANGPNTTVEEGTOSPTVTPASPTLQOGCSAFVQ-ILWAGLOPILCGNNNTTEPEALRNG 431

```

```

QY 382 -----KILYTPDTPATROVAEKNKTOELAVFHDEGM 415
Db 382 -----KILYTPDTPATROVAEKNKTOELAVFHDEGM 415
QY 432 NMSSLGFTSKEQKRNGLLVHMTSNPKLLIYAPAGSADHVIILKANETFAVGNVTHYAOV 491
Db 432 NMSSLGFTSKEQKRNGLLVHMTSNPKLLIYAPAGSADHVIILKANETFAVGNVTHYAOV 491
QY 416 WEELSPKTIWENSOEMDLVRLDSDRNDHFWEQQLDGLDWTKQDIYAFLAKPEDVQ 475
Db 416 WEELSPKTIWENSOEMDLVRLDSDRNDHFWEQQLDGLDWTKQDIYAFLAKPEDVQ 475
QY 492 WNIWISAIRSFLE-----OGRLOQH-----LHM-LQOYVADLRLEPEAMN 530
Db 492 WNIWISAIRSFLE-----OGRLOQH-----LHM-LQOYVADLRLEPEAMN 530
QY 476 SS-----NGSVYTWREAFENETNOAIRTS-----PRMECVNKLKLP 512
Db 476 SS-----NGSVYTWREAFENETNOAIRTS-----PRMECVNKLKLP 512
QY 531 LSLDELPRALRLDYPSLPNGTALL-----QOLDITDANACGMIDPMKSVSDIRKG 581
Db 531 LSLDELPRALRLDYPSLPNGTALL-----QOLDITDANACGMIDPMKSVSDIRKG 581
QY 513 IATEVWLINKSME--LDERKFMAGIVFTGTPSGTELPHHYKTKRIDIDNVERTNKK 570
Db 513 IATEVWLINKSME--LDERKFMAGIVFTGTPSGTELPHHYKTKRIDIDNVERTNKK 570
QY 582 FPDEESIVVTLINQAVODWVFAVSIPTQRDGS--LPHVHYKIKRONSSPTEKTEIR 639
Db 582 FPDEESIVVTLINQAVODWVFAVSIPTQRDGS--LPHVHYKIKRONSSPTEKTEIR 639
QY 571 DGWDGPRPADPEEDMRYYWGFAVLQDVBEAIIIRVLGTG- KRTGYVMQOMPFCYVD 629
Db 571 DGWDGPRPADPEEDMRYYWGFAVLQDVBEAIIIRVLGTG- KRTGYVMQOMPFCYVD 629
QY 640 RAYWRPGRPTNG--GREYFLYGFVWIDMIERAILINTFEVGHVPEPQVOMFPYPCYTR 696
Db 640 RAYWRPGRPTNG--GREYFLYGFVWIDMIERAILINTFEVGHVPEPQVOMFPYPCYTR 696
QY 630 DIFLRVMSRSMPLFTLWAVIYSAVILKGIYKEARKLKTMRIGLDSILFMSFTSS 689
Db 630 DIFLRVMSRSMPLFTLWAVIYSAVILKGIYKEARKLKTMRIGLDSILFMSFTSS 689
QY 697 DDFLFVTEHMDPLCWLIVSVVAMTQIIVAEKHLKLEVKMTGLNNAVHWAMFTTG 756
Db 697 DDFLFVTEHMDPLCWLIVSVVAMTQIIVAEKHLKLEVKMTGLNNAVHWAMFTTG 756
QY 690 LIPFLVAGLLVYILKGLMLPYSDPSVYFVFLSPAVVTIIOCLISTLSRANLAAAC 749
Db 690 LIPFLVAGLLVYILKGLMLPYSDPSVYFVFLSPAVVTIIOCLISTLSRANLAAAC 749
QY 757 FQLSISVLTALAILKYGGVILMHSVLIIMFLAYAAVATIFCPLSVLSKATLASAC 816
Db 757 FQLSISVLTALAILKYGGVILMHSVLIIMFLAYAAVATIFCPLSVLSKATLASAC 816
QY 750 GGIIFYTYLLPYVLVC-----VAMODYVGFTEKIFSLSPVFGGFCYCFALFEEQIGV 804
Db 750 GGIIFYTYLLPYVLVC-----VAMODYVGFTEKIFSLSPVFGGFCYCFALFEEQIGV 804
QY 817 GGIIFYLVYPIYVIAIREVAHDKITAE-KIASIMSTTAFGLGSKYFALYEVAGGI 875
Db 817 GGIIFYLVYPIYVIAIREVAHDKITAE-KIASIMSTTAFGLGSKYFALYEVAGGI 875
QY 805 QWDNLFPESVVEEDENLTTSISMMLPDTFLYGVMTWYIEAVPFGOYGIIPRWYPCYKSY 864
Db 805 QWDNLFPESVVEEDENLTTSISMMLPDTFLYGVMTWYIEAVPFGOYGIIPRWYPCYKSY 864
QY 876 OWHTEFSQSPVEGDDNLLAVTLMVDIVVGVLTWYIEAVPFGYGPFRWYFPLQKSY 935
Db 876 OWHTEFSQSPVEGDDNLLAVTLMVDIVVGVLTWYIEAVPFGYGPFRWYFPLQKSY 935
QY 865 WFEGE--ESDEKSHPGSNOKRMS-----ETC-----MEEPETHLKLIGSIONL 904
Db 865 WFEGE--ESDEKSHPGSNOKRMS-----ETC-----MEEPETHLKLIGSIONL 904
QY 936 WLGSGTTEWMSWPAHAAPRLSWMEEDACAMESRHEETRGMEEPETHLPLVVCYKL 995
Db 936 WLGSGTTEWMSWPAHAAPRLSWMEEDACAMESRHEETRGMEEPETHLPLVVCYKL 995
QY 905 VVYVYRDMKVAVDGLALNFYEGQITSPFLHNGAGKTTMSITLGLPPTSGTAVIIGNDI 964
Db 905 VVYVYRDMKVAVDGLALNFYEGQITSPFLHNGAGKTTMSITLGLPPTSGTAVIIGNDI 964
QY 996 TKYKKDKKTLANKLSTLNLYENQVVSFLHNGAGKTTMSITLGLPPTSGSATIYHDI 1055
Db 996 TKYKKDKKTLANKLSTLNLYENQVVSFLHNGAGKTTMSITLGLPPTSGSATIYHDI 1055
QY 965 RSEKSTIRONLQVCPQHNVLPMLLVEEIRIYALKGLSEKHYAAEEMQALVDGLPSS 1024
Db 965 RSEKSTIRONLQVCPQHNVLPMLLVEEIRIYALKGLSEKHYAAEEMQALVDGLPSS 1024
QY 1056 KTEMEIRIKNLGMCPQHNVLPDQLTVEEHLWFYSRLKSMQAEIERKEMDKMIEDLEL-SN 1114
Db 1056 KTEMEIRIKNLGMCPQHNVLPDQLTVEEHLWFYSRLKSMQAEIERKEMDKMIEDLEL-SN 1114
QY 1025 KLSKTSQLSGGMQRKLSVALAFVVGSKVILDEPTAGVDPRYSGRIWELLKTYROGRTI 1084
Db 1025 KLSKTSQLSGGMQRKLSVALAFVVGSKVILDEPTAGVDPRYSGRIWELLKTYROGRTI 1084
QY 1115 KRHSIVQTLDSGGMKRLKLSALAFVVGSKVILDEPTAGVDPRYSGRIWELLKTYROGRTI 1174
Db 1115 KRHSIVQTLDSGGMKRLKLSALAFVVGSKVILDEPTAGVDPRYSGRIWELLKTYROGRTI 1174
QY 1085 ILSTHMDADVLDGRIALISHGKLCYGVSSLEFLKNOLGTVYTLVKKDYESSLSCRN 1144
Db 1085 ILSTHMDADVLDGRIALISHGKLCYGVSSLEFLKNOLGTVYTLVKKDYESSLSCRN 1144
QY 1175 LSTHMDADVLDGRIALISHGKLCYGVSSLEFLKNOLGTVYTLVKKDYESSLSCRN 1234
Db 1175 LSTHMDADVLDGRIALISHGKLCYGVSSLEFLKNOLGTVYTLVKKDYESSLSCRN 1234
QY 1145 SSSITVYLKEDDESQSSSDAGLSDHDSPTLTIDVANSILNIRKHYEALVIEDIGHEL 1204
Db 1145 SSSITVYLKEDDESQSSSDAGLSDHDSPTLTIDVANSILNIRKHYEALVIEDIGHEL 1204
QY 1235 MASSPSGRPOLNSCEMO-----VSQPIRKHVASSLLVSDSTTEL 1274
Db 1235 MASSPSGRPOLNSCEMO-----VSQPIRKHVASSLLVSDSTTEL 1274
QY 1205 TVVLYPEAKKEGAFVELFHEIDRLSDLGISYGISSETTELEIFLKAEE----- 1254
Db 1205 TVVLYPEAKKEGAFVELFHEIDRLSDLGISYGISSETTELEIFLKAEE----- 1254
QY 1275 SYILPSEAVKKAERFLPQGLEHSLDALHLSFGIMPTTLLEEVFLKSEEDQSLSENSAD 1334
Db 1275 SYILPSEAVKKAERFLPQGLEHSLDALHLSFGIMPTTLLEEVFLKSEEDQSLSENSAD 1334
QY 1255 -----SGVDA-ETSDGTL-----PARRNRA-FGDKOS 1280
Db 1255 -----SGVDA-ETSDGTL-----PARRNRA-FGDKOS 1280
QY 1335 VKESRKDALPGAEGTLAVESQAGNLARCSLEAQSASLOSASVSQASAGDEGAGYTGYG 1394
Db 1335 VKESRKDALPGAEGTLAVESQAGNLARCSLEAQSASLOSASVSQASAGDEGAGYTGYG 1394
QY 1281 CLRPTEDDADPNDSIDDPESRETDLSGMDGSGSYGVKMKTLQOQFALLMKRLILIA 1340
Db 1281 CLRPTEDDADPNDSIDDPESRETDLSGMDGSGSYGVKMKTLQOQFALLMKRLILIA 1340
QY 1395 DYRLPL-DNLQDPD--SVLSDEAEKALARY-GQSKRLLEGMWIKMQLFHLLVKKRHA 1450
Db 1395 DYRLPL-DNLQDPD--SVLSDEAEKALARY-GQSKRLLEGMWIKMQLFHLLVKKRHA 1450
QY 1341 RSRKGFPAQIIVPAVFCIALVFSLIIVPFGKYSLELQPMWINEQY-----FVS 1392
Db 1341 RSRKGFPAQIIVPAVFCIALVFSLIIVPFGKYSLELQPMWINEQY-----FVS 1392

```

```

1451 RNSALSOQLLPAPFVCVATVALSVPEIGDLPPLVLSQYH-NYTORGNFIPIAN 1509
1393 NDAPE-----DTGLELLNALTKDPGFGTCM----- 1419
1510 EERREYRLRLSPDAPQOLVTFRLPSGAGACVLKSPANGSLGPMNLSSGESRLAAR 1569
1420 -----EGNPI-----PD-----TTCQAGEEWTAP 1440
1570 FPDSCMESFTQGLPLSNFPPPPSPAPSDSPSPDEDSLLAMNTSLPPTAGPETWTAP 1629
1441 -VPOTIMOLFONGNMTMQNPSPACCCSDKIKMLPVCPPGAGLPPPOKONTDIIOD 1499
1630 SLPRVHEVYR-----CTCSAGCTFS---CPSSVGG-HPPOMKRVYTDILTD 1673
1500 LTRGNISDYLVTYVOIILAKSLKNKIMWNEFRYGGFSLGVSNTQALPPSOEVNDAIKOMK 1559
1674 TIGHNVSEVLEFTSDRF-----RLHRYGATITG-NIQKSTIPAPIGTRPPLMYR 1720
1560 KHLKLAKDSSADRFPLNSLGRFMTGLDTRNNVYVFNKNGMAHISSEFLVYNNALLRANIQ 1619
1721 K-----IAVRVACVLYNNKGYHSMPTYLNSLNAAILRANLP 1757
1620 KGE-NSHYGITAFNHPNLTKOOLSEVALMTSVDLVLSICVIFAMSVFPAFVFLIQ 1678
1758 KSKGNPAAYGITVTNHPMKTSASLS-LDYLOGDIDVYATFIYAMSVFPAFVFLIYA 1816
1679 ERYSKAKHLQFISGVKPVITWLSNFWDMCNVVPATVLIIFIGFOOKSVYSSNLPVL 1738
1817 EKSTAKHLQFISGVKPVITWLSNFWDMCNVVPATVLIIFIGFOOKSVYSSNLPVL 1876
1739 ALLLLYKSTIPPLMPASFVKRIPSTAVVLTSVNLFINGISVATEVLEFT-DNKLN 1797
1877 LSLFLYKWSITPIMPASFVFEVPSAVVFLIVLNLFGITATYATFLLQEFHDKDLK 1936
1798 NINDILKSVLEFPFHCRLGLIDVYKNOAMADLERFGE-NRFVSPILSMIDVGRNLFAM 1856
1937 VVNSYKSCFLLFPNINLGHMEIAYNEYINERYAKIQOFDKMSPFEMDITVKTAVAM 1996
1857 AVSGVFFLITVLIQYRFFIRPPVNAKLSPLNDEDEDVREORILLDGGQNDILEIKE 1916
1997 TVGFGVFLITVLIQYRFFIRPPVNAKLSPLNDEDEDVREORILLDGGQNDILEIKE 2055
1917 LTKIYRKR---KRPAYDRICVGPPECEGGLGVNGAGSSPFKMLTGTJYTRGDAFIN 1973
2056 LTVVYRSRKIGRLAVDRICLVGRPECGGLGVNGAGKSTFKMLTGTDESTTGGAEFVN 2115
1974 KNSILNIEHVHONMGVYCPQDAITELLTGREHEFFALLRGVPEKEVKGEMAIRKIG 2033
2116 GHSVLADLQVQOSLGTCQFDALPDELTAAREHLOLYTLRGIPMKDEAQVYRMALKEIE 2175
2034 LVYKGEYAGNYSGNKKRLSTAMALIGBPVVFLEDEPTGMDPKARPLMNCALSVKE 2093
2176 LTKCACKRPAISYSGKMKRISTALIGYPAFTLEDEPTGMDPKARPLMNCALSVKE 2235
2094 GRGVNLTSHSEMECALCTPMAITMVGRRFCISVGHKNNRGDGTIVVRLAGSNPDK 2153
2236 GRGVNLTSHSEMECALCTPMAITMVGRRFCISVGHKNNRGDGTIVVRLAGSNPDK 2294
2154 PYDFFGLPFGSVLKEKHNMLQYOLPSSLSIARIFFISLOSQRHLIEDYSVSOTLL 2213
2295 DVVRFNRNRPALMKERHHTKVQYOLKSEHISLAQVFSMEHVAVGLIEDYSVSOTLL 2354
2214 DOYFVNFPAKQSD 2227
2355 DNVEVNFPAKQSDN 2368

```

RESULT 10
Q9HC28 PRELIMINARY; PRT: 2436 AA.
AC Q9HC28;
DT 01-MAR-2001 (TReMBLrel. 16, Created)

```

DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ATP-BINDING CASSETTE SUB-FAMILY A MEMBER 2 (ABC TRANSPORTER
DE ABCA2).
GN ABCA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BBRAIN;
RA Vulevic B., Chen Z., Davis W. Jr., Walsh E.S., Tew K.D.;
RT *Cloning and characterization of human ABCA2.*;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC PubMed=1178988;
RA Kaminski W.E., Plehler A., Pullmann K., Porsch-Ozcuremez M., Duong C.,
RA Bared G.M., Buchler C., Schmitz G.;
RT *Complete Coding Sequence, Promoter Region, and Genomic Structure of
RT the Human ABCA2 Gene and Evidence for Sterol-Dependent Regulation in
RT Macrophages.*;
RL Biochem. Biophys. Res. Commun. 281:249-258(2001).
DR EMBL: AF178941; AGO9372.1; -.
DR EMBL: AF327657; AAK1434.1; -.
DR InterPro: IPR003593; AAA.
DR InterPro: IPR003439; ABC_Transport.
DR InterPro: IPR001687; ATP_GTP_A.
DR Pfam: PF00005; ABC_tran; 2.
DR SMART: SM00382; AAA; 2.
KW ATP-binding
SQ SEQUENCE 2436 AA; 269955 MW; E044A3AF14EA25D1 CRC64;

```

Query Match 35.9%; Score 4240.5; DB 4; Length 2436;
Best Local Similarity 39.8%; Pred. No. 3,7e-271;
Matches 999; Conservative 347; Mismatches 729; Indels 435; Gaps 61;

```

QY 6 QLRLLKNNLFRFRQTOQLLEAVMPLEFILLISVLSVPPYEQHCHPKNK-MPSA 64
11 QQLLLKNNLFRFRQTOQLLEAVMPLEFILLISVLSVPPYEQHCHPKNK-MPSA 65
6 QQLLLKNNLFRFRQTOQLLEAVMPLEFILLISVLSVPPYEQHCHPKNK-MPSA 65
QY 65 GTPVVOGILCANPCFRYPPTGPAFVGVNFKSIYARLFSDARLL-----LYSQKD 120
66 GILPWOISLCPDGOQDEGFL-----QYANSTYTOLERLDRVVEGNNLPDARP 115
DB 121 SKMDKRYVRLTLOQIKSSSNILQDFLVNDFPSG-----FLYHNLSTP 165
116 SLGSELEALR-QHLEALSACGTSGLHDSSTVSFSLDSVARNPOLMFRFLTONLSLP 173
QY 166 KTVKMKLRADY-----ILHVFLOQYOLHLS-LCNLS-----KSEEMI----- 204
174 NSTAQAALLAARDPPEVYHLLFPGSSALDSQGLKHGOEPWSRUGGNLFFMEELLAPA 233
205 ---QI-----GDQVSELGIPKEKLAAB-----RVLSNMDI 235
DB 234 LLEQLTCTPGSELIRILLVPESQKALQYRDVYCSGAAARARFSGLSAELRNQDYL 293
236 LKPIRLTUNSTSPPSKELAE--TKTLHLSTGLTQDELFSKRSMDKROEYMFLLTYNS 293
294 AK-VSQQLGLDAPNCSDSPOAPPPRLQALLGLDLD-----AKRYLDDVDYLS 341
QY 294 SSSSTQIYQAVARIYCGHPEGGLTKISLWYEDNNYKALFGNGTDEDAETFDYDNSTP 353
DB 342 ALALLPQAGCTGRTPGPASAGAGAN-----GTGAGAVMCPNATABEGAPSAALATP 396
QY 354 YCNDLKKNLSSPLSRIIMKALPLVY----- 381
DB 397 ---DTLQGGCSAFVQ--LWAGLQPILCNNRTIEPEARLGNMSSLGFTSKQORNLGLV 451
QY 382 -----KLITPDPDPATROVAAEVNKTFOELAVHDEGMEELSPRIWTFMNSQMD 434

```

```

Db 452 HLMTSPNKILYAPAGSRVDRVILKANETFAFVGNVTHYAOVMINISABELRSFLQCRQO 511
Qy 435 LVMMLDSRDNHFWEOOLDGLDWTADQIVAFIAKHPEDVOSSNGSVYTWREAFNETN-- 492
Db 512 HLMWL-----QOYVAELRLHPE--ALNLSIDELPALRBDNFS 547
Qy 493 -----QAIRTIS-----REMEOVNLNKLEPIATEVWMLNKSME--LDERKFMAG 535
Db 548 LPSGMALLOOLDITDINAAGMIOPMSKVSVDIFKFPDEBSITVTLNOAYQONVTVFAS 607
Qy 536 IFTGTITPGSIELPHHHKKYKIRMDIDNVERTNKKIKDGYDPPGRADPFEDMRVWGFAY 595
Db 608 VIFQTRKDSG--LPHVHHKIRONSSEFTEKTNEIRAYRPPNTO--GREFYLCFW 662
Qy 596 LOPVBOAIIIRVLGTE-KKTGYMOMPYPCVVDIFLRVMSRSPRLMTLAMIYSVAV 654
Db 663 IOMMERAILDITFVGHVYVPGSYVOMFPFPCYTRDPLFVLEHMPMLCOWISWYSVAM 722
Qy 655 IIRGIYVEKARLEKTRMIRGLDNLIMFWSFISLIPPLVSAGLLVTLIKGNLPSD 714
Db 723 TIQIYAEKHEHRLKEVMTKMTGNNAVHVMFITGFVOGISITVTLALTKGVYLMHSH 782
Qy 715 PSVVEFLSEFAVVTILOCFILSTLSRANLAACGGIIFPTLYLYC-----VAMOD 769
Db 783 VVITMLFLAYAVATIMFCEFLVSILSKALASACGGIIFLSYVYVAVAREVADHK 842
Qy 770 YVGFLLIKFASLSPVAFEGCEYFALFEEOGIGVOMDLFESPYVEDCFNLTISML 829
Db 843 ITAFE-KCIASLMSTAFAGSGKRYFALYEVAGIOMHFFSQSPVGDGDFNILLATML 901
Qy 830 FDFLLYGVMTYIEAVFPGQYGIIPRWYPCPKSWFGE--ESDEKSHPGSNOKMS-- 884
Db 902 VDAVYVGIITWYIEAVHPCMYGLPRWYFPLOKSYWLGSGRTFAMWSPMARTPLSYM 961
Qy 885 -----MEEPHKLKGSTONLYKYVRDGMKAVVADSLANFEGQTT 929
Db 962 EELQACAMESRRREETRGHEEPTHLPLVAVCYDKLTKYKDKKALNLSINLENDVY 1021
Qy 930 SFLGNAGAKRTTMSILTLGFPPTSGTAYILGKDIRSEKSTIRONLGVCPQHNVLFDMLT 989
Db 1022 SFLGNAGAKRTTMSILTLGFPPTSGSATIYGHIDFTEDELRKNLGMKQPNVILFRLT 1081
Qy 990 VEHIMFYARILGSLKHYKAEOMALDVLGPPSKLSKTSOLSGMOKRISVALAEVG 1049
Db 1082 VEHIMFYARILGSLKHYKAEOMALDVLGPPSKLSKTSOLSGMOKRISVALAEVG 1140
Qy 1050 GSKVVLIDEPAGVDPYSRGIMELLKXROGRTIILSTHNMDEADVLDRAIISHGL 1109
Db 1141 GSRAILIDEPAGVDPYARARALMDILITKPKPRTIILSHNMDEADVLDRAIISHGL 1200
Qy 1110 CCVGSLSFLKNOLGTYVLLVKKDVESLSSCRNSSSTVSYLKKEDSVSSSDAGLGS 1169
Db 1201 KCCGSPLFLKTYGDGYRLTLKRAPEPG-----GQOPRGLAS 1238
Qy 1170 DHESDTLIDVS--AISNLIRKHVSEARLYVEDIGHETVYLVEAKAKGAPVLFHEID 1227
Db 1239 SEPPGARPLSSGSELOVQFIRKHVASCLVSDTSTELSTILPSEAKKGAERFLQHLER 1298
Qy 1228 RUSDLGSSYGISETTEIEFLKVAE-----SGVDA-ETSDGTLP----- 1267
Db 1299 SIDLHLSFGLMDITLLEVFLKVEEDQSLNSLEADVKESKVDLPAGEGASGEHAG 1358
Qy 1268 -----ARRNRA-FGDKOSCLRPTEDDAADPNDSDIDPESR 1303
Db 1359 NLARSELTOQSASLQASSVGSARGDEAGYTDVYGYRPLF-DNPQDDP--NVSLEOV 1415
Qy 1304 ETDLDSMGDGSGYOVKGKLTQOQFVALLMKRLLIARSRKGFPAVYLAVFICIALV 1363
Db 1416 EMBALSRV-GGSSRKLDGWLNVROFHGLVKRPHCARNSALFSQILLPAFFVCVAMT 1474
Qy 1364 FSLIYPPFGKYSLELQPMWYNEQY-----FVSDABE-----DTGTELELAL 1408
Db 1475 VALSVPEIGDPLPVLSPSOYH-NYTOPRGNFIPYANERREYRRLRSLPDASPOGLVSTF 1533

```

```

Qy 1409 TKDPEGTROM-----EGNPI----- 1424
Db 1534 RLPSGVATCVLKLKSPANGSLGPTLNLSSGESRLARFFDSMCLESFPGILSPNFVPP 1593
Qy 1425 -----PD-----TPQAGEEMETAP-VPOIIMLPONGMNTQNPSPAC 1463
Db 1594 PSPAPSDSPASPDDELQAMNVSLEPTAGPEMWTSPASLPLVREPPV-----C 1641
Qy 1464 QCSSDKIKMLPVCPGAGGLPPPORKONTADIIODLTGRNISDYLYKTVVOLIASKLN 1523
Db 1642 TCSAGCTGS--CPSSVGG-HPQOMRVYGTDLITDIGHVSYLLFTSDRF----- 1590
Qy 1524 KIWNEFRYGGFSIGSVSTQALPSPQEVNDAIKOMKHHLAKOSSADRELNSLGRMTG 1583
Db 1691 -----RLHRYGATIG--NVLKSIIPASFGTRAPVYRK----- 1721
Qy 1584 LDRNNVAVFENNNKGWHAISSFLVANNALIRAMLOGE-NPSHYGITAFNHPNLTKQO 1642
Db 1722 IAVRAAQVFNNNGYHSMPTLYLSNAILRANLPRKSGRPAVAGITVYNNHPRNKTSAS 1781
Qy 1643 LSEVALMTTSDVLYSICVIFRMSFPVPSFVVELIOBRVSKAKHLOPISGVKPYIWSN 1702
Db 1782 LS-IDYLLQGTDVYIAFIIYVMSFVPASFFVFLVAKRSTKAKHLOPISGCPNIIYMLAN 1840
Qy 1703 FVMDKCNVVPATLVIIIFICEQOKSYVSPNLVYVALLLLLGWSTIPLMYPASFEVKI 1762
Db 1841 YVMDKANTVATGCIVIIIFPDLPATTSPIFNPAVLSLELLIGWSTIPLMYPASFEV 1900
Qy 1763 PSTAVVLTYSNLTGINGSVATFVLELT-DNKLNNINDLNSVFLFPFCIGRLID 1821
Db 1901 PSSAVFELIVNLTGIGATVATFELQLEHDKDLKVNLSKCSFLIPFNNGHGLME 1960
Qy 1822 MVKQAMADALERGE-NRFVSPLSMDLVGRNLFAMAVEGVFFLTIVLQYFFITRRP 1880
Db 1961 MAYNEYNEYAKIGOPDKMSPEEMDITVTRGIVAMAVEGVGFLTIMCOYNFLRRPQ 2020
Qy 1881 VNAKLSPLDEDEYVRRERKILDDGGONDLIEKELTKYIRK--RKPAVORICVGP 1937
Db 2021 MPVSTKPEVD-DVYVABERQVNLGADNDNMVKIKENTLKYKSKIGRIILAVDRCLGVR 2079
Qy 1938 PGECFGLGVNAGKSSFTFKMLTGDITVTRQDAFLNKSILSNIEHYHOMNGYCPQDAI 1997
Db 2080 PGECFGLGVNAGKSTFTFKMLTGDSTTGGEAFVNGSHVFLKELHVOQSLGCPQDCL 2139
Qy 1998 TELTGREHVEFFALLRGVEKEVKGVAIRKLGLYKGEYAGYSGGNKRXISTAM 2057
Db 2140 FDELTAHEHIDLYRLNGISWKDEARVAKALELLETKYADKPAAGTYSGNNRKLSTAI 2199
Qy 2058 ALIGPPVVELDEPTTGMKPRARFLNWCALSVYKEGSRVYVLTSHSMECEALCTEMATM 2117
Db 2200 ALIGYPAFIFLDEPTTGMKPRARFLNWLILDKTGRSVVLTSHSMECEALCTFLATM 2259
Qy 2118 VNGFRCLGSVOHLKNRFGGTYTIVRIAGSNPDLEKVDQFGLAPRGVYLAKKHHNMLO 2177
Db 2260 VNGFRCLGSVOHLKNRFGGTYTIVRIAGSNPDLEKVDQFGLAPRGVYLAKKHHNMLO 2218
Qy 2178 YOLPSSLSLARIPSLISQSKRRLIHEDYSVSOTITDQVAVNFAPOXSD 2227
Db 2319 YOLKSEHISLAQVFSKMEQVSGVLGIDYVSQTTLDNVVNFNAKKOSDN 2368

```

```

RESULT 11
Q9UPUO
ID Q9UPUO PRELIMINARY: PRT: 1529 AA.
AC Q9UPUO:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE K1AA1062 PROTEIN (FRAGMENT).
GN K1AA1062.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=9397452; PubMed=10470851;
 RA Kikuno R., Nagase T., Ishikawa K., Hirose M., Miyajima N.,
 Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIV.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL ENA Res. 6:197-205(1999).
 DR EMBL: AB028985; BAA83014.1;
 DR InterPro: IPR003439; ABC_transporter.
 DR InterPro: IPR001687; ATP_GTP_A.
 DR InterPro: IPR000561; EGF-like.
 DR Pfam: PF00005; ABC_tran; 2. Lipocalin_cyflabp.
 DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
 DR PROSITE: PS00213; EGF_1; UNKNOWN_1.
 DR PROSITE: PS00213; LIPOCALIN; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 1529 AA; 170059 MW; BCED65F5E4ACAA1A CRC64;

Query Match 28.4%; Score 3345.5; DB 4; Length 1529;
 Best Local Similarity 46.7%; Pred. No. 3.3e-212;
 Matches 721; Conservative 207; Mismatches 381; Indels 235; Gaps 33;

OY 836 GVMVYIEAVFPGQYIPRPWYFPCSTSYWFG---ESDKSHSGSNOKRMS-----EIC 887
 DB 1 GILWYIEAVHPGMYGLPRPMYFPLKSYLWGSRTAEWMSWMAATPPLSYWEEQAC 60
 OY 888 -----MEEPYHLKLVGSIONLVKVRDGMKAVDGLALNFYSGQTSPTGHN 935
 DB 61 AMESRREETRGMEEPETHPLVVCYVDKLTLYKVDKDLINKSLMLYENQVVSFEGHN 120
 OY 936 GAGGTTMSITLGPPTSGATYILGKDIRSEMSTIRONIGYCPQHVLDTMLTVEEHM 995
 DB 121 GAGTTMSITLGPPTSGATYILGKDIRSEMSTIRONIGYCPQHVLDTMLTVEEHM 180
 OY 996 FYARLKLSEKHKVAKEMOMALDVLPSSSKLKSQTSQLSGMOKRLSVALAFVSGSKVY 1055
 DB 181 FYSLKSKMAQBEIRREDMKIMEDLEL-SNKRHSLVQTLSGMKRKLVALAFVSGSKVY 239
 OY 1056 LDEPTAGVDPYRSRGIVMELLKTYRQGTITLSTHMDADVLRIRIAIISHGKLCYSS 1115
 DB 240 LDEPTAGVDPYARRAIDMLIKYRGTITLSTHMDADVLRIRIAIISHGKLCYSS 299
 OY 1116 LFLKQGLGTYLFLVKKDVSSLSGSSSTVSYLKKEDVSQSSSDAGLSGDHESDT 1175
 DB 300 LFLKQGLGTYLFLVKKDVSSLSGSSSTVSYLKKEDVSQSSSDAGLSGDHESDT 337
 OY 1176 LTIDVS--AISNLIRKHVSEARLEDIGHETLYVLYPEAKEGAFVELFHEIDRLSLG 1233
 DB 338 PLSSCESELQVQFIRKHVASCILVSDTSTELSYILPSEAAKGAERFLQHLERSLDLH 397
 OY 1234 ISSYGISSTLEELFLKVAEE-----SGVDA-ETSDGTLR----- 1267
 DB 398 LSSFGMLDTLLEVLFLKVEEDQSLNSEADYKESRKDVLPAGBPASGECHAGNLRCS 457
 OY 1268 -----ARRRRA-FGDKQGLRPTEDDADPNDDIDPESRETDLS 1309
 DB 458 ELTOSQASLOSASSVSGARDEGAGYTDYDYLPL-DNQDDP--NVSIGVEALALS 514
 OY 1310 GMDGKGYQVGMKLTQOQVYALLMKRLIARRSRKGFPAQIVLPAYVCTALVSLTLP 1369
 DB 515 RV-GGSGSKLDGMLKVKQFGLLVKRFHRCARRSKALFSQILLPAFVVCYAMTVALSV 573
 OY 1370 PFGKPSLEIQPMWYNEQYT-----FVSNDAPE-----DTGTEILNALTDPGF 1414
 DB 574 EIGDLPPLVLTSPSYH-NYTOPRGNFIPIYANEEERETRLRLSPASPQGLVSTRLPDGV 632

OY 1415 GTRCM-----EGNDI----- 1424
 DB 633 GATCVLKSPANGSLGPTLNLSSGESRLAARFDSMCLESTFGGLPLSNFVPPSPAPS 692
 OY 1425 -----PD-----TPQAGEEEMTAP-VPQITMDLPONGNTWMPNSPACOSSDK 1469
 DB 693 DSPASDEDLQAMNVSPLPTAGPEMTWTSAPSLRVLREPR-----CYCSAG 740
 OY 1470 IKKMLVCPGAGGLPPPRKONTADILLODLTGRNISDLVTVYQIITAKSLKNIWNE 1529
 DB 741 TGFS---CPSSVG--HPPMRVATGDLIDTIGHANVEYLFTSDRF-----RL 785
 OY 1530 FRYGFSLSVNTQALPSPQEVNDAIKQMKHLAKDSSADRFNLSIGREMTGIDTRNN 1589
 DB 786 HRRGALTFC--NLKSTPSSPECTRAPPMWR-----LAIVRA 820
 OY 1590 VKVFNKGMHAISFLYNNALIRANLQKE-NPSHYGTAFFHPLNLKQOLEVAL 1648
 DB 821 AQVFNKGYHSMPTVNLNNAIRANLPKSGNPAAGYITVNHMPKTSASLS-LDY 879
 OY 1649 MTSVULVLSICVIFAMSVSPASFYVFLIOERYSKAKHLQFISGYKPYIYMLSNFVDMC 1708
 DB 880 LLOGTGVTAIFLIYAMSEVPASFEVFLVAKSTAKHLQFVSGGNPILLYMLANTVMDL 939
 OY 1709 NYVPATLVIIIFICPOOKSYSTNLPLYALLLLLYGMSITPLMYPASFVEKIPSTAY 1768
 DB 940 NYVPATCCVILLFVVDLPATYSPTEPAVLSLFLTYGMSITPLMYPASFVEKIPSTAY 999
 OY 1769 VLTSVNLFIGINSVATFVLELT-DNKLNNINDILKSVELLFPHFCRGLIDWKNQA 1827
 DB 1000 FLIVMLFIFTATVATFLQLFEHDKDLVNSYLSKCFELFPYNNLGHGEMEAUYEX 1059
 OY 1828 MADALRRGE-NRFSVSLMDLVGRNLFAMAVEGVFFELITLYORFIRPRPNAKLS 1886
 DB 1060 INEYVAKIOFDMKSPFEMDVTTRGLVAVAGVGVLITLMCOQNFLLRRPQMPVSTK 1119
 OY 1887 PLNDEDEDVREERORILDGSGGNDILEIKELTKYRRK--RKPAVDRCVGIPEGCG 1943
 DB 1120 PYED-DYDVASEKQRYLRDADNDVYKIELTKYRSKRIIGHLAVDRCLGVRRGCG 1178
 OY 1944 LIGVNGAGSSPTKMLTGDTTYTRGDAFLNKSILSNIEVQNMNGYCPQPAITBELTG 2003
 DB 1179 LIGVNGAGTSTFKMLTGDESTGGEAFVNGHSVLELLQVOOSLGYCQOCALDELTA 1238
 OY 2004 REHEFFALLRGVPEKEVGEMAIKLGIVYKGYKAGVSGGKRLSTAMALIGSP 2063
 DB 1239 REHLQTLRLRGISWDEARVYKMALEKLETKYADKPGYISGGKRLSTALALIGP 1298
 OY 2064 PVPFLDEPTGMDPKARFLMNCALSVKEGRSVLTLSHMECEALCTRMAIMVNGRFR 2123
 DB 1299 AFIIDEPTGMDPKARFLMNLILDLITGRSVLTLSHMECEALCTRMAIMVNGRFR 1358
 OY 2124 CLGSVOHLKRRFDGTYTYRIAGSNPDLKPYODFGLAFPGSVLKEKIRNMLQVLPSS 2183
 DB 1359 CLGSIOHLKRRFDGYTYTYR-TRSSQSVKDVVFRFNRPPEAMLEKIRHTTVQYOLKSE 1417
 OY 2184 LSSIAFFSTLSQSKRRLHIEDYVSQTTLDVYFVFAKQSD 2227
 DB 1418 HISLAQVFSKMEQVSGVLGIEDYVSQTTLDVYFVFAKQSDN 1461

RESULT 12
 096JUT3
 ID 096JUT3 PRELIMINARY; PRT: 2277 AA.
 AC 096JUT3;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE ATP-BINDING CASSETTE TRANSPORTER FAMILY A MEMBER 12.
 GN ABCA12.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=RETINA;
 RA Donner T.I., Moses T., Detera-Madleigh S.;
 RT "A retinal cDNA for the ATP-binding cassette transporter ABCA12.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF034346; AAK54355.1;
 KW ATP-binding
 SQ SEQUENCE 2277 AA: 256970 MW: EDA2F00280361E2D CRC64;

Query Match 27.4%; Score 3229.5; DB 4; Length 2277;
 Best Local Similarity 33.4%; Pred. No. 3.1e-204;
 Matches 767; Conservative 426; Mismatches 726; Indels 377; Gaps 59;

OY 103 ARLEPSDARLLLYSOKDKMKRKYRLLOQIKKSSNLIKLODEL-----VDNET- 153
 DB 159 AELGTETLASLTHDNVYSKK-----VRDLTGTDPKINLMNMOFLEQALOMNYLENITQ 213
 OY 154 -----FSGFLYHNLSLPKS-----TYDKM----- 173
 DB 214 LIPIETEMLHVNNASADASEKPGQLLMFKNVELEKEDLRRTGMSKRTIDKLALIPDPN 273
 OY 174 RADVILHKVEYLOGYOLHLS-----LCNGSKSEMIOLGDQVSELCG- 217
 DB 274 RAELISQVEFLHSCDTNITTPKLEDAMKEFCNLSERSRO-----SYLIGLTLHYLN 327
 OY 218 -----PKKLAAEKRVLRSMNDILKPLIRLTINSTSPPSKELAEATYTLHSLGT 267
 DB 328 IYVFYKVFPPRKQKPVKEM-----MELFIRLKEILN-----QMASGTPLLD- 371
 OY 268 LAOELFSMSWSMDR-----QEVMLTN-VNSSSSSTQIQVARSICGHPREGGLKI 319
 DB 372 -----KMSLKQMHLPRSVPLTQAMYSRNRMTPOGS-----ESTISQALCSQ-----GITT 418
 OY 320 KSLNMY-----EDNNYALFEGNGTEDEDAETFY--DNSTPYCNDLKNLESPLSRI 370
 DB 419 EYLTAMLPSSORPKGNHTKDFLYKLTKEQASKYGIPIINTPFCFSLYKDIINMPAGV 478
 OY 371 IMKALPVLVGLITPPDIPATROVMAEYNAKTFQOELAVHNDLEGMEEELSPK- 422
 DB 479 IMAFLPMLGLILAPYMPVTKALMEKSDVLRQDLAEIRKESQEMDQSPLEFMSFHL 538
 OY 423 -----IWMENSOEMDLVRMLDSRDHFEQOOLDIGLWTAODIVAF 467
 DB 539 NQAIPLMLQMTLRMPFVQVFKFSVGLDAVELL-----KQDEL-----DILRK 582
 OY 468 AKHREPVOSNGSVYTWRAEFNETNOAITISREMECVLNLKEPIAEVWLINKSMELL 527
 DB 583 LENNIDI-----IDQLNTLSLTVNISSCVLYDRIOAKTIDEMEREAKRLY 629
 OY 528 DERKEWAGIV-----TGITPGSIELPHHVKYKIMQIDONERTKIKIDGWDPGP 578
 DB 630 KSNELGVSITFLPNSRSHRGYDSGNVFLPRVYKITTIRMSLKTQOTRSLRTKIMAGCP 689
 OY 579 RADPEFDMRYWVGGAFLQDVVEQATIRVLTG-TEKTKGVYMQMPFYCYVDIFLRWMS 637
 DB 690 HNSPSHNOIY-GRAFYILODSIERAIIELOTGRNSQELAVQOALPYPCFMKDNFLVSVS 748
 OY 638 RSMPLMTLAWIYSAVAIIKGIYERKEARLKEKTMKIMGLDNLTFEWSFISLILPLVSA 697
 DB 749 YSLPYLWAMVAVYIAAFKPKLVYEKDKLHEYKMMGVCSNHFPAWLISVGLLITI 808
 OY 698 GLLVVLKGLNLPLYSDSVVFEFLSVFAVYIILOCFILISTEFSRANLAACGGIITYPTL 757
 DB 809 VLIILIKLGNLIPKTNGLIFLPSDYSESVIAMSILYSVEFNNTNIALIGSLITYITA 868
 OY 756 YLPYVLCVAMQDYVGFITKIPASLSVPAFGGCTYFALFEBOGIGVQWDMLEFSPVEED 817
 DB 869 FEPFIVLVTENELSYLVKVFMSLSPTAFSAASQIYARIEBOGIGLOMENMYTSPVDD 928
 OY 818 GNLITTSIS-----MMLFDPLVIGVWTWVIEAVFPGQYIIPRPWFPCPKSTW-----FG--E 868

DB 929 -----TTSGWILCCLTLADSYFLYFLAMVVRVFPCTGTGAAPWTFPIIPSTWKRFGCAE 984
 OY 869 ESDERS-----HPGSNOKRMSSEICMEEPHTKLGVSIONLYKVVYBDGKVA 915
 DB 985 VKPEKSNGLMFTNIMQNTNPSASEPWFSSNIEPEPRDLVGVALHGVKITV--GSKVA 1042
 OY 916 VDLGLANVEEQITSEFLGNAGAKTTMSIITGLFPPPSGATYLLGKDINSEKSTIQNL 975
 DB 1043 VDNLMNFEYEGHITSLLGPNAGAKTTISMULTGFSGASAGTIFVYGDIKIDTLTVKRM 1102
 OY 976 GVCPOHNVLPMLVVEEHIWPFYARLK--GLSEKHYKMEQOMALDVGJPSKSKTSQOL 1033
 DB 1103 GYCMQHDVLEFYLTKKEHLILLYGSKYKWHYKKQKQHEVVKRTKLDGTGLYSRRK-RVGT 1161
 OY 1034 SGMQRKLSVALAPVYSGKVVILDEPTAGVDPYSRGIWELLILKYRGRTIISTHME 1093
 DB 1162 SCGMKRKLSIALIGLGRVYILDEPSTGVDPCCSRRSIMVYISKNKARTIISTHIDE 1221
 OY 1094 ADVIGDRIATISHKGLCCVSSSLFLKNQLGTYTLTKKDVESLSSCRSSSTVSYLK 1153
 DB 1222 AEVLSDRIATLEGGGLRCGSPFLYKAEFGDYHLTLTK----- 1261
 OY 1154 KEDSVQSSDAGLGDHESDTLTIDVSAISNLIRKHVSEARLEVEDIGHETVYL-PYEA 1212
 DB 1262 -----KSPNLNANAVCDTM-----AVYAMIQSHLPKAVYLEDIGGELYVLPFPST 1307
 OY 1213 AKGAFVELFHEIDRLSDLGISYSETTELEPIFLKVAEESGVDAETSDGLTPARR-- 1270
 DB 1308 KVSQAYISLRLALNGMDLNLGCGISDTPVEVEFNLTKESQKNSAMSEHLTKIG 1367
 OY 1271 NRRAFGDKQSLRPFTEPDADPNDSDIDPESRETDLLSGMDGSGVYGMKLTQOQFV 1330
 DB 1368 NSNANGIS-----TPDULSVSSSNTFD--RDKTLT-----RGE-RLDGFGLLKKIM 1412
 OY 1331 ALLMKRLIARSRKGFPAQIVLPAVEFCIALVYSILVPPFGKYPSLELOPMWY--NEQY 1388
 DB 1413 ALLIKRFHHTRRMKGLIAQVILPIVFTYAMGLTIRMSNSVPEIQISPSLYGSEQT 1472
 OY 1389 TFSVNDAPEDTGLLELNLALTKDPFGTCRCMEGNPIPDTC--QAGEEWTAPAPOTIM 1446
 DB 1473 AFVANYHP--STBALVSAMWDFPDGNMCLNLS--DLOCLNKSDLEKMTNGTEGERTNP 1526
 OY 1447 DLFONGNMTQNPSPACOSSDKIKKMLPVCPAGGLPPORRKNONTADILQDGTGNIS 1506
 DB 1527 GV-----CSCSEN-----VQBCP--KMYSPRHKRTYSQVITYMLTGQRYE 1565
 OY 1507 DYLVKTYVQITAKSLKMLVWNEF--RYGFSILGVSNTQALPPSOEVNDAIKOMKHK 1563
 DB 1566 NYLIST-----ANEVQKRYGWSFG-----LP 1588
 OY 1564 LAKSSADRFLNSLGRMTGID--TRNNVYKVPNNKGHAISFLYNNALILRANLOKE 1622
 DB 1589 LTKDLRD-----ITGVPAKRITLAKWYIDEGYHSLPATUNSLNNFLLVNNSKID 1639
 OY 1623 NPSHYGTAENHPLNLTKQOLEVALMTTSVDVLSICVIFAMSPVASFVPLIOERVS 1682
 DB 1640 AARH-GIMVSHRPYQOD--EQATISSLIDILVALSILMGSVYTAASPVVYVBEHQT 1696
 OY 1683 KAKHLQISGVKPYTYLNSFWDMCYVVPALVYIIFCFQOKYSVSTNIPVALLL 1742
 DB 1697 KAKQLQHSIXGVYCYWTFNFIYDMVFLVPAVFSIGIIFLPAFYSENNNGAVALLL 1756
 OY 1743 LLYGMSITPLMYPASFEVKIPSTAYVVLVSVNLFIGINGSVATFVLELPDKNLN---- 1798
 DB 1757 LIRGYAFSSMYLILAGLHETGMAFITTYCVVNFPGINSTVLSLSTVYFISKEKRPNDPTE 1816
 OY 1799 -INDILKSVFLFPHFCGLGLIDWYKNOAMADALERFGENRFVSLSDVYGRNLFANA 1857
 DB 1817 LISETLKRIFLIPPOCFYGLIETLSQOQSVLDLKAAGVEYDNEFEMNKIKGAMFVALY 1876
 OY 1858 VEGVVPFLITVLI-----QYRFIRPRPVNAKLSPLANDEDEVREKRRRIIDGGGNDI 1911

Db 1877 SGTMEFSLRLILNESILKRLLEFFR-KFNSSHRETIDEDVBARERLVESGAEEFDL 1935
 Qy 1912 LEIHELKIVR--RRKPAVDRICVGIIPGECFGLLVGNAGKSTFKMLTGDTTVRGD 1969
 Db 1936 VOLCLTRTYOLHKHIIAVNNISIGIPAGCEFGLLVGNAGKTKTKMLTGDIPISSGN 1995
 Qy 1970 AFL--NNKSIISNINEHVONNGMGCPOPAITETELTGREHVEFALLRGVPEKEVKGWEMA 2028
 Db 1996 ILINKKSGSLGHVDSHSIYNOCPOEDALDVLVEEHLIFYAVAHVHPEKDIETVYHKL 2055
 Qy 2029 IRLKGLVYKGYKAVGNSGKRRKRLSPALALIGSPVVFLEDEPTGMDPKARFLMNCAL 2088
 Db 2056 LRLHLMPFKDRATSMCSYGTFRKRLSPALALIGKPSILLIDEPSSGMDPKSRHLKRTIS 2115
 Qy 2089 SYVEGSGSVLTSHMECEALCTRMALIMVNGRRCGSHVONHKNRGDGTIVYRAGS 2148
 Db 2116 EEOVKCSVLTSHMECEALCTRLIMVNGKFCQIGSLQHIKSRGGRGTIVYHKLKN 2175
 Qy 2149 NPDLKPVODFGLAFPSVLEKEKRNMLQYOLPSSLSLARIFSLISQSKRLHIEDYSV 2208
 Db 2176 KVTMETLTKFMQHLFPKTYLKDQHLMSLEHYHVPYTAGGVANIPDLLENTALNTMFLV 2235
 Qy 2209 SQTLLDQVYVFAKQ 2224
 Db 2236 SQTLLLEVFINFADQ 2251
 RESULT 13
 QYVRG4 PRELIMINARY; PRT; 1713 AA.
 AC QYVRG4;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE CG1718 PROTEIN.
 GN CG1718.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; Pubmed=10731132;
 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 Butkus K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
 Dutilleul K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
 Foster K.C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ileguam C.,
 Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Liao X., Liao Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paigled J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL: AE003568; AAF50837.1; -
 DR Flybase: FBgn0031170; CG1718.
 DR InterPro: IPR003439; ABC transporter.
 DR InterPro: IPR001687; ATP_GTP_A.
 DR Pfam: PF00005; ABC_tran; 2.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; Transport.
 SQ SEQUENCE 1713 AA; 192888 MW; 9DE20D3BF9D3C1CA CRC64;

Query Match 21.1%; Score 2485.5; DB: 5; Length 1713;
 Best Local Similarity 32.3%; Pred. No. 3,6e-135;
 Matches 622; Conservative 354; Mismatches 603; Indels 345; Gaps 49;

Qy 410 HDLEGWWEELSPKRTFMENSGEMDLVRLMLDSRND--HFMEQOLDGDMTAQDIAFL 467
 Db 24 HKQWVIELVLPALFSL-----LVLRVLVDPEQGVRYNEQNTLDNL----- 69
 Qy 468 AKHPEDVQSSNG-SVYTWREAFNETNOAIRTI-----SRMECVNLKLEPIATE 516
 Db 70 -----LQKNKGFSEKFEFLCYSPVNPVLKLLVEEAMQSLGKKNICESENATOLE----- 118
 Qy 517 VMLINKSMELDRKKWAGIVFTGIRPGSIE--LPHHKYKIR-----MDIDNVE 564
 Db 119 -----LDTVSKNAF-AGVQFDAMANLTENDPLRDNDFALRFPALERTATIAANW 170
 Qy 565 RTNKIKDGYNDPPRADPDEP---MRYWGFAYLQDVEQAIIIVLTGTEKTKTVYMQ 620
 Db 171 LTRLRLEPTDILGPRNEDGDDGIPPGYLRGLPLQHSLSMAVYLNKQKGEDLPVYVAK 230
 Qy 621 QMPYCYVDIDILVMSRSPLEFMTLAWIYSAVVIKGIYVERKARLKETMIRIMGLDSI 680
 Db 231 RYFPFAVIFDPLLEGSSIMSLIILSFYPCYITKYITAEKEKOLKEMKIMGLSMNL 290
 Qy 681 LMSWPFISLILPLVAGNLVILKLG-----NLRLYSDPSVVFVLSFAVVTILQCL 735
 Db 291 HWTAMVFKSFTMLTISAIIILAIILVKIMSEDAVAVLTHANFTALVFLIITYSSICECPM 350
 Qy 736 ISLTFERANLAACGCIYFTLVLPVLCVAMQDYGFILKIFASLSPVAFGCEPYA 795
 Db 351 MATFFSASATAAVTGLIWIATIPYSFTINSDDLSLSKLSWLSINSTAMGFGIKLL 410
 Qy 796 LPEEOGIGVQWDLFSPVEEDGFNLTTISMLFDTFLGYVWTWIEAVFPQGVGIRP 855
 Db 411 GFEGTGGGLQWSNFFPVSVDDTLTGAIVMMLVSCVIMILCLVEQVMGVSFVPRP 470
 Qy 856 WYRPPCKTSYFGE--SDEKSHGPSNOKRSELCMEEPETHLKGSIONVKKYVADGK 913
 Db 471 WNPFPREFPCGREGYTGVEDIPNGVEQDPRAFTPEDEGKHIGLOMHLK--RFGNK 528
 Qy 914 VAVDGLALNFEEQITSLFNGAGKTTMSILTGLFPTSGTAVYILGDIRSEMSITNO 973
 Db 529 MAVKGLSMNFEDEILVILGHNGAGKTTISMLTGFPPTSGLAIINGSDIRNTIEGARM 588
 Qy 974 NLGVCPOHNVLFMLVVEEHIMVYARLKGISEKHVAEMQALDGLPSSKIKSTQSOL 1033
 Db 589 SLGICPOHNVLFDEMVSNNHIFRFSRMKGRGKAVQEVAKYLMTEL--EDKANVAASKYL 647
 Qy 1034 SGMQKRLSVALAFVGGSKVYILDEPTAGVDPYSRKGIVELLKTYOGTITLSTHMD 1093
 Db 648 SGMKRLSVALCGLDGTQVVLCDPESSGMDPARRQIMDLLOQEKVGRTLLTTHFMD 707

OY	1094	ADVLGDRATIIISHKLOCCVSSSEFLKNNOCTGYUULVLYKADVESSLSORNSSSTVSYLK	1153
Db	708	ADVLGDRATIMOGELKOCQSTSEFLKQYOSGRILVSYQUNLPHYGRCTYTKTCDISLKTVCY	767
OY	1154	KEDSVSOSSSDAGLGSDBESDTLTITDVSAISNLIRKHVSEARLVEDIGHETVYLYPEAA	1213
Db	768	RDD-----CETNEYATLANKYIIGLPECDIGAEISYQLPDSAS	806
OY	1214	KEGAFVELFHEIDRLRSDLSISYGSSETTLEFIPLKVAEBSGVDAEHSDTGLPARRRR	1273
Db	807	AK--FEHFEGOLEQSDLEHLNGLNGVIGVITISMEVFPAKVAE-----KDNVTG	850
OY	1274	AFGDKOSCLR---PTEDDADADENDSIDIPESRETELLSGMDKGSQYQWKMLTOOQFV	1330
Db	851	NIKQOHEIMNGSGCFRED-----DNESVQSD--GIFSENRRILLOGLLSTNQWK	898
OY	1331	ALLMKRLLIARSKKGFADIVLPANFVCIALVFSLITPPFGCKYTSLELOPMYNEQTFE	1390
Db	899	AMLLKLEFLYWRKNLLILLIONIMEVFVVVT1--DLTKQTFQ--ELKPI-----	945
OY	1391	VSNDAPEDGTLELLNMLTKDPGFGFRMGCPNIPPTQAGEBEEMTAPVYQOTIMDL--	1448
Db	946	-----TISL-----TOYPLAVTYLDSN	963
OY	1449	FONGNMWQNEPSPACQSSDKIKMLPYCPGAGGLPPOROKONTADILLDTGRENISDY	1508
Db	964	VONG-----TG-----Y	970
OY	1509	LVKTYVVOIILSKLNKILWANEFRYG--GSLGVSNNQALPPROEVDNATKQMKHKLAKD	1567
Db	971	EIANKYEEDLAS-----YGSNGYELGTGQGF-----EDYIILDKGTIQQVIN	10133
OY	1568	SSADREFLNSLGRFMTGDTLRNNKVVFNKNGWHAISPLFNVINMALIRANLOKGENPBY	1627
Db	1014	S---RYL-----VAATTESKKITAMLNQALHTABLTVNNHVAL--ADKLFG---SSV	10599
OY	1628	GITAFNHPNLTKOOLSEVALMTSDVLYSICVIFAMSFVAFASVPEVLIOGRVSKAHL	1687
Db	1060	KIOVTMAPLPTYSTLLSQJSTGNNGJGTOLASNLQCMQFVSISYILFLIKERESRAKL	1119
OY	1688	QFISGVPVLYWLSNPFWDMCNCNVVPATVITIIIFEOOKRSVSSNLPVLAALLILLLGW	1747
Db	1120	QFVGSVKWMFMLSQFICDPASTYVALIYVITVCGFQSTGELGRLYLLLLLRGF	1179
OY	1748	SITPLMTPASVEXKIBSTAVLTSVNLFGINGSATVYL--ELFTDNKLNNINDILKS	1805
Db	1180	AVEFLPITMSJFEFEPEPTGARVSIVINICGMALFIVVYVMSSELF-DTK--DTADILIG	1236
OY	1806	VELLFPHFCJLGRGIDWKNQAMADALERGENREFSPL-----SMDLV	1849
Db	1237	IFRIFPHSLAMSLNKYTTATIRNMCARAGA---LPIILLOELVPQCCNLKPYRAMEEP	1293
OY	1850	G--RNLPAHAVEGVFLITVLIOYR-----FFIR-----PRVNAKLSPLNDEDED	1894
Db	1294	GVEPELYMAATGVVFLIIVIEFRLINLEMKIKIOLISKPPPTPEGOL-----DDD	1347
OY	1895	VRRERORILDOGGOND-----LEIKELTKYRKRKPAYDRICVGPPEQCGILGVNGA	1950
Db	1348	VANERERILQ--MSSNELATLNLVLDRYTKYQFM--ANQVSLCVQVEYECGELGVNGA	1404
OY	1951	GKSSTFKMLTGDITVTRGDAFLKNKSTLSINHEHVONMGCYCPQDAITELLTGRHEVEF	2010
Db	1405	GKTTTFKMTKEDERISGAAVYQGLSTESNMNSIKYMICYCPQFDLLDDTLGREVLRIE	1464
OY	2011	ALLGCVPEKVGKGEWAIRKGLVYKGEKYGAGNYSGGKKRSLSTAMALIGPPVYVIE	2070
Db	1465	CMKRSVQESRIRJQSTEDLASFSFGMKHIDQTHAYSGGKKRKLSTALAVTIGSPSIYIDE	1524
OY	2071	PTTGMDEKARFELNMCALSVYKGGRSRVYLTSHSEBCEALCTIRMAIMVNGRARCQSVOH	2130
Db	1525	PTTGMDPARARQJLNMNVCYRIRDSGKSLVLTSHSEBCEALCTIRLAIMVNGEKKICGSIQH	1584
OY	2131	LKNRFGDGYITV-----RIAGS--NP-----DLKPYQDEFFGLAF	2163

Db 190 DN-----PLT-----AGIFEDSIADKLNKPDKDFTYIRLSNTH 225
 QY 565 RTNKIKIDGWDPGRADPFEDMRYWG-----GFAV 595
 Db 226 RRR-----NAGDONSYPWDTSVSFAYOVSFPIEDDNDGSGPGYWGSGFMT 273
 QY 596 LQDVEQALIRVLTEK-----TGVYMOQMPYCYVDIDFLRKSRLMPLMTLAWY 650
 Db 274 VQRAVVAITEITTDGADQTLPLDSYVSRFPFGYTKI-TEICAFMPYVIFSMT 332
 QY 651 SVAVIIGIYERKARLKTETRMIGIDNSLWSPISLIPPLVAGLVLKGNL 710
 Db 333 SVIYIRAVVYERKEDRLKEMRYMGLSOFIMVAHFILYNAKLFAYILTIMHFVAL- 391
 QY 711 PYSDPSVPELSEFVAVVITLLOCFILSTESRANLAACGIIYTFLYL----- 759
 Db 392 -KSDMTLEFVFLMAYFADVYFAFMISSEFNSATSLISVFMMLLYWYAFESSIDOT 450
 QY 760 -PYVLCAWADYVFTLKFASLSP-VAFGCEYFALFEEOGIVGMDNLFESFEED 817
 Db 451 NPYPL-----GYRL-----INCINDIALNYGLLAAYETQADGLKNGELFTSPSPN 499
 QY 818 GENUITSISMLFDTFLYGMVYIAVPPGYGIP-REMYFPCTKSYW-GEESDEK 873
 Db 500 NLTFGHALIADIGIIMILTYIAVPIPGEGVPEQKPFV-FLPSYFPPNGSKTVDS 558
 QY 874 SHFGSNOKRSEICMEEPFHLKLSIQNLVY-----RDGKKVAVDGL 919
 Db 559 SDOPFOIYADHVLEKEPDLIPTINVNLTYGTSEFKLLEDCFGSGEKRAVSNL 618
 QY 920 ALNFYEQSITPLFHNGAGKTTMILTGFPSTGTAVALIKDIRSEKSTIQNLGVP 979
 Db 619 NLKMYPGQCTVLLGHNGAGSTTFMSLTGVAOSSAAYNDPITSLPKIRKRGCLP 678
 QY 980 QHNVLEDMITVEEHLMEFYARLKLGS-EKHVKAEMQOMALDGLPSSKLKSKTSQGL 1037
 Db 679 QYNTLFGFMTVMEHLEFFALKERTMDPEAREILARLIDF-----KADFMAGALSQ 733
 QY 1038 QRLSLVALAVGSKYVILDEPTAGVDYRSRGIWELLKRYOGRTIILSTHMDADVL 1097
 Db 734 KRLSLAIALIGSEYVWDEPTSGMDPGARHETWLLIOEKERRITLTHHEMADVL 793
 QY 1098 GDRIAIISHKLCVGSLEPLKNOLGTYLTVKKDVESLSSCNSSSTVYLKEDS 1157
 Db 794 GDRIAIHAHQLECCSGPMLKQOYGDHYTLV----- 827
 QY 1158 VQSSSDAGLGSDESDTLIDVSAISNLIRKHYSEARLYEDIGHLETVLPEAKEGA 1217
 Db 828 -----YDTTSPDVSKTTDILREYIPEAHVPSYIGQATYLL-SATHRPI 871
 QY 1218 FVELFHEIDRLSDLGSSIGISSETILEFLKVAE-----ESGVDAETSDGLPAR 1269
 Db 872 FPLLEKELEHQTCGTTSGVSIITMEYFLVGHADERYNYEKGIEENDISE----- 925
 QY 1270 RNRRAFGDKQSCRLPTEADAAPNDSDIDPESRETDLLSGMGKGYOYKGLTQOOF 1329
 Db 926 -----MEKRD-PPILQD-----KQVRYTGTLLMQRA 993
 QY 1330 VALMKRLIARSRKGFQAIVLPAVFCIALVLSLIVPPFGKYPSSLDELQPMYNEOYT 1389
 Db 954 KAMEYKRAIFFFRKQTQFLQOLVPAVYLVAMFTSQVLPSVKE----- 997
 QY 1390 FVSDAPAEQDTGLELINALTKDQFGRCMGKNPIDTPQOAGEEMTAPVQTIMDLF 1449
 Db 998 -----QDPQTISLA-----PFSDTK-KAG-----HLVSD- 1020
 QY 1450 QNGWMTQNSPACQCSSDKIKMLPVCPPGAGGLPPQKQKONTADILQDTRNSIDYL 1509
 Db 1021 -SGNYVTL-----LOG-----SONLSSWY 1038
 QY 1510 VKTYOIIAKSLNKLWNEFRYRGFSLGVSNQOALPPQSEVDAIKOMKHLKLAKDS 1569

Db 1039 QCTVQ-----LGVTQ-----VDTITSNEKFIQDQNAM 1069
 QY 1570 ADR-----FLNSLGRFMTGLDTRNNVYVFNKGMHAISSFLYINNAAILRANLQK 1620
 Db 1070 GSRTFGLHAYLGFVPSMNFST--VSPSLKTFEFPNLFYLPALAITTDSMILSOKOK 1127
 QY 1621 GENPSHYGITAENHDLNLTKQOLSEVALMTTSVDVLSCVIFAMSFVAPSVFLIOER 1680
 Db 1128 -----QYSTAANHPLPSTQDTLKNTRSGGAFLIAYGLIVSPAVAGYSQFLITER 1182
 QY 1681 VSKAHLOFISGVKRYVYIWSLNFVWDMCNVYPATLVIIIFICPOQKSYSTN-LPYLA 1739
 Db 1183 KKSXKHMOILSGIRPWFMTFAFIDAMFYIRILCFDAIFYIFNITVYTHDFGMMLLT 1242
 QY 1740 LLLLLGMSITPLMYPASVFEKIPSTAVVLTLSVNLFGINGSVATFVLELFTOKLNI 1799
 Db 1243 LSFLLKWTALPFTYWFQFFESAPKGMWYTHIILGMIGIAVPIISQTSIDLQYL 1302
 QY 1800 NDILKSVLIFPHFCLGRGLDMVKNQAMADALERE-----GENRFS 1842
 Db 1303 WSLTFA--WLFPTYNISQATVTFQENVRILACKRLDCTIPMKAVTACGTSABRLYVD 1360
 QY 1843 PLSMVLGN-----LPMAVEGVFFLIYLIQYREF-----IRPPYNAKLSPLND 1890
 Db 1361 NVLF--VGNRKGLIYVIFLAVQGFYIWMFMRENDOFTKLALIRKADNPITDITD 1418
 QY 1891 -----EDEDVRRER---ORLIDGGQNDILEIKELTKYRRKRKPAYDRICVGIIP 1938
 Db 1419 TKVDERVEDSDVIAESVORL--ANNKKTALVSNLKYMGFN--AYKGVAFHNS 1474
 QY 1939 GECFGLGVNAGKSGSTFKMLTGDTTVCDAFLNKSILSNIEHOMMGYCPQDAIT 1998
 Db 1475 KCFGLGVNAGKSTFQMLTGEMSSGDAYVNGSVKNMWRAGANTGYCPQYDALI 1534
 QY 1999 ELLTGREHVEFPALLRGVPEKVGAVGERALRKLGLVYKGYAGNCGKRRKISTAMA 2058
 Db 1535 KEMSGEETLYMFARJRGJPEKDIKKVANAIVHAIGIYASROIKTYGKKRRSLGIA 1594
 QY 2059 LIGSGPYVLEDEPTGMPKARFLMNCALSVYKGRSVLTSHEMCEALCTPMATV 2118
 Db 1595 IYGLPVLLEDEPTSGVDKARITLWNLINLRDGLTALVLSHMDCEALCTELATV 1654
 QY 2119 NGRFCLGSVQHLKRNFGGYITVIRIAGSNPDLKPVDFGLAFPGSVLEKERNMLOY 2178
 Db 1655 YKFRFCYSGCHIKRSGYTYLLRLKRN--DAKRTSTIKQFRGSVINEHLOLNF 1713
 QY 2179 QLPSSLSLARIFFSLISQSKRLHIEDYSVSQTLIDQYVFNPAKD--QSDDD 2228
 Db 1714 DIPRQDSWSRLEFKLETYSTLSLMDDDYLSQTLQVFIERSRDAGVSSDSE 1766
 RESULT 15
 Q9VVJ9 PRELIMINARY; PRT; 1660 AA.
 AC Q9VVJ9;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE CG6052 PROTEIN.
 GN CG6052.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; Pubmed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amaratunga C.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 George R.A., Lewis S.E., Richardson S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikiros G.L.G.,
 Abril J.F., Abdayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 Baller R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 Burks K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Foster C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,
 Glodek A., Gong R., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE005523; AAF49312.2;
 DR Flybase: Fgn0036747; CG6052.
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR001687; ATP_GTP_A.
 DR Pfam: PF00005; ABC_tran; 2.
 DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN 1.
 SO SEQUENCE 1660 AA; 187552 MW; 76622965ECEF7814B CRC64;

Query Match 17.3%; Score 2041.5; DB 5; Length 1660;
 Best Local Similarity 28.9%; Pred. No. 8.8e-126;
 Matches 527; Conservative 332; Mismatches 575; Indels 389; Gaps 48;

532 FMAGIYF---TGITGSIELPHHVKKIIRM-----DINVRRTKKIKGYNDPGR 579
 84 FLAGVOFEDENNVNTNDAGYPLNLTSLRPSRLRTMGPILDTMTSLRFLSTYPTSGSR 143
 580 ----ADPFEDMRVWGGFAYLQDVVEAOAIRVLTGTEKKTG---VYMOQMPYCVVDIIF 632
 144 NRLNDGCVPGVGIYREGFLPIQHALLMSWALASGV-IDTGIPALHLDQRPYRATYYOL 202
 633 LKVMASMPLEMTLAMIYVAVIYKGYEKKARKETRMKGLDNLSTIMSWTISLIP 692
 203 LSGRLRLPFLVILSTFIPASTVTKYVSEKELQKEIMKLIGVHNHLMWAMFVKSYIM 262
 693 LTVSAGLVVILKLG-----NLTPYSDPSVYVPLSVFVAVVYILOCFLISTLSFSAANIA 747
 263 LMLVFLIMSLIMKVFYASVAVLTSSWVPLFLHTYVAVSVCLCFMLAVLFSKASTAS 322
 748 AGCGIITFTLPLVYLCAVADYVGTFLTKIFASL-SPVAFGFCGEYFALFEEOGIGVQ 806
 323 AVAAIFMFLTYIPYSGFYVYERLSIMSKLISLIFSNSALGFGIHVYVMGEGITW 382
 807 DNLFSPEBEDGFNLTTISNMLPFTFLXGYMTWIEVFPQGGIIPRPWTPTCTKSYWF 866
 383 RNMFPVSTDSLFTLYIMTSPFSIMFISICLYVEQVFPGEVGRPRMFMCHKWY- 441
 867 GESEDEKSHPSGN-----QKRMSEICMEEPFHLKLGVSIONLVKYYRODMKAVY 916

442 -----ROYVPSLNTVPSPOTILHGSAAKASCRRAR-----EVGIOLFNIQKNY--GKLKAV 490
 917 DGLNLNPEQGITFLPNNGAGKTTTSLTGLPEPTSGAVIYLGKIRSEMSITRONL 976
 491 KGISLKHARNETIYLLGHNGAGKTTTNTMTITGYKPSGTAIVGDTIRHLKARSLG 550
 977 VCPQHNVLFDMLVIEHIIWFIYARLKL-SEKHVKAEMQALDVLGIPSSKLKST--S 1031
 551 ICPNNILFKEMSVRDIHIFESKLKIRGTAKAVENEGK-----MTMLKLOKSVYAAK 605
 1032 QLSGMRKLSVALAFPGSKVYVLLDEPTAGVDYPSRGIWELLKTRKORGTIILSHHM 1091
 606 NLSGMKRKLSLCCALCGNAKAVYLCDEPSSGIDAGRSIMDLQSEKDRITLLTHYM 665
 1092 DEAVLDRLAIIISHGKLCVGSLSFLKNQDGTGYLLTVKKDVESLSSCRSSSTVSY 1151
 666 DEAVLDGRILAIISGKLCVGSLSFLKNQDGTGYLLTVKKDVESLSSCRSSSTVSY 710
 1152 LKKEDSVSSQSSDGLSDHESDPLTIDVSAISLTKIKHSEARLVYDIGHETLYLPE 1211
 711 -----DGAIVTQILKKYVPIKPERVLTETLYRLPE 743
 1212 AAKGAEVLEFHEIDRLSDLGISSYGISSETLEIFLKY-----AESGYDAETSDGTL 1267
 744 YSKR--FAELLQDDEKCAQQLVGYGLSGATLEDVMAVNTDKRYGAGGPPVDSI- 800
 1268 ARRRRAFGDKQSLRPFEDDAADPNDSDIDPESRETDLSGMDKGSQYVKGWILQ 1327
 801 -----DFKELVDSKTRER-----RRIR 819
 1328 QFV--ALMKRLIARRSRKGFPAQIVLPAVFCIALVSLVPPGKPSLELOPMWY 1384
 820 CFMWQALFLKFTTTRNNWLOIQVLPYAVMALIILNSRCGRITYELPAPISINQY 879
 1385 NEQYTEVSNDAPEDTGLELINALTKD-PGGYTRKMGEPNIPPTPOAGEEWTAPVPO 1443
 880 SSAYVLEDNTDTTKTSS--LADAYSKHLEHYARRC----- 912
 1444 TIDMLFQNGMWTQNPSPACQSSDKIKMLPVCPPAGGLPPQKQNTADILQDUTGR 1503
 913 TLL-----KRGDL----- 920
 1504 NISDYLVKTYVQIIAKSLKKIWNERYGSGSLGVSNTQALPPSOEVDNAIKOMKHK 1563
 921 KFEYDYL-----SHDVNHS-BRIDFH-- 940
 1564 LAKSSADRFLNSIGREMTGD--TRNNVYKVPNNKGNHAISSPLVYNNALILANLOK 1622
 941 -----FLAGLVSENNFIWLNKRPLHTAPLTNLNLHNLAIKL--GQ 982
 1623 NPSHYGITAENHP-----INLTQKQLSSEVALMTTSVDVLVSLCVFAMSFVPSAPV 1673
 983 DASLY--VINEPLPYSDORTLRINKGV-----LGAELISINLSITWCFITAFPA 1030
 1674 VFLIQEYVSAKHLQITISGKVPYIYWSNFWDMCNVDPATLVITIFICFOOKSVYST 1733
 1031 IPIIRETRERAKLQFLSGDVCAVYWTSHIWPYLVFVLSALSSIIITIAFKELIGITPD 1090
 1734 NLPLYALLLLLGKSTIPPLWYPAFVKIPSTPYVYVLTGNGVSAATFVLELFD 1793
 1091 DLSRTFYMLLIFGPGIMLSYASGCSDAATGFTIRISITINTLNG--TGLFLMFTINTFA 1149
 1794 NKLNNINDILKSVLLFPHCLGRGLDM-----VKNQAMADALFEFGEN--RFVSPLS 1845
 1150 FOLKDAVEKLAWFRLSPHSILASSHSIHIGVINRGCISIGIRKLPLQOLRCRNV-PLC 1208
 1846 WDLVGR-----NLPMAVEGVFFLITVLIQYRF-----FIRPPRYNAK 1884
 1209 CDIPGYGWRKPGVLEIYTIMIGSTLFLIYMHAKACNLIAEKLGNCFSKRRKVEEG 1268
 1885 LSPLNDEDEDVREBORILDGGGNDILEIKELIKYIRKRPAYVDRICVGPCCFGL 1944
 1269 TSIENDSVVAEORVYVREKINSGRKVDPLVYKISKRRSKL--AVAKISEHVPHADCFGL 1326

